

# SEQUENCE LISTING

<110> Dumas Milne Edwards, Jean Baptiste  
Bougueleret, Lydie  
Jobert, Severin

<120> FULL-LENGTH HUMAN cDNAs ENCODING POTENTIALLY SECRETED PROTEINS

<130> 78.US4.CIP

<150> US 09/731,872

<151> 2000-12-07

<150> US 60/187,470

<151> 2000-03-06

<150> US 60/169,629

<151> 1999-12-08

<160> 482

<170> Patent.pm

<210> 1

<211> 2201

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 169..1692

<220>

<221> sig\_peptide

<222> 169..249

<223> Von Heijne matrix  
score 7.15265901862021  
seq VLLLLLLLERGMFS/SP

<400> 1

```

agatgtgaat agctccacta taccagcctc gtcttccttc cgggggacaa cgtgggtcag      60
ggcacagaga gatatttaat gtcaccctct tggggctttc atgggactcc ctctgccaca      120
ttttttggag gttgggaaag ttgctagagg cttcagaact ccagccta atg gat ccc      177
                                         Met Asp Pro
                                         -25
aaa ctc ggg aga atg gct gcg tcc ctg ctg gct gtg ctg ctg ctg ctg      225
Lys Leu Gly Arg Met Ala Ala Ser Leu Leu Ala Val Leu Leu Leu Leu
          -20                      -15                      -10
ctg ctg gag cgc ggc atg ttc tcc tca ccc tcc ccg ccc ccg gcg ctg      273
Leu Leu Glu Arg Gly Met Phe Ser Ser Pro Ser Pro Pro Pro Ala Leu
          -5                      1                      5
tta gag aaa gtc ttc cag tac att gac ctc cat cag gat gaa ttt gtg      321
Leu Glu Lys Val Phe Gln Tyr Ile Asp Leu His Gln Asp Glu Phe Val
          10                      15                      20
cag acg ctg aag gag tgg gtg gcc atc gag agc gac tct gtc cag cct      369
Gln Thr Leu Lys Glu Trp Val Ala Ile Glu Ser Asp Ser Val Gln Pro
25                      30                      35                      40
gtg cct cgc ttc aga caa gag ctc ttc aga atg atg gcc gtg gct gcg      417

```

Val	Pro	Arg	Phe	Arg	Gln	Glu	Leu	Phe	Arg	Met	Met	Ala	Val	Ala	Ala	
				45					50					55		
gac	acg	ctg	cag	cgc	ctg	ggg	gcc	cgt	gtg	gcc	tcg	gtg	gac	atg	ggg	465
Asp	Thr	Leu	Gln	Arg	Leu	Gly	Ala	Arg	Val	Ala	Ser	Val	Asp	Met	Gly	
			60					65					70			
cct	cag	cag	ctg	ccc	gat	ggg	cag	agt	ctt	cca	ata	cct	ccc	gtc	atc	513
Pro	Gln	Gln	Leu	Pro	Asp	Gly	Gln	Ser	Leu	Pro	Ile	Pro	Pro	Val	Ile	
			75				80					85				
ctg	gcc	gaa	ctg	ggg	agc	gat	ccc	acg	aaa	ggc	acc	gtg	tgc	ttc	tac	561
Leu	Ala	Glu	Leu	Gly	Ser	Asp	Pro	Thr	Lys	Gly	Thr	Val	Cys	Phe	Tyr	
			90			95					100					
ggc	cac	ttg	gac	gtg	cag	cct	gct	gac	cgg	ggc	gat	ggg	tgg	ctc	acg	609
Gly	His	Leu	Asp	Val	Gln	Pro	Ala	Asp	Arg	Gly	Asp	Gly	Trp	Leu	Thr	
			105		110				115						120	
gac	ccc	tat	gtg	ctg	acg	gag	gta	gac	ggg	aaa	ctt	tat	gga	cga	gga	657
Asp	Pro	Tyr	Val	Leu	Thr	Glu	Val	Asp	Gly	Lys	Leu	Tyr	Gly	Arg	Gly	
				125					130					135		
gcg	acc	gac	aac	aaa	ggc	cct	gtc	ttg	gct	tgg	atc	aat	gct	gtg	agc	705
Ala	Thr	Asp	Asn	Lys	Gly	Pro	Val	Leu	Ala	Trp	Ile	Asn	Ala	Val	Ser	
			140					145					150			
gcc	ttc	aga	gcc	ctg	gag	caa	gat	ctt	cct	gtg	aat	atc	aaa	ttc	atc	753
Ala	Phe	Arg	Ala	Leu	Glu	Gln	Asp	Leu	Pro	Val	Asn	Ile	Lys	Phe	Ile	
			155				160					165				
att	gag	ggg	atg	gaa	gag	gct	ggc	tct	gtt	gcc	ctg	gag	gaa	ctt	gtg	801
Ile	Glu	Gly	Met	Glu	Glu	Ala	Gly	Ser	Val	Ala	Leu	Glu	Glu	Leu	Val	
			170			175					180					
gaa	aaa	gaa	aag	gac	cga	ttc	ttc	tct	ggg	gtg	gac	tac	att	gta	att	849
Glu	Lys	Glu	Lys	Asp	Arg	Phe	Phe	Ser	Gly	Val	Asp	Tyr	Ile	Val	Ile	
			185		190				195						200	
tca	gat	aac	ctg	tgg	atc	agc	caa	agg	aag	cca	gca	atc	act	tat	gga	897
Ser	Asp	Asn	Leu	Trp	Ile	Ser	Gln	Arg	Lys	Pro	Ala	Ile	Thr	Tyr	Gly	
				205					210					215		
acc	cgg	ggg	aac	agc	tac	ttc	atg	gtg	gag	gtg	aaa	tgc	aga	gac	cag	945
Thr	Arg	Gly	Asn	Ser	Tyr	Phe	Met	Val	Glu	Val	Lys	Cys	Arg	Asp	Gln	
			220					225					230			
gat	ttt	cac	tca	gga	acc	ttt	ggg	ggc	atc	ctt	cat	gaa	cca	atg	gct	993
Asp	Phe	His	Ser	Gly	Thr	Phe	Gly	Gly	Ile	Leu	His	Glu	Pro	Met	Ala	
			235				240					245				
gat	ctg	gtt	gct	ctt	ctc	ggg	agc	ctg	gta	gac	tcg	tct	ggg	cat	atc	1041
Asp	Leu	Val	Ala	Leu	Leu	Gly	Ser	Leu	Val	Asp	Ser	Ser	Gly	His	Ile	
			250			255					260					
ctg	gtc	cct	gga	atc	tat	gat	gaa	gtg	gtt	cct	ctt	aca	gaa	gag	gaa	1089
Leu	Val	Pro	Gly	Ile	Tyr	Asp	Glu	Val	Val	Pro	Leu	Thr	Glu	Glu	Glu	
					270					275					280	
ata	aat	aca	tac	aaa	gcc	atc	cat	cta	gac	cta	gaa	gaa	tac	cgg	aat	1137
Ile	Asn	Thr	Tyr	Lys	Ala	Ile	His	Leu	Asp	Leu	Glu	Glu	Tyr	Arg	Asn	
				285					290					295		
agc	agc	cgg	gtt	gag	aaa	ttt	ctg	ttc	gat	act	aag	gag	gag	att	cta	1185
Ser	Ser	Arg	Val	Glu	Lys	Phe	Leu	Phe	Asp	Thr	Lys	Glu	Glu	Ile	Leu	
			300					305					310			
atg	cac	ctc	tgg	agg	tac	cca	tct	ctt	tct	att	cat	ggg	atc	gag	ggc	1233
Met	His	Leu	Trp	Arg	Tyr	Pro	Ser	Leu	Ser	Ile	His	Gly	Ile	Glu	Gly	
			315				320					325				
gcg	ttt	gat	gag	cct	gga	act	aaa	aca	gtc	ata	cct	ggc	cga	gtt	ata	1281
Ala	Phe	Asp	Glu	Pro	Gly	Thr	Lys	Thr	Val	Ile	Pro	Gly	Arg	Val	Ile	
			330			335					340					
gga	aaa	ttt	tca	atc	cgt	cta	gtc	cct	cac	atg	aat	gtg	tct	gcg	gtg	1329
Gly	Lys	Phe	Ser	Ile	Arg	Leu	Val	Pro	His	Met	Asn	Val	Ser	Ala	Val	

```

345          350          355          360
gaa aaa cag gtg aca cga cat ctt gaa gat gtg ttc tcc aaa aga aat 1377
Glu Lys Gln Val Thr Arg His Leu Glu Asp Val Phe Ser Lys Arg Asn
          365          370          375
agt tcc aac aag atg gtt gtt tcc atg act cta gga cta cac ccg tgg 1425
Ser Ser Asn Lys Met Val Val Ser Met Thr Leu Gly Leu His Pro Trp
          380          385          390
att gca aat att gat gac acc cag tat ctc gca gca aaa aga gcg atc 1473
Ile Ala Asn Ile Asp Asp Thr Gln Tyr Leu Ala Ala Lys Arg Ala Ile
          395          400          405
aga aca gtg ttt gga aca gaa cca gat atg atc cgg gat gga tcc acc 1521
Arg Thr Val Phe Gly Thr Glu Pro Asp Met Ile Arg Asp Gly Ser Thr
          410          415          420
att cca att gcc aaa atg ttc cag gag atc gtc cac aag agc gtg gtg 1569
Ile Pro Ile Ala Lys Met Phe Gln Glu Ile Val His Lys Ser Val Val
425          430          435          440
cta att ccg ctg gga gct gtt gat gat gga gaa cat tcg cag aat gag 1617
Leu Ile Pro Leu Gly Ala Val Asp Asp Gly Glu His Ser Gln Asn Glu
          445          450          455
aaa atc aac agg tgg aac tac ata gag gga acc aaa tta ttt gct gcc 1665
Lys Ile Asn Arg Trp Asn Tyr Ile Glu Gly Thr Lys Leu Phe Ala Ala
          460          465          470
ttt ttc tta gag atg gcc cag ctc cat taatcacaag aaccttctag 1712
Phe Phe Leu Glu Met Ala Gln Leu His
          475          480
tctgatctga tccactgaca gattcacctc cccacatcc ctagacaggg atggaatgta 1772
aatatccaga gaatttgggt ctagtatagt acattttccc ttccatttaa aatgtcttgg 1832
gatatctgga tcagtaataa aatatttcaa aggcacagat gttggaaatg gtttaagggtc 1892
ccccactgca cacccttcctc aagtcatagc tgcttgacgc aacttgattt cccaaggtcc 1952
tgtgcaatag cccaggatt ggattccttc caacctttta gcatactctcc aaccttgcaa 2012
tttgattggc ataactactc cagtttgctt tctaggtcct caagtgtctg tgacacataa 2072
tcattccatc caatgatcgc ctttgcttta ccactctttc cttttatctt attaataaaa 2132
atgttggtct ccaccactga aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaagaaaaaa 2192
aaaaaaaaa 2201

```

<210> 2  
 <211> 1631  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 148..1140

<220>  
 <221> sig\_peptide  
 <222> 148..240  
 <223> Von Heijne matrix  
       score 10.0910253445132  
       seq LVLLLVTRSPVNA/CL

```

<400> 2
gtctgtgccc gccattgtgc ggcgtgtgtc cctcagagg gttcctgctg ctgccgggtgc 60
cttgaccct cccctcgtc tctgttcta ctgcccagg agcccggcgg gtccgggact 120
cccgctcgtg ccggtgcggg cgccggc atg tgg ctg tgg gag gac cag ggc ggc 174
                               Met Trp Leu Trp Glu Asp Gln Gly Gly
                               -30          -25
ctc ctg ggc cct ttc tcc ttc ctg ctg cta gtg ctg ctg gtg acg 222

```

Leu	Leu	Gly -20	Pro	Phe	Ser	Phe	Leu -15	Leu	Leu	Val	Leu	Leu -10	Leu	Val	Thr	
cgg	agc	ccg	gtc	aat	gcc	tgc	ctc	ctc	acc	ggc	agc	ctc	ttc	gtt	cta	270
Arg	Ser	Pro	Val	Asn	Ala	Cys	Leu	Leu	Thr	Gly	Ser	Leu	Phe	Val	Leu	
	-5					1				5					10	
ctg	cgc	gtc	ttc	agc	ttt	gag	ccg	gtg	ccc	tct	tgc	agg	gcc	ctg	cag	318
Leu	Arg	Val	Phe	Ser	Phe	Glu	Pro	Val	Pro	Ser	Cys	Arg	Ala	Leu	Gln	
			15						20					25		
gtg	ctc	aag	ccc	cgg	gac	cgc	att	tct	gcc	atc	gcc	cac	cgt	ggc	ggc	366
Val	Leu	Lys	Pro	Arg	Asp	Arg	Ile	Ser	Ala	Ile	Ala	His	Arg	Gly	Gly	
			30					35					40			
agc	cac	gac	gcg	ccc	gag	aac	acg	ctg	gcg	gcc	att	cgg	cag	gca	gct	414
Ser	His	Asp	Ala	Pro	Glu	Asn	Thr	Leu	Ala	Ala	Ile	Arg	Gln	Ala	Ala	
		45					50					55				
aag	aat	gga	gca	aca	ggc	gtg	gag	ttg	gac	att	gag	ttt	act	tct	gac	462
Lys	Asn	Gly	Ala	Thr	Gly	Val	Glu	Leu	Asp	Ile	Glu	Phe	Thr	Ser	Asp	
	60					65					70					
ggg	att	cct	gtc	tta	atg	cac	gat	aac	aca	gta	gat	agg	acg	act	gat	510
Gly	Ile	Pro	Val	Leu	Met	His	Asp	Asn	Thr	Val	Asp	Arg	Thr	Thr	Asp	
				80						85					90	
ggg	act	ggg	cga	ttg	tgt	gat	ttg	aca	ttt	gaa	caa	att	agg	aag	ctg	558
Gly	Thr	Gly	Arg	Leu	Cys	Asp	Leu	Thr	Phe	Glu	Gln	Ile	Arg	Lys	Leu	
			95						100					105		
aat	cct	gca	gca	aac	cac	aga	ctc	agg	aat	gat	ttc	cct	gat	gaa	aag	606
Asn	Pro	Ala	Ala	Asn	His	Arg	Leu	Arg	Asn	Asp	Phe	Pro	Asp	Glu	Lys	
			110					115					120			
atc	cct	acc	cta	atg	gaa	gct	gtt	gca	gag	tgc	cta	aac	cat	aac	ctc	654
Ile	Pro	Thr	Leu	Met	Glu	Ala	Val	Ala	Glu	Cys	Leu	Asn	His	Asn	Leu	
			125				130					135				
aca	atc	ttc	ttt	gat	gtc	aaa	ggc	cat	gca	cac	aag	gct	act	gag	gct	702
Thr	Ile	Phe	Phe	Asp	Val	Lys	Gly	His	Ala	His	Lys	Ala	Thr	Glu	Ala	
	140					145					150					
cta	aag	aaa	atg	tat	atg	gaa	ttt	cct	caa	ctg	tat	aat	aat	agt	gtg	750
Leu	Lys	Lys	Met	Tyr	Met	Glu	Phe	Pro	Gln	Leu	Tyr	Asn	Asn	Ser	Val	
	155				160					165					170	
gtc	tgt	tct	ttc	ttg	cca	gaa	gtt	atc	tac	aag	atg	aga	caa	aca	gat	798
Val	Cys	Ser	Phe	Leu	Pro	Glu	Val	Ile	Tyr	Lys	Met	Arg	Gln	Thr	Asp	
			175						180					185		
cgg	gat	gta	ata	aca	gca	tta	act	cac	aga	cct	tgg	agc	cta	agc	cat	846
Arg	Asp	Val	Ile	Thr	Ala	Leu	Thr	His	Arg	Pro	Trp	Ser	Leu	Ser	His	
			190					195								



	285	290	295	
cac ttc tagacttttca cgggtgggagc aaacgggttc agaaactgcc agggggcctca				1190
His Phe				
300				
tacaggggata tcaaaaatacc ctttgtgcta gcccaggcccc tgggggaatca ggtgactcac				1250
acaaatgcaa tagttgggtca ctgcattttt acctgaacca aagctaaacc cgggtgttgcc				1310
accatgcacc atggcatgcc agagtccaac actggttgctc ttgaaaaatct ggggtctgaa				1370
aaaacgcaca agagccccctg ccctgcccta gctgaggcac acagggagac ccagttagga				1430
taagcacaga ttgaattgta caatttgcag atgcagatgt aaatgcatgg gacatgcatg				1490
ataactcaga gttgacattt taaaacttgc cacacttatt tcaaatattt gtactcagct				1550
atgttaacat gtactgtaga catcaaactt gtggccatac taataaaaatt attaaaagga				1610
gcacaaaaaaaa aaaaaaaaaa a				1631
<210>	3			
<211>	1245			
<212>	DNA			
<213>	Homo sapiens			
<220>				
<221>	CDS			
<222>	85..906			
<220>				
<221>	sig_peptide			
<222>	85..135			
<223>	Von Heijne matrix			
	score 3.86022363031904			
	seq GFVAALVAGGVAG/VS			
<400>	3			
aaaacatggc ggcgcccagc gcgcgaggac gtgatccgct tctgctccgg cttggattgt				60
agccttgacg aggtctgagc gacc atg gac cgg ccg ggg ttc gtg gca gcg				111
	Met Asp Arg Pro Gly Phe Val Ala Ala			
	-15 -10			
ctg gtg gct ggt ggg gta gca ggt gtt tct gtt gac ttg ata tta ttt				159
Leu Val Ala Gly Gly Val Ala Gly Val Ser Val Asp Leu Ile Leu Phe				
	-5 1 5			
cct ctg gat acc att aaa acc agg ctg cag agt ccc caa gga ttt agt				207
Pro Leu Asp Thr Ile Lys Thr Arg Leu Gln Ser Pro Gln Gly Phe Ser				
	10 15 20			
aag gct ggt ggt ttt cat gga ata tat gct ggc gtt cct tct gct gct				255
Lys Ala Gly Gly Phe His Gly Ile Tyr Ala Gly Val Pro Ser Ala Ala				
	25 30 35 40			
att gga tcc ttt cct aat gct gct gca ttt ttt atc acc tat gaa tat				303
Ile Gly Ser Phe Pro Asn Ala Ala Ala Phe Phe Ile Thr Tyr Glu Tyr				
	45 50 55			
gtg aag tgg ttt ttg cat gct gat tca tct tca tat ttg aca cct atg				351
Val Lys Trp Phe Leu His Ala Asp Ser Ser Ser Tyr Leu Thr Pro Met				
	60 65 70			
aaa cat atg ttg gct gcc tct gct gga gaa gtg gtt gcc tgc ctg att				399
Lys His Met Leu Ala Ala Ser Ala Gly Glu Val Val Ala Cys Leu Ile				
	75 80 85			
cga gtt cca tct gaa gtg gtt aag cag agg gca cag gta tct gct tct				447
Arg Val Pro Ser Glu Val Val Lys Gln Arg Ala Gln Val Ser Ala Ser				
	90 95 100			
aca aga aca ttt cag att ttc tct aac atc tta tat gaa gag ggt atc				495
Thr Arg Thr Phe Gln Ile Phe Ser Asn Ile Leu Tyr Glu Glu Gly Ile				
	105 110 115 120			

```

caa ggg ttg tat cga ggc tat aaa agc aca gtt tta aga gag att cct      543
Gln Gly Leu Tyr Arg Gly Tyr Lys Ser Thr Val Leu Arg Glu Ile Pro
      125      130      135
ttt tct ttg gtc cag ttt ccc tta tgg gag tcc tta aaa gcc ctc tgg      591
Phe Ser Leu Val Gln Phe Pro Leu Trp Glu Ser Leu Lys Ala Leu Trp
      140      145      150
tcc tgg agg cag gat cat gtg gtg gat tct tgg cag tca gca gtc tgt      639
Ser Trp Arg Gln Asp His Val Val Asp Ser Trp Gln Ser Ala Val Cys
      155      160      165
gga gct ttt gca ggt gga ttt gcc gct gca gtc acc acc cct cta gac      687
Gly Ala Phe Ala Gly Gly Phe Ala Ala Val Thr Thr Pro Leu Asp
      170      175      180
gtg gca aag aca aga att atg ctg gca aag gct ggc tcc agc act gct      735
Val Ala Lys Thr Arg Ile Met Leu Ala Lys Ala Gly Ser Ser Thr Ala
      185      190      195      200
gat ggg aat gtg ctc tct gtc ctg cat ggg gtc tgg cgg tca cag ggg      783
Asp Gly Asn Val Leu Ser Val Leu His Gly Val Trp Arg Ser Gln Gly
      205      210      215
ctg gca gga tta ttt gca ggt gtc ttc cct cga atg gca gcc atc agt      831
Leu Ala Gly Leu Phe Ala Gly Val Phe Pro Arg Met Ala Ala Ile Ser
      220      225      230
ctg gga ggt ttc atc ttt ctg ggg gct tat gac cga acg cac agc ttg      879
Leu Gly Gly Phe Ile Phe Leu Gly Ala Tyr Asp Arg Thr His Ser Leu
      235      240      245
ctg ttg gaa gtt ggc aga aag agt cct tgaagcagag acaagcctca      926
Leu Leu Glu Val Gly Arg Lys Ser Pro
      250      255
cctccacttc tgtcaagaga ggggctgca gtgcaaacc tcttccgctg agcagctgtc      986
tgaactatag gccccagtgc tgaagaccag ttgtgctaag ataccggcat ggagattgtg      1046
ccatccgtgg tataggctgg ctgggtatgaa gtcattggcc tgtatgccag agagctaaga      1106
gaagaaaacg gggctgtgg cggtactctg aacaatttcc tcagaacctc ttaataaata      1166
agtttggtaa tgctgagaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa      1226
agaaaaaaaa aaaaaaaaaa

```

<210> 4  
 <211> 1623  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 31..1248

<220>  
 <221> sig\_peptide  
 <222> 31..135  
 <223> Von Heijne matrix  
 score 6.3770152988307  
 seq TLLLFAAPFGLLG/EK

```

<400> 4
aacctcttcc gtcggctgaa ttgcggccgt atg cgc ggc tct gtg gag tgc acc      54
Met Arg Gly Ser Val Glu Cys Thr
      -35      -30
tgg ggt tgg ggg cac tgt gcc ccc agc ccc ctg ctc ctt tgg act cta      102
Trp Gly Trp Gly His Cys Ala Pro Ser Pro Leu Leu Trp Thr Leu
      -25      -20      -15
ctt ctg ttt gca gcc cca ttt ggc ctg ctg ggg gag aag acc cgc cag      150

```

Leu	Leu	Phe	Ala	Ala	Pro	Phe	Gly	Leu	Leu	Gly	Glu	Lys	Thr	Arg	Gln		
-10						-5				1					5		
gtg	tct	ctg	gag	gtc	atc	cct	aac	tgg	ctg	ggc	ccc	ctg	cag	aac	ctg		198
Val	Ser	Leu	Glu	Val	Ile	Pro	Asn	Trp	Leu	Gly	Pro	Leu	Gln	Asn	Leu		
				10					15					20			
ctt	cat	ata	cgg	gca	gtg	ggc	acc	aat	tcc	aca	ctg	cac	tat	gtg	tgg		246
Leu	His	Ile	Arg	Ala	Val	Gly	Thr	Asn	Ser	Thr	Leu	His	Tyr	Val	Trp		
			25					30					35				
agc	agc	ctg	ggg	cct	ctg	gca	gtg	gta	atg	gtg	gcc	acc	aac	acc	ccc		294
Ser	Ser	Leu	Gly	Pro	Leu	Ala	Val	Val	Met	Val	Ala	Thr	Asn	Thr	Pro		
		40					45				50						
cac	agc	acc	ctg	agc	gtc	aac	tgg	agc	ctc	ctg	cta	tcc	cct	gag	ccc		342
His	Ser	Thr	Leu	Ser	Val	Asn	Trp	Ser	Leu	Leu	Leu	Ser	Pro	Glu	Pro		
	55					60					65						
gat	ggg	ggc	ctg	atg	gtg	ctc	cct	aag	gac	agc	att	cag	ttt	tct	tct		390
Asp	Gly	Gly	Leu	Met	Val	Leu	Pro	Lys	Asp	Ser	Ile	Gln	Phe	Ser	Ser		
	70				75						80				85		
gcc	ctt	gtt	ttt	acc	agg	ctg	ctt	gag	ttt	gac	agc	acc	aac	gtg	tcc		438
Ala	Leu	Val	Phe	Thr	Arg	Leu	Leu	Glu	Phe	Asp	Ser	Thr	Asn	Val	Ser		
				90					95					100			
gat	acg	gca	gca	aag	cct	ttg	gga	aga	cca	tat	cct	cca	tac	tcc	ttg		486
Asp	Thr	Ala	Ala	Lys	Pro	Leu	Gly	Arg	Pro	Tyr	Pro	Pro	Tyr	Ser	Leu		
			105					110					115				
gcc	gat	ttc	tct	tgg	aac	aac	atc	act	gat	tca	ttg	gat	cct	gcc	acc		534
Ala	Asp	Phe	Ser	Trp	Asn	Asn	Ile	Thr	Asp	Ser	Leu	Asp	Pro	Ala	Thr		
		120				125						130					
ctg	agt	gcc	aca	ttt	caa	ggc	cac	ccc	atg	aac	gac	cct	acc	agg	act		582
Leu	Ser	Ala	Thr	Phe	Gln	Gly	His	Pro	Met	Asn	Asp	Pro	Thr	Arg	Thr		
	135					140					145						
ttt	gcc	aat	ggc	agc	ctg	gcc	ttc	agg	gtc	cag	gcc	ttt	tcc	agg	tcc		630
Phe	Ala	Asn	Gly	Ser	Leu	Ala	Phe	Arg	Val	Gln	Ala	Phe	Ser	Arg	Ser		
	150				155					160					165		
agc	cga	cca	gcc	caa	ccc	cct	cgc	ctc	ctg	cac	aca	gca	gac	acc	tgt		678
Ser	Arg	Pro	Ala	Gln	Pro	Pro	Arg	Leu	Leu	His	Thr	Ala	Asp	Thr	Cys		
				170					175					180			
cag	cta	gag	gtg	gcc	ctg	att	gga	gcc	tct	ccc	cgg	gga	aac	cgt	tcc		726
Gln	Leu	Glu	Val	Ala	Leu	Ile	Gly	Ala	Ser	Pro	Arg	Gly	Asn	Arg	Ser		
			185					190					195				
ctg	ttt	ggg	ctg	gag	gta	gcc	aca	ttg	ggc	cag	ggc	cct	gac	tgc	ccc		774
Leu	Phe	Gly	Leu	Glu	Val	Ala	Thr	Leu	Gly	Gln	Gly	Pro	Asp	Cys	Pro		
		200					205					210					
tca	atg	cag	gag	cag	cac	tcc	atc	gac	gat	gaa	tat	gca	ccg	gcc	gtc		822
Ser	Met	Gln	Glu	Gln	His	Ser	Ile	Asp	Asp	Glu	Tyr	Ala	Pro	Ala	Val		
	215					220					225						
ttc	cag	ttg	gac	cag	cta	ctg	tgg	ggc	tcc	ctc	cca	tca	ggc	ttt	gca		870
Phe	Gln	Leu	Asp	Gln	Leu	Leu	Trp	Gly	Ser	Leu	Pro	Ser	Gly	Phe	Ala		
	230				235						240				245		
cag	tgg	cga	cca	gtg	gct	tac	tcc	cag	aag	ccg	ggg	ggc	cga	gaa	tca		918
Gln	Trp	Arg	Pro	Val	Ala	Tyr	Ser	Gln	Lys	Pro	Gly	Gly	Arg	Glu	Ser		
				250					255					260			
gcc	ctg	ccc	tgc	caa	gct	tcc	cct	ctt	cat	cct	gcc	tta	gca	tac	tct		966
Ala	Leu	Pro	Cys	Gln	Ala	Ser	Pro	Leu	His	Pro	Ala	Leu	Ala	Tyr	Ser		
			265				270						275				
ctt	ccc	cag	tca	ccc	att	gtc	cga	gcc	ttc	ttt	ggg	tcc	cag	aat	aac		1014
Leu	Pro	Gln	Ser	Pro	Ile	Val	Arg	Ala	Phe	Phe	Gly	Ser	Gln	Asn	Asn		
		280					285					290					
ttc	tgt	gcc	ttc	aat	ctg	acg	ttc	ggg	gct	tcc	aca	ggc	cct	ggc	tat		1062
Phe	Cys	Ala	Phe	Asn	Leu	Thr	Phe	Gly	Ala	Ser	Thr	Gly	Pro	Gly	Tyr		

295	300	305	
tgg gac caa cac tac ctc agc tgg tgc atg ctc ctg ggt gtg ggc ttc			1110
Trp Asp Gln His Tyr Leu Ser Trp Ser Met Leu Leu Gly Val Gly Phe			
310	315	320	325
cct cca gtg gac ggc ttg tcc cca cta gtc ctg ggc atc atg gca gtg			1158
Pro Pro Val Asp Gly Leu Ser Pro Leu Val Leu Gly Ile Met Ala Val			
330	335	340	
gcc ctg ggt gcc cca ggg ctc atg ctg cta ggg ggc ggc ttg gtt ctg			1206
Ala Leu Gly Ala Pro Gly Leu Met Leu Leu Gly Gly Gly Leu Val Leu			
345	350	355	
ctg ctg cac cac aag aag tac tca gag tac cag tcc ata aat			1248
Leu Leu His His Lys Lys Tyr Ser Glu Tyr Gln Ser Ile Asn			
360	365	370	
taaggccgcg tctctggagg gaaggacatt actgaacctg tcttgctgtg cctcgaaact			1308
ctggagggtg gagcatcaag ttccagcccc cttcactccc ccactcttgc tttctgtgga			1368
acctcagagg ccagcctcga cttcctggag acccccaggt ggggcttcct tcatactttg			1428
ttgggggact ttggaggcgg gcaggggaca gggctattga taagggtcccc ttggtgttgc			1488
cttcttgcac ctccacacat ttcccttgga tgggacttgc aggcctaaat gagaggcatt			1548
ctgactgggt ggctgccctg gaaggcaaga aaatagattt attttttttt cacagggcaa			1608
aaaaaaaaaa aaaaaa			1623

<210> 5  
 <211> 1454  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 72..143

<220>  
 <221> sig\_peptide  
 <222> 72..119  
 <223> Von Heijne matrix  
 score 5.68931280801877  
 seq LGMLLGLLMAACT/PS

<400> 5	
gtgtctgccca ctgcgctgcc ggaggccgaa ggtccctgac tatggctccc cagagcctgc	60
cttcatctag g atg gct cct ctg ggc atg ctg ctt ggg ctg ctg atg gcc	110
Met Ala Pro Leu Gly Met Leu Leu Gly Leu Leu Met Ala	
-15 -10 -5	
gcc tgc aca cct tct gcc tca gtc atc aga acc tgaaggagtt tgccctgacc	163
Ala Cys Thr Pro Ser Ala Ser Val Ile Arg Thr	
1 5	
aacccagaga agagcagcac caaagaaaacg gagagaaaaag aaaccaaagc cgaggaggag	223
ctggatgccg aagtccttga ggtgttccac ccgacgcacg agtggcaggc ccttcagcca	283
gggcaggctg tccctgcagg atcccacgta cggctgaatc ttcagactgg ggaaagagag	343
gcaaaactcc aatatgagga caagtccga aataatttga aaggcaaaag gctggatatc	403
aacaccaaca cctacacatc tcaggatctc aagagtgcac tggcaaaatt caaggagggg	463
gcagagatgg agagttcaaa ggaagacaag gcaaggcagg ctgaggtaaa gcggctcttc	523
cgccccattg aggaactgaa gaaagacttt gatgagctga atgttgtcat tgagactgac	583
atgcagatca tggtagcggc gatcaacaag ttcaatagtt ccagctccag tttggaagag	643
aagattgctg cgctctttga tcttgaatat tatgtccatc agatggacaa tgcgcaggac	703
ctgctttcct ttggtggtct tcaagtgggt atcaatgggc tgaacagcac agagcccctc	763
gtgaaggagt atgctgcgtt tgtgctgggc gctgcctttt ccagcaacct caagggtccag	823
gtggaggcca tcgaaggggg agccctgcag aagctgctgg tcatcctggc cacggagcag	883
ccgctcactg caaagggagg tgctcacctg gcgcgtgggc aactgctct acgacctggt	943

```

cacggagaag atgttcgccg aggaggaggc tgagctgacc caggagatgt cccagagaa 1003
gctgcagcag tatcgccagg tacacctcct gccakgcctg tgggaacagg gctggtgcga 1063
gatcacggcc cactccttg cgtgccccga gcatgatgcc ygtgagaagg tgctgcwgac 1123
actgggcgtc ctccctgacca cctgccggga ccgctaccgt caggaccccc agctcggcag 1183
gacactggcc agcctgcagg ctgagtagca ggtgctggcc agcctggagc tgcaggatgg 1243
tgaggacgag ggtacttcc aggagctgct gggctctgtc aacagcttgc tgaaggagct 1303
gagatgaggc cccacaccag gactggactg ggatgccgct agtgaggctg aggggtgcca 1363
gcgtgggttg gcttctcagg caggaggaca tcttgccagt gctggcttgg ccattaaatg 1423
gaaacctgaa ggccaaaaaa aaaaaaaaaa a 1454

```

<210> 6  
 <211> 1639  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 111..1154

<220>  
 <221> sig\_peptide  
 <222> 111..197  
 <223> Von Heijne matrix  
 score 4.68065944212013  
 seq LLGPLMAACFTFC/LS

```

<400> 6
agacggtcgc cgccgcgttt gcgcaggggg agctggtcgc cgccgcggcc gcctggaatt 60
gtgggagttg tgtctgccac tcggctgccg gaggccgaag gtccctgact atg gct 116
                                     Met Ala
ccc cag agc ctg cct tca tct agg atg gct cct ctg ggc atg ctg ctt 164
Pro Gln Ser Leu Pro Ser Ser Arg Met Ala Pro Leu Gly Met Leu Leu
      -25                      -20                      -15
ggg ccg ctg atg gcc gcc tgc ttc acc ttc tgc ctc agt cat cag aac 212
Gly Pro Leu Met Ala Ala Cys Phe Thr Phe Cys Leu Ser His Gln Asn
      -10                      -5                      1                      5
ctg aag gag ttt gcc ctg acc aac cca gag aag agc agc acc aaa gaa 260
Leu Lys Glu Phe Ala Leu Thr Asn Pro Glu Lys Ser Ser Thr Lys Glu
      10                      15                      20
aca gag aga aaa gaa acc aaa gcc gag gag gag ctg gat gcc gaa gtc 308
Thr Glu Arg Lys Glu Thr Lys Ala Glu Glu Glu Leu Asp Ala Glu Val
      25                      30                      35
ctg gag gtg ttc cac ccg acg cat gag tgg cag gcc ctt cag cca ggg 356
Leu Glu Val Phe His Pro Thr His Glu Trp Gln Ala Leu Gln Pro Gly
      40                      45                      50
cag gct gtc cct gca gga tcc cac gta cgg ctg aat ctt cag act ggg 404
Gln Ala Val Pro Ala Gly Ser His Val Arg Leu Asn Leu Gln Thr Gly
      55                      60                      65
gaa aga gag gca aaa ctc caa tat gag gac aag ttc cga aat aat ttg 452
Glu Arg Glu Ala Lys Leu Gln Tyr Glu Asp Lys Phe Arg Asn Asn Leu
      70                      75                      80                      85
aaa ggc aaa agg ctg gat atc aac acc aac acc tac aca tct cag gat 500
Lys Gly Lys Arg Leu Asp Ile Asn Thr Asn Thr Tyr Thr Ser Gln Asp
      90                      95                      100
ctc aag agt gca ctg gca aaa ttc aag gag ggg gca gag atg gag agt 548
Leu Lys Ser Ala Leu Ala Lys Phe Lys Glu Gly Ala Glu Met Glu Ser
      105                      110                      115
tca aag gaa gac aag gca agg cag gct gag gta aag cgg ctc ttc cgc 596

```

Ser	Lys	Glu	Asp	Lys	Ala	Arg	Gln	Ala	Glu	Val	Lys	Arg	Leu	Phe	Arg		
		120					125				130						
ccc	att	gag	gaa	ctg	aag	aaa	gac	ttt	gat	gag	ctg	aat	gtt	gtc	att	644	
Pro	Ile	Glu	Glu	Leu	Lys	Lys	Asp	Phe	Asp	Glu	Leu	Asn	Val	Val	Ile		
		135				140					145						
gag	act	gac	atg	cag	atc	atg	gta	cgg	ctg	atc	aac	aag	ttc	aat	agt	692	
Glu	Thr	Asp	Met	Gln	Ile	Met	Val	Arg	Leu	Ile	Asn	Lys	Phe	Asn	Ser		
150					155					160					165		
tcc	agc	tcc	agt	ttg	gaa	gag	aag	att	gct	gcg	ctc	ttt	gat	ctt	gaa	740	
Ser	Ser	Ser	Ser	Leu	Glu	Glu	Lys	Ile	Ala	Ala	Leu	Phe	Asp	Leu	Glu		
				170					175					180			
tat	tat	gtc	cat	cag	atg	gac	aat	gcg	cag	gac	ctg	ctt	tcc	ttt	ggt	788	
Tyr	Tyr	Val	His	Gln	Met	Asp	Asn	Ala	Gln	Asp	Leu	Leu	Ser	Phe	Gly		
		185					190					195					
ggt	ctt	caa	gtg	gtg	atc	aat	ggg	ctg	aac	agc	aca	gag	ccc	ctc	gtg	836	
Gly	Leu	Gln	Val	Val	Ile	Asn	Gly	Leu	Asn	Ser	Thr	Glu	Pro	Leu	Val		
		200				205					210						
aag	gag	tat	gct	gcg	ttt	gtg	ctg	ggc	gct	gcc	ttt	tcc	agc	aac	ccc	884	
Lys	Glu	Tyr	Ala	Ala	Phe	Val	Leu	Gly	Ala	Ala	Phe	Ser	Ser	Asn	Pro		
		215				220					225						
aag	gtc	cag	gtg	gag	gcc	atc	gaa	ggg	gga	gcc	ctg	cag	aag	ctg	ctg	932	
Lys	Val	Gln	Val	Glu	Ala	Ile	Glu	Gly	Gly	Ala	Leu	Gln	Lys	Leu	Leu		
230					235					240					245		
gtc	atc	ctg	gcc	acg	gag	cag	ccg	ctc	act	gca	aag	aag	aag	gtc	ctg	980	
Val	Ile	Leu	Ala	Thr	Glu	Gln	Pro	Leu	Thr	Ala	Lys	Lys	Lys	Val	Leu		
			250						255					260			
ttt	gca	ctg	tgc	tcc	ctg	ctg	cgc	cac	ttc	ccc	tat	gcc	cag	cgg	cag	1028	
Phe	Ala	Leu	Cys	Ser	Leu	Leu	Arg	His	Phe	Pro	Tyr	Ala	Gln	Arg	Gln		
		265					270					275					
ttc	ctg	aag	ctc	ggg	ggg	ctg	cag	gtc	ctg	agg	acc	ctg	gtg	cag	gag	1076	
Phe	Leu	Lys	Leu	Gly	Gly	Leu	Gln	Val	Leu	Arg	Thr	Leu	Val	Gln	Glu		
		280				285					290						
aag	ggc	acg	gag	gtg	ctc	gcc	gtg	cgc	gtg	gtc	aca	ctg	ctc	tac	gac	1124	
Lys	Gly	Thr	Glu	Val	Leu	Ala	Val	Arg	Val	Val	Thr	Leu	Leu	Tyr	Asp		
		295				300				305							
ctg	gtc	acg	gag	aag	atg	ttc	gcc	gag	gag	taggctgagc	tgacccagga					1174	
Leu	Val	Thr	Glu	Lys	Met	Phe	Ala	Glu	Glu								
310					315												
gatgtcccca	gagaagctgc	agcagtatcg	ccaggtacac	ctcctgccag	gcctgtggga											1234	
acagggctgg	tgcgagatca	cggccacct	cctggcgctg	cccagcatg	atgcccgtga											1294	
gaaggtgctg	cagacactgg	gcgtcctcct	gaccacctgc	cgggaccgct	accgtcagga											1354	
ccccagctc	ggcaggacac	tggccagcct	gcaggctgag	taccaggtgc	tggccagcct											1414	
ggagctgcag	gatggtgagg	acgagggcta	cttccaggag	ctgctgggct	ctgtcaacag											1474	
cttgctgaag	gagctgagat	gaggccccac	accaggactg	gactgggatg	ccgctagtga											1534	
ggctgagggg	tgccagcgtg	ggtgggcttc	tcaggcagga	ggacatcttg	gcagtgtctg											1594	
cttggccatt	aaatggaaac	ctgaaggcaa	aaaaaaaaaa	aaaaa												1639	

<210> 7  
 <211> 1768  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 66..1256

<220>  
 <221> sig\_peptide

<222> 66..173

<223> Von Heijne matrix

score 4.89555877630516

seq LLLLLRLNDAALRA/LQ

<400> 7

agaggagg	tg	gcggtg	ggtg	ccctgc	cctg	tggcccc	cgt	gctg	cttgca	ctcga	actcg	60				
tcgcc	atg	gag	gag	ctc	cag	gag	cct	ctg	aga	gga	cag	ctc	110			
Met	Glu	Glu	Leu	Gln	Glu	Pro	Leu	Arg	Gly	Gln	Leu	Arg	Leu	Cys		
	-35				-30				-25							
ttc	acg	caa	gct	gcc	cgg	act	agc	ctc	tta	ctg	ctc	agg	ctc	aac	gac	158
Phe	Thr	Gln	Ala	Ala	Arg	Thr	Ser	Leu	Leu	Leu	Arg	Leu	Arg	Leu	Asn	Asp
	-20				-15				-10							
gct	gcc	ctg	cgg	gcg	ctg	caa	gag	tgt	cag	cgg	caa	cag	gta	cgg	ccg	206
Ala	Ala	Leu	Arg	Ala	Leu	Gln	Glu	Cys	Gln	Arg	Gln	Gln	Val	Arg	Pro	
	-5				1				5					10		
gtg	att	gct	ttc	caa	ggc	cac	cga	ggg	tat	ctg	aga	ctc	cca	ggc	cct	254
Val	Ile	Ala	Phe	Gln	Gly	His	Arg	Gly	Tyr	Leu	Arg	Leu	Pro	Gly	Pro	
			15					20					25			
ggt	tgg	tcc	tgc	ctc	ttc	tcc	ttc	ata	gtg	tcc	cag	tgt	tgt	cag	gag	302
Gly	Trp	Ser	Cys	Leu	Phe	Ser	Phe	Ile	Val	Ser	Gln	Cys	Cys	Gln	Glu	
		30					35					40				
ggc	gct	ggt	ggt	agc	ttg	gac	ctt	gtg	tgc	caa	cgc	ttc	ctc	agg	tct	350
Gly	Ala	Gly	Gly	Ser	Leu	Asp	Leu	Val	Cys	Gln	Arg	Phe	Leu	Arg	Ser	
	45					50				55						
ggg	cct	aac	agc	ctc	cac	tgc	ctg	ggc	tca	ctc	agg	gag	cgc	ctc	att	398
Gly	Pro	Asn	Ser	Leu	His	Cys	Leu	Gly	Ser	Leu	Arg	Glu	Arg	Leu	Ile	
	60				65				70					75		
att	tgg	gca	gcc	atg	gat	tct	atc	cca	gcc	cca	tca	tca	gtt	cag	gga	446
Ile	Trp	Ala	Ala	Met	Asp	Ser	Ile	Pro	Ala	Pro	Ser	Ser	Val	Gln	Gly	
				80					85					90		
cac	aac	ctg	act	gaa	gat	gcc	aga	cat	cct	gag	agt	tgg	cag	aac	aca	494
His	Asn	Leu	Thr	Glu	Asp	Ala	Arg	His	Pro	Glu	Ser	Trp	Gln	Asn	Thr	
			95					100					105			
gga	ggc	tat	tct	gaa	gga	gat	gca	gta	tca	cag	cca	cag	atg	gca	cta	542
Gly	Gly	Tyr	Ser	Glu	Gly	Asp	Ala	Val	Ser	Gln	Pro	Gln	Met	Ala	Leu	
		110					115					120				
gag	gag	gtg	tca	gtg	tca	gat	cca	ctg	gca	agc	aac	caa	gga	cag	tca	590
Glu	Glu	Val	Ser	Val	Ser	Asp	Pro	Leu	Ala	Ser	Asn	Gln	Gly	Gln	Ser	
		125				130					135					
ctc	cca	gga	tcc	tca	agg	gag	cac	atg	gca	cag	tgg	gaa	gtg	aga	agc	638
Leu	Pro	Gly	Ser	Ser	Arg	Glu	His	Met	Ala	Gln	Trp	Glu	Val	Arg	Ser	
					145				150					155		
cag	acc	cat	gtt	cca	aac	aga	gaa	cct	gtt	cag	gca	ctg	cct	tcc	tct	686
Gln	Thr	His	Val	Pro	Asn	Arg	Glu	Pro	Val	Gln	Ala	Leu	Pro	Ser	Ser	
				160					165					170		
gcc	agc	cgg	aaa	cgt	ctg	gac	aag	aaa	cgt	tca	gtg	cct	gta	gcc	act	734
Ala	Ser	Arg	Lys	Arg	Leu	Asp	Lys	Lys	Arg	Ser	Val	Pro	Val	Ala	Thr	
			175				180						185			
gta	gaa	ctg	gaa	gaa	aag	agg	ttc	aga	act	ctg	cct	tta	gtg	cca	agc	782
Val	Glu	Leu	Glu	Glu	Lys	Arg	Phe	Arg	Thr	Leu	Pro	Leu	Val	Pro	Ser	
			190				195					200				
ccc	cta	caa	ggc	ctg	acc	aat	cag	gat	tta	caa	gag	gga	gaa	gat	tgg	830
Pro	Leu	Gln	Gly	Leu	Thr	Asn	Gln	Asp	Leu	Gln	Gly	Glu	Asp	Trp		
		205				210					215					
gag	caa	gaa	gat	gag	gac	atg	gac	ccc	aga	tta	gaa	cac	agt	tcc	tca	878
Glu	Gln	Glu	Asp	Glu	Asp	Met	Asp	Pro	Arg	Leu	Glu	His	Ser	Ser	Ser	
					225				230						235	

```

gtt caa gaa gat tct gaa tcc cca agt cct gaa gat ata cca gac tac      926
Val Gln Glu Asp Ser Glu Ser Pro Ser Pro Glu Asp Ile Pro Asp Tyr
      240      245      250
ctc ctg caa tac agg gcc atc cac agt gca gaa cag caa cat gcc tat      974
Leu Leu Gln Tyr Arg Ala Ile His Ser Ala Glu Gln Gln His Ala Tyr
      255      260      265
gag cag gac ttt gag aca gat tat gct gaa tac cgc atc ctg cat gcc      1022
Glu Gln Asp Phe Glu Thr Asp Tyr Ala Glu Tyr Arg Ile Leu His Ala
      270      275      280
cgt gtt ggg act gca agc caa agg ttc ata gag ctg gga gca gag att      1070
Arg Val Gly Thr Ala Ser Gln Arg Phe Ile Glu Leu Gly Ala Glu Ile
      285      290      295
aaa aga gtt cgg cga gga act cca gaa tac aag gtc ctg gaa gac aag      1118
Lys Arg Val Arg Arg Gly Thr Pro Glu Tyr Lys Val Leu Glu Asp Lys
      300      305      310      315
ata atc cag gaa tat aaa aag ttc agg aag cag tac cca agt tac aga      1166
Ile Ile Gln Glu Tyr Lys Lys Phe Arg Lys Gln Tyr Pro Ser Tyr Arg
      320      325      330
gaa gaa aag cgt cgc tgt gag tac ctt cac cag aaa ttg tcc cac att      1214
Glu Glu Lys Arg Arg Cys Glu Tyr Leu His Gln Lys Leu Ser His Ile
      335      340      345
aaa ggt ctc atc ctg gag ttt gag gaa aag aac agg ggc agc      1256
Lys Gly Leu Ile Leu Glu Phe Glu Glu Lys Asn Arg Gly Ser
      350      355      360
tgaagttatc aaggggaatct ttgagcctct gcttagtgaa acacaaagga acaaagcagc      1316
tataaactaa atagaatgca actatctgct tttcttatgc tgaccactgg agtccatggc      1376
ggcaagtaga gagctgctct aggttcttga gggttggttt tcattattaa tttttagggt      1436
atgggcactg tgcaaagact ccatagctgt gcctaggagt ctaggaaaag tgacagaggc      1496
ttggcttttt taccttttagt tcagccaagt cattttcaag tcctgagaaa tgacatcatc      1556
ttcaggataa aataatgagg acattagaca aaccaaacta agtgaatttt agcctggtag      1616
cctctctaag gaaacagtaa taataacttc tgataagagt taaaagaact tgtagcatac      1676
ctggatataa tgggaaaagg cctgggtgtt acccatgtac tgaaaatgaa cttttaccaa      1736
catggctaaa aaattaaaaa aaaaaaaaaa aa      1768

```

<210> 8  
 <211> 1510  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 190..1398

<220>  
 <221> sig\_peptide  
 <222> 190..252  
 <223> Von Heijne matrix  
 score 5.8172934575094  
 seq ALLWAQEVGQVLA/GR

```

<400> 8
acgggttggc tggcagcgcg cgaggctggt gagtcggcag ccctgtggca gccggcgggc      60
tggtttccat gggtgcacga ttaggaacca ccagctgctg catcccatgg ccaggggtgg      120
cgtccagggtg gcagagcagc taggaacgca aggctgaac ctggggccag acaccctgct      180
ctcccgccc atg gtc aac gac cct cca gta cct gcc tta ctg tgg gcc cag      231
      Met Val Asn Asp Pro Pro Val Pro Ala Leu Leu Trp Ala Gln
      -20      -15      -10
gag gtg ggc caa gtc ttg gca ggc cgt gcc cgc agg ctg ctg ctg cag      279

```



Glu	Val	Gly	Gln	Val	Leu	Ala	Gly	Arg	Ala	Arg	Arg	Leu	Leu	Leu	Gln	
		-5					1			5						
ttt	ggg	gtg	ctc	ttc	tgc	acc	atc	ctc	ctt	ttg	ctc	tgg	gtg	tct	gtc	327
Phe	Gly	Val	Leu	Phe	Cys	Thr	Ile	Leu	Leu	Leu	Leu	Trp	Val	Ser	Val	
10					15					20					25	
ttc	ctc	tat	ggc	tcc	ttc	tac	tat	tcc	tat	atg	ccg	aca	gtc	agc	cac	375
Phe	Leu	Tyr	Gly	Ser	Phe	Tyr	Tyr	Ser	Tyr	Met	Pro	Thr	Val	Ser	His	
				30					35						40	
ctc	agc	cct	gtg	cat	ttc	tac	tac	agg	acc	gac	tgt	gat	tcc	tcc	acc	423
Leu	Ser	Pro	Val	His	Phe	Tyr	Tyr	Arg	Thr	Asp	Cys	Asp	Ser	Ser	Thr	
				45				50							55	
acc	tca	ctc	tgc	tcc	ttc	cct	gtt	gcc	aat	gtc	tcg	ctg	act	aag	ggc	471
Thr	Ser	Leu	Cys	Ser	Phe	Pro	Val	Ala	Asn	Val	Ser	Leu	Thr	Lys	Gly	
		60					65					70				
gga	cgt	gat	cgg	gtg	ctg	atg	tat	gga	cag	ccg	tat	cgt	gtt	acc	tta	519
Gly	Arg	Asp	Arg	Val	Leu	Met	Tyr	Gly	Gln	Pro	Tyr	Arg	Val	Thr	Leu	
	75				80				85							
gag	ctt	gag	ctg	cca	gag	tcc	cct	gtg	aat	caa	gat	ttg	ggc	atg	ttc	567
Glu	Leu	Glu	Leu	Pro	Glu	Ser	Pro	Val	Asn	Gln	Asp	Leu	Gly	Met	Phe	
	90				95				100						105	
ttg	gtc	acc	att	tcc	tgc	tac	acc	aga	ggc	ggc	cga	atc	atc	tcc	act	615
Leu	Val	Thr	Ile	Ser	Cys	Tyr	Thr	Arg	Gly	Gly	Arg	Ile	Ile	Ser	Thr	
				110					115						120	
tct	tcg	cgt	tcg	gtg	atg	ctg	cat	tac	cgc	tca	gac	ctg	ctc	cag	atg	663
Ser	Ser	Arg	Ser	Val	Met	Leu	His	Tyr	Arg	Ser	Asp	Leu	Leu	Gln	Met	
				125				130						135		
ctg	gac	aca	ctg	gtc	ttc	tct	agc	ctc	ctg	cta	ttt	ggc	ttt	gca	gag	711
Leu	Asp	Thr	Leu	Val	Phe	Ser	Ser	Leu	Leu	Leu	Phe	Gly	Phe	Ala	Glu	
		140					145					150				
cag	aag	cag	ctg	ctg	gag	gtg	gaa	ctc	tac	gca	gac	tat	aga	gag	aac	759
Gln	Lys	Gln	Leu	Leu	Glu	Val	Glu	Leu	Tyr	Ala	Asp	Tyr	Arg	Glu	Asn	
		155				160					165					
tcg	gtg	agt	gag	tac	gtg	ccg	acc	act	gga	gcg	atc	att	gag	atc	cac	807
Ser	Val	Ser	Glu	Tyr	Val	Pro	Thr	Thr	Gly	Ala	Ile	Ile	Glu	Ile	His	
	170				175				180						185	
agc	aag	cgc	atc	cag	ctg	tat	gga	gcc	tac	ctc	cgc	atc	cac	gcg	cac	855
Ser	Lys	Arg	Ile	Gln	Leu	Tyr	Gly	Ala	Tyr	Leu	Arg	Ile	His	Ala	His	
				190					195					200		
ttc	act	ggg	ctc	aga	tac	ctg	cta	tac	aac	ttc	ccg	atg	acc	tgc	gcc	903
Phe	Thr	Gly	Leu	Arg	Tyr	Leu	Leu	Tyr	Asn	Phe	Pro	Met	Thr	Cys	Ala	
				205				210						215		
ttc	ata	ggc	gtt	gcc	agc	aac	ttc	acc	ttc	ctc	agc	gtc	atc	gtg	ctc	951
Phe	Ile	Gly	Val	Ala	Ser	Asn	Phe	Thr	Phe	Leu	Ser	Val	Ile	Val	Leu	
		220				225						230				
ttc	agc	tac	atg	cag	tgg	gtg	tgg	ggg	ggc	atc	tgg	ccc	cga	cac	cgc	999
Phe	Ser	Tyr	Met	Gln	Trp	Val	Trp	Gly	Gly	Ile	Trp	Pro	Arg	His	Arg	
		235				240					245					
ttc	tct	ttg	cag	gtt	aac	atc	cga	aaa	aga	gac	aat	tcc	cgg	aag	gaa	1047
Phe	Ser	Leu	Gln	Val	Asn	Ile	Arg	Lys	Arg	Asp	Asn	Ser	Arg	Lys	Glu	
					255					260					265	
gtc	caa	cga	agg	atc	tct	gct	cat	cag	cca	ggc	gca	ggg	cct	gaa	ggc	1095
Val	Gln	Arg	Arg	Ile	Ser	Ala	His	Gln	Pro	Gly	Ala	Gly	Pro	Glu	Gly	
				270					275					280		
cag	gag	gag	tca	act	ccg	caa	tca	gat	gtt	aca	gag	gat	ggc	gag	agc	1143
Gln	Glu	Glu	Ser	Thr	Pro	Gln	Ser	Asp	Val	Thr	Glu	Asp	Gly	Glu	Ser	
				285				290					295			
cct	gaa	gat	ccc	tca	ggg	aca	gag	ggc	cag	ctg	tcc	gag	gag	gag	aaa	1191
Pro	Glu	Asp	Pro	Ser	Gly	Thr	Glu	Gly	Gln	Leu	Ser	Glu	Glu	Glu	Lys	

```

      300              305              310
cca gat cag cag ccc ctg agc gga gaa gag gag cta gag cct gag gcc      1239
Pro Asp Gln Gln Pro Leu Ser Gly Glu Glu Glu Leu Glu Pro Glu Ala
      315              320              325
agt gat ggt tca ggc tcc tgg gaa gat gca gct ttg ctg acg gag gcc      1287
Ser Asp Gly Ser Gly Ser Trp Glu Asp Ala Ala Leu Leu Thr Glu Ala
      330              335              340              345
aac ctg cct gct cct gct cct gct tct gct tct gcc cct gtc cta gag      1335
Asn Leu Pro Ala Pro Ala Pro Ala Ser Ala Ser Ala Pro Val Leu Glu
      350              355              360
act ctg ggc agc tct gaa cct gct ggg ggt gct ctc cga cag cgc ccc      1383
Thr Leu Gly Ser Ser Glu Pro Ala Gly Ala Leu Arg Gln Arg Pro
      365              370              375
acc tgc tct agt tcc tgaagaaaag gggcagactc ctcacattcc agcactttcc      1438
Thr Cys Ser Ser Ser
      380
cacctgactc ctctcccctc gtttttcctt caataaacta ttttgtgtca gctccaaaaa      1498
aaaaaaaaaa aa      1510

<210> 9
<211> 882
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 78..410

<220>
<221> sig_peptide
<222> 78..155
<223> Von Heijne matrix
      score 10.0731536331164
      seq LWLALVSCILTQA/SA

<400> 9
atggctggcc agaggaggaa cgctttgtgt tctcatcgga gctgcatggg aagtctgcat      60
acagcaaagt gacctgc atg cct cac ctt atg gaa agg atg gtg ggc tct      110
      Met Pro His Leu Met Glu Arg Met Val Gly Ser
      -25              -20
ggc ctc ctg tgg ctg gcc ttg gtc tcc tgc att ctg acc cag gca tct      158
Gly Leu Leu Trp Leu Ala Leu Val Ser Cys Ile Leu Thr Gln Ala Ser
      -15              -10              -5              1
gca gtg cag cga ggt tat gga aac ccc att gaa gcc agt tcg tat ggg      206
Ala Val Gln Arg Gly Tyr Gly Asn Pro Ile Glu Ala Ser Ser Tyr Gly
      5              10              15
ctg gac ctg gac tgc gga gct cct ggc acc cca gag gct cat gtc tgt      254
Leu Asp Leu Asp Cys Gly Ala Pro Gly Thr Pro Glu Ala His Val Cys
      20              25              30
ttt gac ccc tgt cag aat tac acc ctc cta gat ttg ggg ccc atc act      302
Phe Asp Pro Cys Gln Asn Tyr Thr Leu Leu Asp Leu Gly Pro Ile Thr
      35              40              45
cgg aga ggt gca cag tct ccc ggt gtc atg aat gga acc cct agc act      350
Arg Arg Gly Ala Gln Ser Pro Gly Val Met Asn Gly Thr Pro Ser Thr
      50              55              60              65
gca ggg ttc ctg gtg gcc tgg cct atg gtc ctc ctg act gtc ctc ctg      398
Ala Gly Phe Leu Val Ala Trp Pro Met Val Leu Leu Thr Val Leu Leu
      70              75              80

```

```

gct tgg ctg ttc tgagagctcc gctgagcatc tggccttgaa gtttgtgttc      450
Ala Trp Leu Phe
      85
ttccctctgg caatggctcc cttcagcact tctgctttcc actccaattc acacaggctt      510
gggtattaaca gaatcaaggc caggctaggt taggaaaagg gaagagcttt caccttcttt      570
aaaactctcg gctgggcgca gtggctcatg cctgtaatcc cagcattttg ggaggctgag      630
gcagggtgat cacctgaggt cagcagttca aaatcagcct ggccaaaatg ctgaaactcc      690
gtctctacta aaaatacaaa aattagccag gcatggtgac aggcgcctgt aatcccagct      750
actcgggagg ccaaggcagg agaattgctc gaactcaggg ggtggagggtt gcagtgagtt      810
gagattgtgc cattgcactc cagcctgggc aacagagcaa gactctgtct caggcaaaaaa      870
aaaaaaaaaa aa                                                         882

<210> 10
<211> 1849
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 84..299

<220>
<221> sig_peptide
<222> 84..134
<223> Von Heijne matrix
      score 3.86022363031904
      seq GFVAALVAGGVAG/VS

<400> 10
aaacatggcg gcgcccagcg cgcgaggacg tgatccgctt ctgctccggc ttggattgta      60
gccttgacga ggtctgagcg acc atg gac cgg ccg ggg ttc gtg gca gcg ctg      113
                        Met Asp Arg Pro Gly Phe Val Ala Ala Leu
                        -15                                -10

gtg gct ggt ggg gta gca ggt gtt tct gtt gac ttg ata tta ttt cct      161
Val Ala Gly Gly Val Ala Gly Val Ser Val Asp Leu Ile Leu Phe Pro
      -5                                1                                5

ctg gat acc att aaa acc agg ctg cag agt ccc caa gga ttt aat aag      209
Leu Asp Thr Ile Lys Thr Arg Leu Gln Ser Pro Gln Gly Phe Asn Lys
      10                                15                                20                                25

gct ggt ggt ttt cat gga ata tat gct ggc gtt cct tct gct gct att      257
Ala Gly Gly Phe His Gly Ile Tyr Ala Gly Val Pro Ser Ala Ala Ile
                        30                                35                                40

gga tcc ttt cct aat ggt tgc ctg cct gat tcg agt tcc atc      299
Gly Ser Phe Pro Asn Gly Cys Leu Pro Asp Ser Ser Ser Ile
      45                                50                                55

tgaagtgggt aagcagaggg cacagggtatc tgcttctaca agaacatttc agattttctc      359
taacatctta tatgaagagg gtatccaagg gttgtatcga ggctataaaa gcacagtttt      419
aagagagatt cctttttctt tgggtccagtt tcccttatgg gagtccttaa aagccctctg      479
gtcctggagg caggatcatg tgggtggattc ttggcagtcg gcagtctgtg gagcttttgc      539
aggtggattt gccgctgcag tcaccacccc tctagacgtg gcgaagacaa gaattatgct      599
ggcaaaggct ggctccagca ctgctgatgg gaatgtgctc tctgtcctgc atggggctctg      659
gcggtcacag gggctggcag gattatttgc aggtgtcttc cctcgaatgg cagccatcag      719
tctgggaggt ttcattcttc tgggggctta tgaccgaacg cacagcttgc tgttgggaagt      779
tggcagaaaag agtccttgaa gcagagacaa gcctcacctc cacttctgtc aagagagggg      839
cctgcagtgt aaaccctctt ccgctgagca gctgtctgaa ctataggccc cagtgtgtaa      899
gaccagttgt gctaagatac cggcatggag attgtgccat ccgtgggtata ggctggctgg      959
tatgaagtca ttggcctgta tgccagagag ctaagagaag aaaacggggg ctgtggcagt      1019
actctgaaca atttcctcag aacctcttaa taaataagtt tggtaatgct gaggccaggc      1079

```

```

cttttagagc tttcatttga tctgtatctg atcttttcatt tcttgccacc tgatggtgga 1139
ttcagcagaa ggcaagatgg ttataattct aaaagaatag cttgtttggt tgtttggttg 1199
ggaaaaggag acttggggaa gagttgtgta tgtgggtggt tctcccccta gttaattcct 1259
gttgtgtaag ggtaggcttt gttgaaaaag aaagaaagat tgaactacag gtgcatagca 1319
agcactcttt ctgggtaact aggctgctgg ttttaattac cctcagattt caccataaaa 1379
aacgcacaat tgtattattt tacagagatg tgtccagcgc cccctgtggt gtgtgagaga 1439
aagcagctgc aactcaagtg actagggtggg cccagctggc ttcgtgcagg agggcacggt 1499
gggtgagcca ttctcgccat tctcatgtca gactgaaagg agggcctggg ccagctttga 1559
aaaggcagga tgaaatggaa aggtcaccac acttagggat tttagacctt gactaacaag 1619
ctccaggtgt agaaaaattc aaaacaaaat gtcaggaatc tagcagtgtt gtctgccctg 1679
gagcaaacaa acagtatgtg attttgcttc gcctattttt tttttctttt ttgggggaag 1739
ataattaaag gcagaatgac tgcgtttgta aaagaaggac caccaactat actgacattt 1799
ataaatgaac ctttattaaa gacacttcaa tgcaaaaaaa aaaaaaaaaa 1849

```

```

<210> 11
<211> 565
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 55..468

<220>
<221> sig_peptide
<222> 55..99
<223> Von Heijne matrix
      score 8.96936032049195
      seq FTLLFLAAVAGA/LV

```

```

<400> 11
attccccaga ctttctgcag attctgtggt tatactcact cctcatccca aaga atg      57
                                     Met
                                     -15
aaa ttt acc act ctc ctc ttc ttg gca gct gta gca ggg gcc ctg gtc      105
Lys Phe Thr Thr Leu Leu Phe Leu Ala Ala Val Ala Gly Ala Leu Val
                                     -10
tat gct gaa gat gcc tcc tct gac tcg acg ggt gct gat cct gcc cag      153
Tyr Ala Glu Asp Ala Ser Ser Asp Ser Thr Gly Ala Asp Pro Ala Gln
      5
gaa gct ggg acc tct aag cct aat gaa gag atc tca ggt cca gca gaa      201
Glu Ala Gly Thr Ser Lys Pro Asn Glu Glu Ile Ser Gly Pro Ala Glu
      20
cca gct tca ccc cca gag aca acc aca aca gcc cag gag act tcg gcg      249
Pro Ala Ser Pro Pro Glu Thr Thr Thr Thr Ala Gln Glu Thr Ser Ala
      35
gca gca gtt cag ggg aca gcc aag gtc acc tca agc agg cag gaa cta      297
Ala Ala Val Gln Gly Thr Ala Lys Val Thr Ser Ser Arg Gln Glu Leu
      55
aac ccc ctg aaa tcc ata gtg gag aaa agt atc tta cta aca gaa caa      345
Asn Pro Leu Lys Ser Ile Val Glu Lys Ser Ile Leu Leu Thr Glu Gln
      70
gcc ctt gca aaa gca gga aaa gga atg cac gga ggc gtg cca ggt gga      393
Ala Leu Ala Lys Ala Gly Lys Gly Met His Gly Gly Val Pro Gly Gly
      85
aaa caa ttc atc gaa aat gga agt gaa ttt gca caa aaa tta ctg aag      441
Lys Gln Phe Ile Glu Asn Gly Ser Glu Phe Ala Gln Lys Leu Leu Lys
      100
                                     105
                                     110

```



```

ggaatccagg ttgttggttg gactgttaat acctttgatg aaaagagtta ctacgaatcc 1115
catcttggtt ccagctatat cactgacagc atggtagaag actgcgaacc tcacttctag 1175
actttcacgg tgggacgaaa cgggttcaga aactgccagg ggccctcatac agggatatca 1235
aaataccctt tgtgctagcc caggccctgg ggaatcaggt gactcacaca aatgcaatag 1295
ttggtcactg catttttacc tgaaccaaag ctaaaccagg tgttgccacc atgcacccatg 1355
gcatgccaga gttcaacact gttgctcttg aaaatctggg tctgaaaaaa cgcacaagag 1415
cccctgccct gccctagctg aggcacacag ggagaccag tgaggataag cacagattga 1475
attgtacaat ttgcagatgc agatgtaaat gcatgggaca tgcagataa ctcagagttg 1535
acattttaaa acttgccaca cttatttcaa atatttgtac tcagctatgt taacatgtac 1595
tgtagacatc aaacttgtgg ccatactaata aaaattatta aaaggagcac taaaaaaaaa 1655
aaaaaaaaa 1663

```

<210> 13  
 <211> 744  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 112..552  
  
 <220>  
 <221> sig\_peptide  
 <222> 112..183  
 <223> Von Heijne matrix  
         score 11.7298925418815  
         seq FVLGLGLTPPTLA/QD

```

<400> 13
tcacaactgg aacccatctc caggaacaaa cagctggaac ccatctcccg ttgaagggaa 60
actgccagat ttttgtaaga ttcttctctc tgggagcctg tgttggaaga g atg gtg 117
                                     Met Val
atg ggc ctg ggc gtt ttg ttg ttg gtc ttc gtg ctg ggt ctg ggt ctg 165
Met Gly Leu Gly Val Leu Leu Leu Val Phe Val Leu Gly Leu Gly Leu
      -20                      -15          -10
acc cca ccg acc ctg gct cag gat aac tcc agg tac aca cac ttc ctg 213
Thr Pro Pro Thr Leu Ala Gln Asp Asn Ser Arg Tyr Thr His Phe Leu
      -5                      1          5          10
acc cag cac tat gat gcc aaa cca cag ggc cgg gat gac aga tac tgt 261
Thr Gln His Tyr Asp Ala Lys Pro Gln Gly Arg Asp Asp Arg Tyr Cys
      15                      20          25
gaa agc atc atg agg aga cgg ggc ctg acc tca ccc tgc aaa gac atc 309
Glu Ser Ile Met Arg Arg Arg Gly Leu Thr Ser Pro Cys Lys Asp Ile
      30                      35          40
aac aca ttt att cat ggc aac aag cgc acg atc aag gcc atc tgt gaa 357
Asn Thr Phe Ile His Gly Asn Lys Arg Thr Ile Lys Ala Ile Cys Glu
      45                      50          55
aac aag aat gga aac cct cac aga gaa aac cta aga ata agc aag tct 405
Asn Lys Asn Gly Asn Pro His Arg Glu Asn Leu Arg Ile Ser Lys Ser
      60                      65          70
tct ttc cag gtc acc act tgc aag cta cat gga ggt tcc ccc tgg cct 453
Ser Phe Gln Val Thr Thr Cys Lys Leu His Gly Gly Ser Pro Trp Pro
      75                      80          85          90
cca tgc cag tac cga gcc aca gcg ggg ttc aga aac gtt gtt gtt gct 501
Pro Cys Gln Tyr Arg Ala Thr Ala Gly Phe Arg Asn Val Val Val Ala
      95                      100         105
tgt gaa aat ggc tta cct gtc cac ttg gat cag tca att ttc cgt cgt 549
Cys Glu Asn Gly Leu Pro Val His Leu Asp Gln Ser Ile Phe Arg Arg

```

```

110      115      120
ccg taaccagcgg gcccttggtc aagtgtggc tctgtgtgcc ttgccttcca 602
Pro
tttccctctt gcaccagaaa cagtgggtggc aacattcatt gccaaagggcc caaagaaaaga 662
gctacctgga ccttttgttt tctgtttgac aacatgttta ataaataaaa atgtcttgat 722
atcagcaaaa aaaaaaaaaa aa 744

<210> 14
<211> 1759
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 101..1243

<220>
<221> sig_peptide
<222> 101..199
<223> Von Heijne matrix
      score 3.57142340200611
      seq FLCLGMALCPRQA/TR

<400> 14
gtagagtgtc gaaggctctg ccaacgggtc tcttggcgtc tcaacgttcg gatcagcagc 60
ttttttccat tctctctctc cacttcttca gtgagcagcc atg agt tgg act gtg 115
                        Met Ser Trp Thr Val
                        -30
cct gtt gtg cgg gcc agc cag aga gtg agc tcg gtg gga gcg aat ttc 163
Pro Val Val Arg Ala Ser Gln Arg Val Ser Ser Val Gly Ala Asn Phe
      -25      -20      -15
cta tgc ctg ggg atg gcc ctg tgt ccg cgt caa gca acg cgc atc ccg 211
Leu Cys Leu Gly Met Ala Leu Cys Pro Arg Gln Ala Thr Arg Ile Pro
      -10      -5      1
ctc aac ggc acc tgg ctc ttc acc ccc gtg agc aag atg gcg act gtg 259
Leu Asn Gly Thr Trp Leu Phe Thr Pro Val Ser Lys Met Ala Thr Val
5      10      15      20
aag agt gag ctt att gag cgt ttc act tcc gag aag ccc gtt cat cac 307
Lys Ser Glu Leu Ile Glu Arg Phe Thr Ser Glu Lys Pro Val His His
      25      30      35
agt aag gtc tcc atc ata gga act gga tcg gtg ggc atg gcc tgc gct 355
Ser Lys Val Ser Ile Ile Gly Thr Gly Ser Val Gly Met Ala Cys Ala
      40      45      50
atc agc atc tta tta aaa ggc ttg agt gat gaa ctt gcc ctt gtg gat 403
Ile Ser Ile Leu Leu Lys Gly Leu Ser Asp Glu Leu Ala Leu Val Asp
      55      60      65
ctt gat gaa gac aaa ctg aag ggt gag acg atg gat ctt caa cat ggc 451
Leu Asp Glu Asp Lys Leu Lys Gly Glu Thr Met Asp Leu Gln His Gly
70      75      80
agc cct ttc acg aaa atg cca aat att gtt tgt agc aaa gat tac ttt 499
Ser Pro Phe Thr Lys Met Pro Asn Ile Val Cys Ser Lys Asp Tyr Phe
85      90      95      100
gtc aca gca aac tcc aac cta gtg att atc aca gca ggt gca cgc caa 547
Val Thr Ala Asn Ser Asn Leu Val Ile Ile Thr Ala Gly Ala Arg Gln
      105      110      115
gaa aag gga gaa acg cgc ctt aat tta gtc cag cga aat gtg gcc atc 595
Glu Lys Gly Glu Thr Arg Leu Asn Leu Val Gln Arg Asn Val Ala Ile
120      125      130

```

ttc aag tta atg att tcc agt att gtc cag tac agc ccc cac tgc aaa	643
Phe Lys Leu Met Ile Ser Ser Ile Val Gln Tyr Ser Pro His Cys Lys	
135 140 145	
ctg att att gtt tcc aat cca gtg gat atc tta act tat gta gct tgg	691
Leu Ile Ile Val Ser Asn Pro Val Asp Ile Leu Thr Tyr Val Ala Trp	
150 155 160	
aag ttg agt gca ttt ccc aaa aac cgt att att gga agc ggc tgt aat	739
Lys Leu Ser Ala Phe Pro Lys Asn Arg Ile Ile Gly Ser Gly Cys Asn	
165 170 175 180	
ctg gat act gct cgt ttt cgt ttc ttg att gga caa aag ctt ggt atc	787
Leu Asp Thr Ala Arg Phe Arg Phe Leu Ile Gly Gln Lys Leu Gly Ile	
185 190 195	
cat tct gaa agc tgc cat gga tgg atc ctc gga gag cat gga gac tca	835
His Ser Glu Ser Cys His Gly Trp Ile Leu Gly Glu His Gly Asp Ser	
200 205 210	
agt gtt cct gtg tgg agt gga gtg aac ata gct ggt gtc cct ttg aag	883
Ser Val Pro Val Trp Ser Gly Val Asn Ile Ala Gly Val Pro Leu Lys	
215 220 225	
gat ctg aac tct gat ata gga act gat aaa gat cct gag caa tgg aaa	931
Asp Leu Asn Ser Asp Ile Gly Thr Asp Lys Asp Pro Glu Gln Trp Lys	
230 235 240	
aat gtc cac aaa gaa gtg act gca act gcc tat gag att att aaa atg	979
Asn Val His Lys Glu Val Thr Ala Thr Ala Tyr Glu Ile Ile Lys Met	
245 250 255 260	
aaa ggt tat act tct tgg gcc att ggc cta tct gtg gcc gat tta aca	1027
Lys Gly Tyr Thr Ser Trp Ala Ile Gly Leu Ser Val Ala Asp Leu Thr	
265 270 275	
gaa agt att ttg aag aat ctt agg aga ata cat cca gtt tcc acc ata	1075
Glu Ser Ile Leu Lys Asn Leu Arg Arg Ile His Pro Val Ser Thr Ile	
280 285 290	
att aag ggc ctc tat gga ata gat gaa gaa gta ttc ctc agt att cct	1123
Ile Lys Gly Leu Tyr Gly Ile Asp Glu Glu Val Phe Leu Ser Ile Pro	
295 300 305	
tgt atc ctg gga gag aac ggt att acc aac ctt ata aag ata aag ctg	1171
Cys Ile Leu Gly Glu Asn Gly Ile Thr Asn Leu Ile Lys Ile Lys Leu	
310 315 320	
acc cct gaa gaa gag gcc cat ctg aaa aaa agt gca aaa aca ctc tgg	1219
Thr Pro Glu Glu Glu Ala His Leu Lys Lys Ser Ala Lys Thr Leu Trp	
325 330 335 340	
gaa att cag aat aag ctt aag ctt taaagttgcc taaaactacc attccgaaat	1273
Glu Ile Gln Asn Lys Leu Lys Leu	
345	
tattgaagag atcatagata caggattata taacgaaatt ttgaataaac ttgaattcct	1333
aaaagatgga aacaggaaag taggtagagt gattttccta tttatttagt cctccagctc	1393
ttttattgag catccacgtg ctggacgata cttattttaca attcctaagt atttttggtg	1453
cctctgatgt agcagcactt gccatgttat atatatgtag ttggcatttg gttcccaaaa	1513
agtaggatgt aggtatttat tgtgttctag aaattccgac tcttttcatt agatatatgc	1573
tattttctttc attcttgctg gtttatacct atgttccattt atatgctgta aaaaagtagt	1633
agcttcttct acaatgtaaa aataaatgta catacaaaaa aatgcagtag tatatacaat	1693
cttttggttt gcttcctttg atagttaata aattccggtt gttgaatcaa taaaaaaaaa	1753
aaaaaa	1759

<210> 15

<211> 1755

<212> DNA

<213> Homo sapiens

<220>



<221> CDS  
<222> 101..517

<220>  
<221> sig\_peptide  
<222> 101..199  
<223> Von Heijne matrix  
score 3.57613483592743  
seq FLCLGMALCLRQA/TR

<400> 15  
gtagagtgtc gaaggtcctg ccaacggctc tcttggcgtc tcaacgttcg gatcagcagc 60  
ttttttccat tctctctctc cacttcttca gtgagcagcc atg agt tgg act gtg 115  
Met Ser Trp Thr Val  
-30  
cct gtt gtg cgg gcc agc cag aga atg agc tcg gtg gga gcg aat ttc 163  
Pro Val Val Arg Ala Ser Gln Arg Met Ser Ser Val Gly Ala Asn Phe  
-25 -20 -15  
cta tgc ctg ggg atg gcc ctg tgt ctg cgt caa gca acg cgc atc ccg 211  
Leu Cys Leu Gly Met Ala Leu Cys Leu Arg Gln Ala Thr Arg Ile Pro  
-10 -5 1  
ctc aac ggc acc tgg ctc ttc aca ccc gtg agc aag atg gcg act gtg 259  
Leu Asn Gly Thr Trp Leu Phe Thr Pro Val Ser Lys Met Ala Thr Val  
5 10 15 20  
aag agt gag ctt att gag cgt ttc act tcc gag aag ccc gtt cat cac 307  
Lys Ser Glu Leu Ile Glu Arg Phe Thr Ser Glu Lys Pro Val His His  
25 30 35  
agt aag gtc tcc atc ata gga act gga tcg gtg ggc atg gcc tgc gct 355  
Ser Lys Val Ser Ile Ile Gly Thr Gly Ser Val Gly Met Ala Cys Ala  
40 45 50  
atc agc atc ttg tta aaa ggc ttg agt gat gaa ctt gcc ctt gtg gat 403  
Ile Ser Ile Leu Leu Lys Gly Leu Ser Asp Glu Leu Ala Leu Val Asp  
55 60 65  
ctt gat gaa gac aaa ctg aag ggt gag acg atg gat ctt caa cat ggc 451  
Leu Asp Glu Asp Lys Leu Lys Gly Glu Thr Met Asp Leu Gln His Gly  
70 75 80  
agc cct ttc acg aaa atg cca ata ttg ttt gta gca aag att act ttg 499  
Ser Pro Phe Thr Lys Met Pro Ile Leu Phe Val Ala Lys Ile Thr Leu  
85 90 95 100  
tca cag caa act cca acc tagtgattat cacagcaggt gcacgccaaag 547  
Ser Gln Gln Thr Pro Thr  
105  
aaaagggaga aacgcgcctt aatttagtcc agcgaaatgt ggccatcttc aagtaatgat 607  
ttccagtatt gtccagtaca gccccactg caaactgatt attgtttcca atccagtgga 667  
tatcttaact tatgtagctt ggaagttagg tgcatttccc aaaaaccgta ttattggaag 727  
cggctgtaat ctggatactg ctcgttttcg tttcttgatt ggacaaaagc ttggtatcca 787  
ttctgaaagc tgccatggat ggatcctcgg agagcatgga gactcaagtg ttccgtgtgtg 847  
gagtggagtg aacatagctg gtgtcccttt gaaggatctg aactctgata taggaaactga 907  
taaagatcct gagcaggaaa aatgtccaca aagaagtgac tgcaactgcc tatgagatta 967  
ttaaaatgaa aggttatact tcttgggccca ttggcctatc tgtggccgat ttaacagaaa 1027  
gtattttgaa gaatcttagg agaatacatc cagtttccac cataactaag ggcctctatg 1087  
gaatagatga agaagtattc ctgagtattc cttgtatcct gggagagaac ggtattacca 1147  
accttataaa gataaagctg acccctgaag aagaggccca tctgaaaaaa agtgcaaaaa 1207  
cactctggga aattcagaat aagcttaagc tttaaagttg cctaaaaacta ccattccgaa 1267  
attattgaag agatcataga tacaggatta tataacgaaa ttttgaataa acttgaattc 1327  
ctaaaagatg gaaacaggaa agtaggtaga gtgattttcc tatttattta gtcctccagc 1387  
tcttttattg agcatccacg tgctggacga tacttattta caattcctaa gtatttttgg 1447  
tacctctgat gtagcagcac ttgccatgtt atatatatgt agttggcatt tggttcccaa 1507

09876997-060801

```

aaagtaggat gtaggtatattt attgtgttct agaaattccg actctttttca ttagatatat 1567
gctattttctt tcattcttgc tggttttatac ctatgttcat ttatatgctg taaaaaagta 1627
gtagctttctt ctacaatgta aaaataaatg tacatacaaa aaaatgcagt agtatataca 1687
atcttttggtt ttgcttcctt tgatagttaa taaattccgt ttgttgaatc aataaaaaaa 1747
aaaaaaa 1755

```

```

<210> 16
<211> 936
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 59..853

```

```

<220>
<221> sig_peptide
<222> 59..100
<223> Von Heijne matrix
      score 5.2402423806254
      seq NFILFIFIPGVFS/LK

```

```

<400> 16
agaaaggagg ctctgggtag acgcactaga ttactggata aatcacttca atttccca 58
atg aat ttt ata ttg ttt att ttt ata cct gga gtt ttt tcc tta aaa 106
Met Asn Phe Ile Leu Phe Ile Phe Ile Pro Gly Val Phe Ser Leu Lys
      -10      -5      1
agt agc act ttg aag cct act att gaa gca ttg cct aat gtg cta cct 154
Ser Ser Thr Leu Lys Pro Thr Ile Glu Ala Leu Pro Asn Val Leu Pro
      5      10      15
tta aat gaa gat gtt aat aag cag gaa gaa aag aat gaa gat cat act 202
Leu Asn Glu Asp Val Asn Lys Gln Glu Glu Lys Asn Glu Asp His Thr
      20      25      30
ccc aat tat gct cct gct aat gag aaa aat ggc aat tat tat aaa gat 250
Pro Asn Tyr Ala Pro Ala Asn Glu Lys Asn Gly Asn Tyr Tyr Lys Asp
      35      40      45      50
ata aaa caa tat gtg ttc aca aca caa aat cca aat ggc act gag tct 298
Ile Lys Gln Tyr Val Phe Thr Thr Gln Asn Pro Asn Gly Thr Glu Ser
      55      60      65
gaa ata tct gtg aga gcc aca act gac ctg aat ttt gct cta aaa aac 346
Glu Ile Ser Val Arg Ala Thr Thr Asp Leu Asn Phe Ala Leu Lys Asn
      70      75      80
gga tca acc cca aac gtg cct gca ttt tgg aca atg tta gct aaa gct 394
Gly Ser Thr Pro Asn Val Pro Ala Phe Trp Thr Met Leu Ala Lys Ala
      85      90      95
ata aat gga aca gca gtg gtc atg gat gat aaa gat caa tta ttt cac 442
Ile Asn Gly Thr Ala Val Val Met Asp Asp Lys Asp Gln Leu Phe His
      100      105      110
cca att cca gag tct gat gtg aat gct aca cag gga gaa aat cag cca 490
Pro Ile Pro Glu Ser Asp Val Asn Ala Thr Gln Gly Glu Asn Gln Pro
      115      120      125      130
gat cta gag gat ctg aag atc aaa ata atg ctg gga atc tcg ttg atg 538
Asp Leu Glu Asp Leu Lys Ile Lys Ile Met Leu Gly Ile Ser Leu Met
      135      140      145
acc ctc ctc ctc ttt gtg gtc ctc ttg gca ttc tgt agt gct aca ctg 586
Thr Leu Leu Leu Phe Val Val Leu Leu Ala Phe Cys Ser Ala Thr Leu
      150      155      160
tac aaa ctg agg cat ctg agt tat aaa agt tgt gag agt cag tac tct 634

```

Tyr	Lys	Leu	Arg	His	Leu	Ser	Tyr	Lys	Ser	Cys	Glu	Ser	Gln	Tyr	Ser		
		165					170					175					
gtc	aac	cca	gag	ctg	gcc	acg	atg	tct	tac	ttt	cat	cca	tca	gaa	ggt	682	
Val	Asn	Pro	Glu	Leu	Ala	Thr	Met	Ser	Tyr	Phe	His	Pro	Ser	Glu	Gly		
		180					185				190						
ggt	tca	gat	aca	tcc	ttt	tcc	aag	agt	gca	gag	agc	agc	aca	ttt	ttg	730	
Val	Ser	Asp	Thr	Ser	Phe	Ser	Lys	Ser	Ala	Glu	Ser	Ser	Thr	Phe	Leu		
		195				200				205					210		
ggt	acc	act	tct	tca	gat	atg	aga	aga	tca	ggc	aca	aga	aca	tca	gaa	778	
Gly	Thr	Thr	Ser	Ser	Asp	Met	Arg	Arg	Ser	Gly	Thr	Arg	Thr	Ser	Glu		
				215					220					225			
tct	aag	ata	atg	acg	gat	atc	att	tcc	ata	ggc	tca	gat	aat	gag	atg	826	
Ser	Lys	Ile	Met	Thr	Asp	Ile	Ile	Ser	Ile	Gly	Ser	Asp	Asn	Glu	Met		
			230					235					240				
cat	gaa	aac	gat	gag	tcg	gtt	acc	cgg	tgaagaaatc	aaggaacccg						873	
His	Glu	Asn	Asp	Glu	Ser	Val	Thr	Arg									
		245					250										
gtgaagaaat	cttattgatg	aataaataac	tttaattatt	ttgtcatcaa	aaaaaaaaaa											933	
aaa																936	

<210> 17  
 <211> 747  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 73..672

<220>  
 <221> sig\_peptide  
 <222> 73..132  
 <223> Von Heijne matrix  
 score 5.21332530399231  
 seq SPVFLVFPPEITA/SE

<400> 17																	
acaagaaaaag	aacatggtct	agactgaagt	accaactaaa	tcattctcctt	tcaaattatc											60	
accgacacca	tc atg gat	tca agc acc	gca cac agt	ccg gtg	ttt ctg gta											111	
	Met Asp	Ser Ser	Thr Ala	His Ser	Pro Val	Phe Leu	Val										
	-20		-15		-10												
ttt cct	cca gaa	atc act	gct tca	gaa tat	gag tcc	aca gaa	ctt tca									159	
Phe Pro	Pro Glu	Ile Thr	Ala Ser	Glu Tyr	Glu Ser	Thr Glu	Leu Ser										
	-5		1		5												
gcc acg	acc ttt	tca act	caa agc	ccc ttg	caa aaa	tta ttt	gct aga									207	
Ala Thr	Thr Phe	Ser Thr	Gln Ser	Pro Leu	Gln Lys	Leu Phe	Ala Arg										
	10		15		20		25										
aaa atg	aaa atc	tta tta	ggg act	atc cag	atc ctg	ttt gga	att atg	acc								255	
Lys Met	Lys Ile	Leu Gly	Thr Ile	Gln Ile	Leu Phe	Gly Ile	Met Thr										
		30		35		40											
ttt tct	ttt gga	gtt atc	ttc ctt	ttc act	ttg tta	aaa cca	tat cca									303	
Phe Ser	Phe Gly	Val Ile	Phe Leu	Phe Thr	Leu Leu	Lys Pro	Tyr Pro										
	45		50		55												
agg ttt	ccc ttt	ata ttt	ctt tca	gga tat	cca ttc	tgg ggc	tct gtt									351	
Arg Phe	Pro Phe	Ile Phe	Leu Ser	Gly Tyr	Pro Phe	Trp Gly	Ser Val										
	60		65		70												
ttg ttc	att aat	tct gga	gcc ttc	cta att	gca gtg	aaa aga	aaa acc									399	
Leu Phe	Ile Asn	Ser Gly	Ala Phe	Leu Ile	Ala Val	Lys Arg	Lys Thr										

```

      75              80              85
aca gaa act ctg ata ata ttg agc cga ata atg aat ttt ctt agt gcc      447
Thr Glu Thr Leu Ile Ile Leu Ser Arg Ile Met Asn Phe Leu Ser Ala
90              95              100
ctg gga gca ata gct gga atc att ctc ctc aca ttt ggt ttc atc cta      495
Leu Gly Ala Ile Ala Gly Ile Ile Leu Leu Thr Phe Gly Phe Ile Leu
      110              115              120
gat caa aac tac att tgt ggt tat tct cac caa aat agt cag tgt aag      543
Asp Gln Asn Tyr Ile Cys Gly Tyr Ser His Gln Asn Ser Gln Cys Lys
      125              130              135
gct gtt act gtc ctg ttc ttg gga att ttg att aca ttg atg act ttc      591
Ala Val Thr Val Leu Phe Leu Gly Ile Leu Ile Thr Leu Met Thr Phe
      140              145              150
agc att att gaa tta ttc att tct ctg cct ttc tca att ttg ggg tgc      639
Ser Ile Ile Glu Leu Phe Ile Ser Leu Pro Phe Ser Ile Leu Gly Cys
      155              160              165
cac tca gag gat tgt gat tgt gaa caa tgt tgt tgactagcac tgtgagaata      692
His Ser Glu Asp Cys Asp Cys Glu Gln Cys Cys
170              175              180
aagatgtgtt aaaatattaa aaaaaaaaaa aaaaaaaaaag aaaaaaaaaa aaaaa      747

<210> 18
<211> 1884
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 94..1275

<220>
<221> sig_peptide
<222> 94..210
<223> Von Heijne matrix
      score 4.55778392992629
      seq LVLVKRLLAIVSVS/CI

<400> 18
acagcgctg cagcctcgtg cagctcttct ggtctccggc gcccgccct cagacgtaat      60
gttgaattaa agaaaatact ttatcagaag aag atg gcc act gcc cag ttg cag      114
                        Met Ala Thr Ala Gln Leu Gln
                        -35
agg act ccc atg agt gca ctg gta ttt ccc aat aag ata tca act gaa      162
Arg Thr Pro Met Ser Ala Leu Val Phe Pro Asn Lys Ile Ser Thr Glu
      -30              -25              -20
cac cag tct ttg gtg tta gtg aag agg ctt cta gca gtt tca gta tcc      210
His Gln Ser Leu Val Leu Val Lys Arg Leu Leu Ala Val Ser Val Ser
      -15              -10              -5
tgt atc acg tat ttg agg gga ata ttc cca gaa tgc gct tat gga aca      258
Cys Ile Thr Tyr Leu Arg Gly Ile Phe Pro Glu Cys Ala Tyr Gly Thr
1              5              10              15
aga tat cta gat gat ctt tgt gtc aaa ata ctg aga gaa gat aaa aat      306
Arg Tyr Leu Asp Asp Leu Cys Val Lys Ile Leu Arg Glu Asp Lys Asn
      20              25              30
tgc cca gga tct aca cag tta gtg aaa tgg att cta gga tgt tat gat      354
Cys Pro Gly Ser Thr Gln Leu Val Lys Trp Ile Leu Gly Cys Tyr Asp
      35              40              45
gct tta cag aaa aaa tat cta agg atg gtt gtt cta gct gta tac aca      402

```



```

355
caccatttaa actgaaggac cctatattat atttccttaa ctctgaagat gtatatgtag 1375
tttaaagcag tttatacact aaaactaagt ttttggctga ctgtcatatt gtggtcctta 1435
atcttgagat aaatccaata gaacttttga ataaaagcaa aagtacaaat gtcataattg 1495
attcggtaat aagtaaaatt tcaaaattga ttttgttcat tacctactta atatttcctt 1555
taaatatata ctaactgtta aggccctcta atgccatttt tctaaacagt aatgtttact 1615
ttggtattaa aatttggtat tgattcactt tttacttatg ttaaaattat accatttaac 1675
tggctctttt gtcattgtgc tgttattaaa acaatgttct tcaatatttt gacataatgt 1735
attaacattt taatatataa tgtacaattt aagaattggg gctttacctt tactatgctt 1795
tttttacagg acaaaaaagac tgatttttaa agtatggcat tttttgcagc ataaataaaa 1855
tattgttcag tacgaaaaaa aaaaaaaaaa 1884

```

```

<210> 19
<211> 691
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 42..515

```

```

<220>
<221> sig_peptide
<222> 42..92
<223> Von Heijne matrix
      score 10.7019149919754
      seq  VLMLLAVLIWTGA/EN

```

```

<400> 19
gagttgtcct gtgctggagg tctgctcaga cgaaggcttc c atg gcg tta gaa gtc      56
                                   Met Ala Leu Glu Val
                                   -15
ttg atg ctc ctc gct gtc ttg att tgg acc ggt gct gag aac ctc cat      104
Leu Met Leu Leu Ala Val Leu Ile Trp Thr Gly Ala Glu Asn Leu His
                                   -10                                   -5                                   1
gtg aaa ata agt tgc tct ctg gac tgg ttg atg gtc tca gtt atc cca      152
Val Lys Ile Ser Cys Ser Leu Asp Trp Leu Met Val Ser Val Ile Pro
5                                   10                                   15                                   20
gtt gca gaa agc aga aat ctg tat ata ttt gcg gat gaa tta cat ctg      200
Val Ala Glu Ser Arg Asn Leu Tyr Ile Phe Ala Asp Glu Leu His Leu
                                   25                                   30                                   35
gga atg ggc tgc cct gca aat cgg ata cat aca tat gta tat gag ttt      248
Gly Met Gly Cys Pro Ala Asn Arg Ile His Thr Tyr Val Tyr Glu Phe
                                   40                                   45                                   50
ata tat ctt gtt cgt gat tgt ggc atc agg aca agg gta gtt tct gag      296
Ile Tyr Leu Val Arg Asp Cys Gly Ile Arg Thr Arg Val Val Ser Glu
                                   55                                   60                                   65
gaa act ctc ctt ttt caa acc gag ctg tac ttt acc cca agg aat ata      344
Glu Thr Leu Leu Phe Gln Thr Glu Leu Tyr Phe Thr Pro Arg Asn Ile
                                   70                                   75                                   80
gat cat gac cct cag gaa atc cat ttg gag tgt tcc acc tct agg aaa      392
Asp His Asp Pro Gln Glu Ile His Leu Glu Cys Ser Thr Ser Arg Lys
85                                   90                                   95                                   100
tca gtg tgg ctt aca cca gtt tct act gag aat gaa ata aaa ttg gat      440
Ser Val Trp Leu Thr Pro Val Ser Thr Glu Asn Glu Ile Lys Leu Asp
                                   105                                   110                                   115
cct agt cct ttt att gct gac ttt cag aca aca gca gaa gag tta gga      488
Pro Ser Pro Phe Ile Ala Asp Phe Gln Thr Thr Ala Glu Glu Leu Gly

```



```

ttc tgg aaa aag tac cgc act ttc tgg aag gag gat aag gcc ttc tgg      678
Phe Trp Lys Lys Tyr Arg Thr Phe Trp Lys Glu Asp Lys Ala Phe Trp
   90               95               100
aaa gag gac aat gcc tta tgg gaa aga gac cgg aac ctt ctt cag gag      726
Lys Glu Asp Asn Ala Leu Trp Glu Arg Asp Arg Asn Leu Leu Gln Glu
105               110               115               120
gac aag gcc ctg tgg gag gaa gaa aag gcc ctg tgg gta gag gaa aga      774
Asp Lys Ala Leu Trp Glu Glu Glu Lys Ala Leu Trp Val Glu Glu Arg
               125               130               135
gcc ctc ctt gag ggg gag aaa gcc ctg tgg gaa gat aaa acg tcc ctc      822
Ala Leu Leu Glu Gly Glu Lys Ala Leu Trp Glu Asp Lys Thr Ser Leu
               140               145               150
tgg gag gaa gag aat gcc ctc tgg gag gaa gag agg gcc ttc tgg atg      870
Trp Glu Glu Glu Asn Ala Leu Trp Glu Glu Glu Arg Ala Phe Trp Met
               155               160               165
gag aac aat ggc cac att gcc gga gag cag atg ctc gaa gat ggg ccc      918
Glu Asn Asn Gly His Ile Ala Gly Glu Gln Met Leu Glu Asp Gly Pro
               170               175               180
cac aac gcc aac aga ggg cag cgc ttg ctg gcc ttc tcc cga ggc agg      966
His Asn Ala Asn Arg Gly Gln Arg Leu Leu Ala Phe Ser Arg Gly Arg
185               190               195               200
gcg tagccagcat gcaggtgcan gggccctgtg gtccagactc ccctgggttg      1019
Ala
ggattcaagt ccagggtgag cccatgtgct ggagaaaata cacactcatt ggtctccttg      1079
ctttgaaaaga tccaataaag tcctgaggca aggtttggaa aaccaaaaaa aaaaaaaaaa      1138

```

<210> 21  
 <211> 468  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 76..276

<220>  
 <221> sig\_peptide  
 <222> 76..135  
 <223> Von Heijne matrix  
 score 5.21332530399231  
 seq SPVFLVFPPEITA/SE

```

<400> 21
agcacaagaa aagaacatgg tctagactga agtaccact aaatcatctc ctttcaaatt      60
atcaccgaca ccatac atg gat tca agc acc gca cac agt ccg gtg ttt ctg      111
               Met Asp Ser Ser Thr Ala His Ser Pro Val Phe Leu
               -20               -15               -10
gta ttt cct cca gaa atc act gct tca gaa tat gag tcc aca gaa ctt      159
Val Phe Pro Pro Glu Ile Thr Ala Ser Glu Tyr Glu Ser Thr Glu Leu
               -5               1               5
tca gcc acg acc ttt tca act caa agc ccc ttg caa aaa tta ttt gct      207
Ser Ala Thr Thr Phe Ser Thr Gln Ser Pro Leu Gln Lys Leu Phe Ala
               10               15               20
aga aaa atg aaa atc tta ggg gat atc cat tct ggg gct ctg ttt tgt      255
Arg Lys Met Lys Ile Leu Gly Asp Ile His Ser Gly Ala Leu Phe Cys
25               30               35               40
tca tta att ctg gag cct tcc taattgcagt gaaaagaaaa accacagaaa      306
Ser Leu Ile Leu Glu Pro Ser

```



45  
ctctgggaat tttgattaca ttgatgactt tcagcattat tgaattattc atttctctgc 366  
ctttctcaat tttggggtgc cactcagagg attgtgattg tgaacaatgt tgttgactag 426  
cactgtgaga ataaagatgt gttaaaataa aaaaaaaaaa aa 468

<210> 22  
<211> 720  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 6..287

<220>  
<221> sig\_peptide  
<222> 6..80  
<223> Von Heijne matrix  
score 4.17710408129886  
seq ISLSHLFLDLSRS/LW

<400> 22  
atttg atg tgc ttc tta gtc tcg ttt aac ttg ccg att cat ata tcc ctg 50  
Met Cys Phe Leu Val Ser Phe Asn Leu Pro Ile His Ile Ser Leu  
-25 -20 -15  
tct cat ttg ttc tta gat ttg tca cga agc ctc tgg ttt ttg gct tgt 98  
Ser His Leu Phe Leu Asp Leu Ser Arg Ser Leu Trp Phe Leu Ala Cys  
-10 -5 1 5  
cct ggt ttg aac ttg gtg tat ctg gct ctt gac tca ttt tct gac ctc 146  
Pro Gly Leu Asn Leu Val Tyr Leu Ala Leu Asp Ser Phe Ser Asp Leu  
10 15 20  
aga cca tcc tta aat ctg ctt ttc tac ttt gta cca ggc ttt ggc gtc 194  
Arg Pro Ser Leu Asn Leu Leu Phe Tyr Phe Val Pro Gly Phe Gly Val  
25 30 35  
tcc aag tac ctg acc tca gct caa cct gtc ttg ggt ttt ctt ctc ctc 242  
Ser Lys Tyr Leu Thr Ser Ala Gln Pro Val Leu Gly Phe Leu Leu Leu  
40 45 50  
cct gac att gac aac cca gcc ctc cta ggc aca gag aga tgg agc 287  
Pro Asp Ile Asp Asn Pro Ala Leu Leu Gly Thr Glu Arg Trp Ser  
55 60 65  
tgagtgtggt tttcctgaaa taaagcttgc attatgagag ggaataaaca gaagaaaaaa 347  
atagtaagta aaatcttgct tgctcttcag taaaataaag ctctattttt cgtttttttt 407  
ttttccaact tcctgtacaa aaaagggaaa actttagctt ttgggggaaa tttggagcta 467  
gcctgttggt actgttgagc ttagtgtatc tataactata tattattcca caatatctta 527  
aatactttat aaagatattt tcataaatta cagcaatcct ggcttttagat gattgatggc 587  
catttttaaa caattaaagc taatttctag ctttttatga gtttggtatt aagcacagta 647  
gtttcttaga aagtctccag ggaatgcatt ttgcaaaata aaaatcagct aatgacccaa 707  
aaaaaaaaaa aaa 720

<210> 23  
<211> 727  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 171..692

```

<220>
<221> sig_peptide
<222> 171..227
<223> Von Heijne matrix
      score 4.17573075349936
      seq LLLGQRCSLKVSQ/QE

<400> 23
attgtgacat caccgtgcac tagccaatgg ctgcctgcct aagctgggtc cctggtctcc      60
tgggactact agccctttgt tgatagggag aagccaacat ctcccgagg accccctaata      120
cttcagggca gctcccagag catggatccc tcctgattcc actcagcccg atg ttc      176
                                     Met Phe
ctc aca gtc aag ctg ctc ctg ggc cag aga tgc agt ctg aag gtg tca      224
Leu Thr Val Lys Leu Leu Leu Gly Gln Arg Cys Ser Leu Lys Val Ser
      -15                                     -10                                     -5
ggg caa gag agt gta gcc acg ctg aag aga ctg gtg tcc agg cgg ctg      272
Gly Gln Glu Ser Val Ala Thr Leu Lys Arg Leu Val Ser Arg Arg Leu
      1                                     5                                     10                                     15
aag gtg cct gag gag cag cag cac ctg ctt ttc cgt ggc cag ctc ctg      320
Lys Val Pro Glu Glu Gln Gln His Leu Leu Phe Arg Gly Gln Leu Leu
      20                                     25                                     30
gag gat gac aag cac ctc tct gac tac tgc att ggg ccc aat gcc tct      368
Glu Asp Asp Lys His Leu Ser Asp Tyr Cys Ile Gly Pro Asn Ala Ser
      35                                     40                                     45
atc aat gtc atc atg cag ccc ttg gag aag atg gcg cta aag gag gcc      416
Ile Asn Val Ile Met Gln Pro Leu Glu Lys Met Ala Leu Lys Glu Ala
      50                                     55                                     60
cac cag ccg cag acc cag ccc ctg tgg cac cag ctg gga ctg gtc cta      464
His Gln Pro Gln Thr Gln Pro Leu Trp His Gln Leu Gly Leu Val Leu
      65                                     70                                     75
gct aaa cac ttt gaa cca cag gat gcc aag gcc gtg ctg cag ctg cta      512
Ala Lys His Phe Glu Pro Gln Asp Ala Lys Ala Val Leu Gln Leu Leu
      80                                     85                                     90                                     95
agg cag gag cac gag gag cgc ctg cag aag ata agc ctg gag cac ctg      560
Arg Gln Glu His Glu Glu Arg Leu Gln Lys Ile Ser Leu Glu His Leu
      100                                     105                                     110
gag cag ctg gcc cag tac ctc ctg gca gag gag cct cac gtg gag cca      608
Glu Gln Leu Ala Gln Tyr Leu Leu Ala Glu Glu Pro His Val Glu Pro
      115                                     120                                     125
gct gga gag agg gag ctt gag gcg aag gca cgg cct cag agc tcc tgt      656
Ala Gly Glu Arg Glu Leu Glu Ala Lys Ala Arg Pro Gln Ser Ser Cys
      130                                     135                                     140
gac atg gag gag aag gag gag gca gca gct gat cag taaacggggc      702
Asp Met Glu Glu Lys Glu Glu Ala Ala Ala Asp Gln
      145                                     150                                     155
atcctacccg aaaaaaaaaa aaaaaa      727

<210> 24
<211> 470
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 137..454

<220>
<221> sig_peptide

```

<222> 137..187

<223> Von Heijne matrix

score 10.7019149919754

seq VLMLLAVLIWTGA/EN

<400> 24

atcctgtgaa ctacccaaaa ggaggaaaac gaacgcagct gagcatggga tgccatataa 60  
 aaatcactta aaccagtcgc cactccttgt ttcctgagtt gtcctgtgct ggaggtctgc 120  
 tcagacgaag gtctcc atg gcg tta gaa gtc ttg atg ctc ctc gct gtc ttg 172  
 Met Ala Leu Glu Val Leu Met Leu Leu Ala Val Leu

-15

-10

att tgg acc ggt gct gag aac ctc cat gtg aaa ata agt tgc tct ctg 220  
 Ile Trp Thr Gly Ala Glu Asn Leu His Val Lys Ile Ser Cys Ser Leu  
 -5 1 5 10

gac tgg ttg atg gtc tca gtt atc cca gtt gca gaa agc aga aat ctg 268  
 Asp Trp Leu Met Val Ser Val Ile Pro Val Ala Glu Ser Arg Asn Leu  
 15 20 25

tat ata ttt gcg gat gaa tta cat ctg gga atg ggc tgc cct gca aat 316  
 Tyr Ile Phe Ala Asp Glu Leu His Leu Gly Met Gly Cys Pro Ala Asn  
 30 35 40

cgg ata cat aca tat gta tat gag ttt ata tat ctt gtt cgt gat tgt 364  
 Arg Ile His Thr Tyr Val Tyr Glu Phe Ile Tyr Leu Val Arg Asp Cys  
 45 50 55

ggc atc agg aca agg gta aga aca gtg att gtc tgt aaa aaa tac tgc 412  
 Gly Ile Arg Thr Arg Val Arg Thr Val Ile Val Cys Lys Lys Tyr Cys  
 60 65 70 75

atg ttt tgt cag act ttt atg cct agt att aaa att gtc ttt 454  
 Met Phe Cys Gln Thr Phe Met Pro Ser Ile Lys Ile Val Phe  
 80 85

taaaaaaaa aaaaaa 470

<210> 25

<211> 987

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 238..609

<220>

<221> sig\_peptide

<222> 238..291

<223> Von Heijne matrix

score 10.0374888212272

seq LLLLVMALPPGTT/GV

<400> 25

attccattca cagactcttg ttgggcagca gccacccgct cacctccatc cccaggactt 60  
 agagggacgc agggcggttg gaacagagga cactccaggc gctgaccctg ggaggccagg 120  
 accagggcca aagtcccgct ggcaagagga gtcctcagag gtccttcatt cagcggttcc 180  
 gggaggtctg ggaagcccac ggcctggctg gggcagggtc aacgccgcca ggccgcc 237  
 atg gtc ctg tgc tgg ctg ctg ctt ctg gtg atg gct ctg ccc cca ggc 285  
 Met Val Leu Cys Thr Trp Leu Leu Leu Val Met Ala Leu Pro Gly

-15

-10

-5

acg acg ggc gtc aag gac tgc gtc ttc tgt gag ctc acc gac tcc atg 333  
 Thr Thr Gly Val Lys Asp Cys Val Phe Cys Glu Leu Thr Asp Ser Met  
 1 5 10

```

cag tgt cct ggt acc tac atg cac tgt ggc gat gac gag gac tgc ttc      381
Gln Cys Pro Gly Thr Tyr Met His Cys Gly Asp Asp Glu Asp Cys Phe
15                20                25                30
aca ggc cac ggg gtc gcc ccg ggc act ggt ccg gtc atc aac aaa ggc      429
Thr Gly His Gly Val Ala Pro Gly Thr Gly Pro Val Ile Asn Lys Gly
                35                40                45
tgc ctg cga gcc acc agc tgc ggc ctt gag gaa ccc gtc agc tac agg      477
Cys Leu Arg Ala Thr Ser Cys Gly Leu Glu Glu Pro Val Ser Tyr Arg
                50                55                60
ggc gtc acc tac agc ctc acc acc aac tgc tgc acc ggc cgc ctg tgt      525
Gly Val Thr Tyr Ser Leu Thr Thr Asn Cys Cys Thr Gly Arg Leu Cys
        65                70                75
aac aga gcc ccg agc agc cag aca gtg ggg gcc acc acc agc ctg gca      573
Asn Arg Ala Pro Ser Ser Gln Thr Val Gly Ala Thr Thr Ser Leu Ala
        80                85                90
ctg ggg ctg ggt atg ctg ctt cct cca cgt ttg ctg tgaccaacag      619
Leu Gly Leu Gly Met Leu Leu Pro Pro Arg Leu Leu
        95                100                105
ggaggacagg gcctgggact gttctcccag atccgccact ccccatgtcc ccatgtcctt      679
ccccactaa atggccagag aggccctgga caacctcttg cgccctggc ttcattcctt      739
ctaaggctgt ccaccaggag cccggtgcta ggggaagcat cccaggcct gactgagcgg      799
caggggagca cggcccgtgg gtttgattgt attactctgt tccactgggt ctaagacgca      859
gagcttctca catctcaatc aggatgcttc tctccattgg tagcacttta gagtccatga      919
aatatggtaa aaaatatata tatatcataa taaatgacag ctgatgttca tggaaaaaaaa      979
aaaaaaaaa      987

<210> 26
<211> 908
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 80..862

<220>
<221> sig_peptide
<222> 80..127
<223> Von Heijne matrix
      score 3.66725851505537
      seq FSLLSISGPPISS/SA

<400> 26
gaatgtttat cctctggaca aaccagccag cctctccaga gcaggcgtgt gatctctgta      60
ccccgcagtg ggtcagaat atg gag aac ttc tca ctc ctc agc atc tct gga      112
                Met Glu Asn Phe Ser Leu Leu Ser Ile Ser Gly
                -15                -10

cct cca atc tct tcc tcc gcc ctg agt gct ttt ccc gac att atg ttc      160
Pro Pro Ile Ser Ser Ser Ala Leu Ser Ala Phe Pro Asp Ile Met Phe
-5                1                5                10
tct cgt gcc acc agc ctg cca gac att gca aag aca gca gta ccc act      208
Ser Arg Ala Thr Ser Leu Pro Asp Ile Ala Lys Thr Ala Val Pro Thr
        15                20                25
gag gca tcc agc cca gct cag gcc ctg cca ccc cag tac caa agc atc      256
Glu Ala Ser Ser Ser Pro Ala Gln Ala Leu Pro Pro Gln Tyr Gln Ser Ile
        30                35                40
att gtc agg caa ggg ata cag aac aca gtg ctc tca cca gac tgc agc      304
Ile Val Arg Gln Gly Ile Gln Asn Thr Val Leu Ser Pro Asp Cys Ser

```

```

      45              50              55
ttg ggg gac acc cag cac gga gag aag ctg agg cgg aac tgc act atc      352
Leu Gly Asp Thr Gln His Gly Glu Lys Leu Arg Arg Asn Cys Thr Ile
60              65              70
tac cgg ccc tgg ttc ccc tac agc tac ttc gtg tgt gca gac aaa      400
Tyr Arg Pro Trp Phe Ser Pro Tyr Ser Tyr Phe Val Cys Ala Asp Lys
      80              85              90
gag agc cag ctg gag gcc tat gac ttc cca gag gtg cag cag gat gag      448
Glu Ser Gln Leu Glu Ala Tyr Asp Phe Pro Glu Val Gln Gln Asp Glu
      95              100              105
ggc aag tgg gac aac tgc ctt tct gag gac atg gct gag aac atc tgt      496
Gly Lys Trp Asp Asn Cys Leu Ser Glu Asp Met Ala Glu Asn Ile Cys
      110              115              120
tcg tcc tct tcc tcc cca gag aac act tgc cct cga gaa gcc acc aag      544
Ser Ser Ser Ser Ser Pro Glu Asn Thr Cys Pro Arg Glu Ala Thr Lys
      125              130              135
aaa tcc agg cat ggc ctg gac tcc atc aca tcc cag gac atc cta atg      592
Lys Ser Arg His Gly Leu Asp Ser Ile Thr Ser Gln Asp Ile Leu Met
      140              145              150
gct tcc aga tgg cac cca gca cag cag aat ggc tac aag tgc gtg gcc      640
Ala Ser Arg Trp His Pro Ala Gln Gln Asn Gly Tyr Lys Cys Val Ala
      160              165              170
tgc tgc cgc atg tac ccc acc ctg gac ttc ctc aag agc cac atc aag      688
Cys Cys Arg Met Tyr Pro Thr Leu Asp Phe Leu Lys Ser His Ile Lys
      175              180              185
agg ggc ttc agg gag ggc ttc agc tgc aag gtg tac tac cgc aag ctc      736
Arg Gly Phe Arg Glu Gly Phe Ser Cys Lys Val Tyr Tyr Arg Lys Leu
      190              195              200
aaa gcc ctc tgg agc aag gag cag aag gcc cgg ctg gga gac agg ctc      784
Lys Ala Leu Trp Ser Lys Glu Gln Lys Ala Arg Leu Gly Asp Arg Leu
      205              210              215
tcc tcc ggc agc tgc cag gcc ttc aat agt cct gct gaa cac ctt agg      832
Ser Ser Gly Ser Cys Gln Ala Phe Asn Ser Pro Ala Glu His Leu Arg
      220              225              230              235
caa att ggc ggt gaa gcc tac tta tgt ctc tagagagatg ccaataaagt      882
Gln Ile Gly Gly Glu Ala Tyr Leu Cys Leu
      240              245
tagtcacagc caaaaaaaaa aaaaaa      908

<210> 27
<211> 762
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 83..310

<220>
<221> sig_peptide
<222> 83..157
<223> Von Heijne matrix
      score 4.72955689475746
      seq LCALLSNFCPSTT/VK

<400> 27
ttttttctac tacaaacgcc atggggatgc ggggtctggga acagcggaaa accctaccct      60
gccctgaaaa gtccctggct ca atg tgc atg tcc ctt tct atg aaa gtt cct      112

```

```

Met Cys Met Ser Leu Ser Met Lys Val Pro
-25 -20
tgc tgc cta tgc gcc ttg ctc tct aac ttc tgt ccc tcc aca act gtg 160
Cys Cys Leu Cys Ala Leu Ser Asn Phe Cys Pro Ser Thr Thr Val
-15 -10 -5 1
aaa gga gac gtc gtg act tcc ttc ttt cgt gct gac tat gac tta gcc 208
Lys Gly Asp Val Val Thr Ser Phe Phe Arg Ala Asp Tyr Asp Leu Ala
5 10 15
agt agg tct gca gat cag tcc tcc cag aaa gtg aag ttg cgc atg ttc 256
Ser Arg Ser Ala Asp Gln Ser Ser Gln Lys Val Lys Leu Arg Met Phe
20 25 30
act ggg cgt ctt ccc atc ggc ccc ttc gcc agt gtg ggg aac gcg gcg 304
Thr Gly Arg Leu Pro Ile Gly Pro Phe Ala Ser Val Gly Asn Ala Ala
35 40 45
gag ctg tgagccggcg actcgggtcc ctgaggtctg gattctttct ccgctactga 360
Glu Leu
50
gacacggcgg acacacacaa acacagaacc acacagccag tcccaggagc ccagtaatgg 420
agagcccaa aaagaagaac cagcagctga aagtccgggat cctacacctg ggcagcagac 480
agaagaagat caggatacag ctgagatccc agtgcgcgac atggaagggtg atctgcaaga 540
gctgcatcag tcaaacaccg gggataaatc tggatttggtg ttccggcgctc aagggtgaaga 600
taatacctaa agaggaacac tgtaaaatgc cagaagcagg tgaagagcaa ccacaagttt 660
aatgaagac aagctgaaac aacgcaagct ggttttatat tagatatattg acttaaaacta 720
tctcaataaa gttttgcagc tttcaccaaa aaaaaaaaaa aa 762

<210> 28
<211> 1102
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 310..906

<220>
<221> sig_peptide
<222> 310..357
<223> Von Heijne matrix
score 11.0931109030915
seq FPLLLLSLGLVLA/EA

<400> 28
atacagtgac ctagagcagg catgggtggg tcacaggctt tggagagcac tctctgtcct 60
gatcttttca gttgagagac ttcagctggt cattgctcat ttggacttag ttcaagggtca 120
tgtcaaagaa gaagggtgcac ttacgctagt tgtagctct gtcttttgta accatcaagt 180
tccatgcgat tgatcagatt taggaggggg cggtggggga taatcaattt tgggtgtcac 240
caggtaaaca gagccctcag catctgaata gaaactgaac aggaacagaa gagattcact 300
acatctgag atg gag acc ttt cct ctg ctg ctg ctc agc ctg ggc ctg gtt 351
Met Glu Thr Phe Pro Leu Leu Leu Leu Ser Leu Gly Leu Val
-15 -10 -5
ctt gca gaa gca tca gaa agc aca atg aag ata att aaa gaa gaa ttt 399
Leu Ala Glu Ala Ser Glu Ser Thr Met Lys Ile Ile Lys Glu Glu Phe
1 5 10
aca gac gaa gag atg caa tat gac atg gca aaa agt ggc caa gaa aaa 447
Thr Asp Glu Glu Met Gln Tyr Asp Met Ala Lys Ser Gly Gln Glu Lys
15 20 25 30
cag acc att gag ata tta atg aac ccg atc ctg tta gtt aaa aat acc 495
Gln Thr Ile Glu Ile Leu Met Asn Pro Ile Leu Leu Val Lys Asn Thr

```

	35		40		45	
agc ctc agc atg tcc aag gat gat atg tct tcc aca tta ctg aca ttc						543
Ser Leu Ser Met Ser Lys Asp Asp Met Ser Ser Thr Leu Leu Thr Phe						
	50		55		60	
aga agt tta cat tat aat gac ccc aag gga aac agt tcg ggt aat gac						591
Arg Ser Leu His Tyr Asn Asp Pro Lys Gly Asn Ser Ser Gly Asn Asp						
	65		70		75	
aaa gag tgt tgc aat gac atg aca gtc tgg aga aaa gtt tca gaa gca						639
Lys Glu Cys Cys Asn Asp Met Thr Val Trp Arg Lys Val Ser Glu Ala						
	80		85		90	
aac gga tcg tgc aag tgg agc aat aac ttc atc cgc agc tcc aca gaa						687
Asn Gly Ser Cys Lys Trp Ser Asn Asn Phe Ile Arg Ser Ser Thr Glu						
	95		100		105	
gtg atg cgc agg gtc cac agg gcc ccc agc tgc aag ttt gta cag aat						735
Val Met Arg Arg Val His Arg Ala Pro Ser Cys Lys Phe Val Gln Asn						
	115		120		125	
cct ggc ata agc tgc tgt gag agc cta gaa ctg gaa aat aca gtg tgc						783
Pro Gly Ile Ser Cys Cys Glu Ser Leu Glu Leu Glu Asn Thr Val Cys						
	130		135		140	
cag ttc act aca ggc aaa caa ttc ccc agg tgc caa tac cat agt gtt						831
Gln Phe Thr Thr Gly Lys Gln Phe Pro Arg Cys Gln Tyr His Ser Val						
	145		150		155	
acc tca tta gag aag ata ttg aca gtg ctg aca ggt cat tct ctg atg						879
Thr Ser Leu Glu Lys Ile Leu Thr Val Leu Thr Gly His Ser Leu Met						
	160		165		170	
agc tgg tta gtt tgt ggc tct aag ttg taaatccac agagctttag						926
Ser Trp Leu Val Cys Gly Ser Lys Leu						
	175		180			
gactagggtc ttactaaaga aggacctctt cttgttcatt cttgtttaaa cctttcctta						986
atatctactc tttagcacta tagtgaactc ctgattatctt attctaactg gaggagttaa						1046
aaatccaaaa ttgtggataa ttcaattaaa agttatgact gaaaaaaaaa aaaaaa						1102

<210> 29  
 <211> 436  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 24..287

<220>  
 <221> sig\_peptide  
 <222> 24..131  
 <223> Von Heijne matrix  
 score 3.79790641648006  
 seq ILMRDFSPSGIFG/AF

<400> 29	
acagcggaca ccaggactcc aaa atg gcg tca gtt gta cca gtg aag gac aag	53
Met Ala Ser Val Val Pro Val Lys Asp Lys	
	-35
aaa ctt ctg gag gtc aaa ctg ggg gag ctg cca agc tgg atc ttg atg	101
Lys Leu Leu Glu Val Lys Leu Gly Glu Leu Pro Ser Trp Ile Leu Met	
	-25
cgg gac ttc agt cct agt ggc att ttc gga gcg ttt caa aga ggt tac	149
Arg Asp Phe Ser Pro Ser Gly Ile Phe Gly Ala Phe Gln Arg Gly Tyr	
	-10
	-5
	1
	5

```

tac cgg tac tac aac aag tac atc aat gtg aag aag ggg agc atc tcg      197
Tyr Arg Tyr Tyr Asn Lys Tyr Ile Asn Val Lys Lys Gly Ser Ile Ser
      10      15      20
ggg att acc atg gtg ctg gca tgc tac gtg ctc ttt agc tac tcc ttt      245
Gly Ile Thr Met Val Leu Ala Cys Tyr Val Leu Phe Ser Tyr Ser Phe
      25      30      35
tcc tac aag cat ctc aag cac gag cgg ctc cgc aaa tac cac      287
Ser Tyr Lys His Leu Lys His Glu Arg Leu Arg Lys Tyr His
      40      45      50
tgaagaggac acactctgca cccccccacc ccacgacctt ggcccgagcc cctccgtgag      347
gaacacaatc tcaatcggtg ctgaatcctt tcatatccta ataggaatta acctccaaat      407
aaaacatgac tggtaaaaaa aaaaaaaaaa      436

<210> 30
<211> 1938
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 132..1574

<220>
<221> sig_peptide
<222> 132..206
<223> Von Heijne matrix
      score 11.1130239236827
      seq LALLLTSTPEALG/AN

<400> 30
ctcccccttcc cgctcccagg aacccatcca gcctcaggaa ctgccccag ccacgagcc      60
ttggctactt aaggacctg ggcccaatcc acagctggga cagtcctggc ccaactgcact      120
gggaatctag g atg ggg gcc ttg gcc aga gcc ctg ccg tcc ata ctg ctg      170
      Met Gly Ala Leu Ala Arg Ala Leu Pro Ser Ile Leu Leu
      -25      -20      -15
gca ttg ctg ctt acg tcc acc cca gag gct ctg ggt gcc aac ccc ggc      218
Ala Leu Leu Leu Thr Ser Thr Pro Glu Ala Leu Gly Ala Asn Pro Gly
      -10      -5      1
ttg gtc gcc agg atc acc gac aag gga ctg cag tat gcg gcc cag gag      266
Leu Val Ala Arg Ile Thr Asp Lys Gly Leu Gln Tyr Ala Ala Gln Glu
      5      10      15      20
ggg cta ttg gct ctg cag agt gag ctg ctc agg atc acg ctg cct gac      314
Gly Leu Leu Ala Leu Gln Ser Glu Leu Leu Arg Ile Thr Leu Pro Asp
      25      30      35
ttc acc ggg gac ttg agg atc ccc cac gtc ggc cgt ggg cgc tat gag      362
Phe Thr Gly Asp Leu Arg Ile Pro His Val Gly Arg Gly Arg Tyr Glu
      40      45      50
ttc cac agc ctg aac atc cac agc tgt gag ctg ctt cac tct gcg ctg      410
Phe His Ser Leu Asn Ile His Ser Cys Glu Leu Leu His Ser Ala Leu
      55      60      65
agg cct gtc cct ggc cag ggc ctg agt ctc agc atc tcc gac tcc tcc      458
Arg Pro Val Pro Gly Gln Gly Leu Ser Leu Ser Ile Ser Asp Ser Ser
      70      75      80
atc cgg gtc cag ggc agg tgg aag gtg cgc aag tca ttc ttc aaa cta      506
Ile Arg Val Gln Gly Arg Trp Lys Val Arg Lys Ser Phe Phe Lys Leu
      85      90      95      100
cag ggc tcc ttt gat gtc agt gtc aag ggc atc agc att tcg gtc aac      554
Gln Gly Ser Phe Asp Val Ser Val Lys Gly Ile Ser Ile Ser Val Asn

```



															105																110																115																	
ctc	ctg	ttg	ggc	agc	gat	tcc	tcc	ggg	agg	ccc	aca	gtt	act	gcc	tcc																602																																	
Leu	Leu	Leu	Gly	Ser	Asp	Ser	Ser	Gly	Arg	Pro	Thr	Val	Thr	Ala	Ser																																																	
															120																125																130																	
agc	tgc	agc	agt	gac	atc	gct	gac	gtg	gag	gtg	gac	atg	tcg	gga	gac																650																																	
Ser	Cys	Ser	Ser	Asp	Ile	Ala	Asp	Val	Glu	Val	Asp	Met	Ser	Gly	Asp																																																	
															135																140																145																	
ttg	ggg	tgg	ctg	ttg	aac	ctc	ttc	cac	aac	cag	att	gag	tcc	aag	ttc																698																																	
Leu	Gly	Trp	Leu	Leu	Asn	Leu	Phe	His	Asn	Gln	Ile	Glu	Ser	Lys	Phe																																																	
															150																155																160																	
cag	aaa	gta	ctg	gag	agc	agg	att	tgc	gaa	atg	atc	cag	aaa	tcg	gtg																746																																	
Gln	Lys	Val	Leu	Glu	Ser	Arg	Ile	Cys	Glu	Met	Ile	Gln	Lys	Ser	Val																																																	
															165																170																175																180	
tcc	tcc	gat	cta	cag	cct	tat	ctc	caa	act	ctg	aca	gtt	aca	aca	gag																794																																	
Ser	Ser	Asp	Leu	Gln	Pro	Tyr	Leu	Gln	Thr	Leu	Thr	Val	Thr	Thr	Glu																																																	
															185																190																195																	
att	gac	agt	ttc	gcc	gac	att	gat	tat	agc	tta	gtg	gaa	gcc	cct	cgg																842																																	
Ile	Asp	Ser	Phe	Ala	Asp	Ile	Asp	Tyr	Ser	Leu	Val	Glu	Ala	Pro	Arg																																																	
															200																205																210																	
gca	aca	gcc	cag	atg	ctg	gag	gtg	atg	ttt	aag	ggg	gaa	atc	ttt	cat																890																																	
Ala	Thr	Ala	Gln	Met	Leu	Glu	Val	Met	Phe	Lys	Gly	Glu	Ile	Phe	His																																																	
															215																220																225																	
cgt	aac	cac	cgt	tct	cca	gtt	acc	ctc	ctt	gct	gca	gtc	atg	agc	ctt																938																																	
Arg	Asn	His	Arg	Ser	Pro	Val	Thr	Leu	Leu	Ala	Ala	Val	Met	Ser	Leu																																																	
															230																235																240																	
cct	gag	gaa	cac	aac	aaa	atg	gtc	tac	ttt	gcc	atc	tcg	gat	tat	gtc																986																																	
Pro	Glu	Glu	His	Asn	Lys	Met	Val	Tyr	Phe	Ala	Ile	Ser	Asp	Tyr	Val																																																	
															245																250																255																260	
ttc	aac	acg	gcc	agc	ctg	gtt	tat	cat	gag	gaa	gga	tat	ctg	aac	ttc																1034																																	
Phe	Asn	Thr	Ala	Ser	Leu	Val	Tyr	His	Glu	Glu	Gly	Tyr	Leu	Asn	Phe																																																	
															265																270																275																	
tcc	atc	aca	gat	gac	atg	ata	ccg	cct	gac	tct	aat	atc	cga	ctg	acc																1082																																	
Ser	Ile	Thr	Asp	Asp	Met	Ile	Pro	Pro	Asp	Ser	Asn	Ile	Arg	Leu	Thr																																																	
															280																285																290																	
acc	aag	tcc	ttc	cga	ccc	ttc	gtc	cca	cgg	tta	gcc	agg	ctc	tac	ccc																1130																																	
Thr	Lys	Ser	Phe	Arg	Pro	Phe	Val	Pro	Arg	Leu	Ala	Arg	Leu	Tyr	Pro																																																	
															295																300																305																	
aac	atg	aac	ctg	gaa	ctc	cag	gga	tca	gtg	ccc	tct	gct	ccg	ctc	ctg																1178																																	
Asn	Met	Asn	Leu	Glu	Leu	Gln	Gly	Ser	Val	Pro	Ser	Ala	Pro	Leu	Leu																																																	

```

gaa ggc ttc ccc ctt cct ctg ctg aag cgt gtt cag ctc tac gac ctt      1514
Glu Gly Phe Pro Leu Pro Leu Leu Lys Arg Val Gln Leu Tyr Asp Leu
                425                      430                      435

ggg ctg cag atc cat aag gac ttc ctg ttc ttg ggt gcc aat gtc caa      1562
Gly Leu Gln Ile His Lys Asp Phe Leu Phe Leu Gly Ala Asn Val Gln
                440                      445                      450

tac atg aga gtt tgaggacaag aaagatgaag cttggaggtc acagctggat      1614
Tyr Met Arg Val
                455

ctgcttggtt catttccagc tgtgcagcac gtctcagaga ttcttgaaga atgaagacat      1674
ttctgctctc agctccgggg gtgaggtgtg cctggcctct gcctccaccc tctctctctt      1734
caccaggtgc atgcatgccc tctctgagtc tggactttgc ttccctcca ggagggacca      1794
ccctccctga ctggcctggg atatctttac aagcaggcac tgtatttttt tattcgccat      1854
ctgatcccca tgcttagcag agtgctggca cttagtaggt cctcaataaa tatttattaa      1914
atgatgacaa aaaaaaaaaa aaaa      1938

<210> 31
<211> 1116
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 117..545

<220>
<221> sig_peptide
<222> 117..245
<223> Von Heijne matrix
      score 5.65876793443964
      seq VVSFALIALVYA/LF

<400> 31
ataagggggac gtctagtggg ttgcccggga ggggtggcgg gagcgggtcct ggaaataatc      60
tgtcctctgt cgccgggaac tggcgaggta gttccttcgc ggtggagaga cctgga atg      119
                                   Met

gcc aaa tat caa ggt gaa gtt caa agt ttg aaa ctg gat gat gat tca      167
Ala Lys Tyr Gln Gly Glu Val Gln Ser Leu Lys Leu Asp Asp Asp Ser
      -40                      -35                      -30

gtt ata gaa gga gta agc gac caa gta ctt gtg gca gtt gtg gtc agt      215
Val Ile Glu Gly Val Ser Asp Gln Val Leu Val Ala Val Val Val Ser
      -25                      -20                      -15

ttc gct ttg att gct acc ctg gta tat gca ctt ttc aga aat gta cat      263
Phe Ala Leu Ile Ala Thr Leu Val Tyr Ala Leu Phe Arg Asn Val His
      -10                      -5                      1                      5

caa aac att cac cca gaa aac cag gag cta gta agg gta ctt cga gaa      311
Gln Asn Ile His Pro Glu Asn Gln Glu Leu Val Arg Val Leu Arg Glu
      10                      15                      20

cag ctt caa aca gaa cag gat gca cct gct gcc act cga cag cag ttc      359
Gln Leu Gln Thr Glu Gln Asp Ala Pro Ala Ala Thr Arg Gln Gln Phe
      25                      30                      35

tac act gac atg tac tgt ccc atc tgc ctg cac caa gcc tcc ttc ccg      407
Tyr Thr Asp Met Tyr Cys Pro Ile Cys Leu His Gln Ala Ser Phe Pro
      40                      45                      50

gtg gag acc aac tgt gga cat ctt ttt tgt ggt gcc tgc att att gct      455
Val Glu Thr Asn Cys Gly His Leu Phe Cys Gly Ala Cys Ile Ile Ala
      55                      60                      65                      70

tac tgg cga tat ggt tca tgg ctt ggg gca atc agt tgt cca atc tgt      503

```

Tyr	Trp	Arg	Tyr	Gly	Ser	Trp	Leu	Gly	Ala	Ile	Ser	Cys	Pro	Ile	Cys	
			75					80						85		
aga	caa	acg	aga	cat	ggc	cac	att	gca	ttg	tcc	aga	aca	gct			545
Arg	Gln	Thr	Arg	His	Gly	His	Ile	Ala	Leu	Ser	Arg	Thr	Ala			
			90					95					100			
tagaccatga	cagtttagcat	cgaagccacc	tgaggaggga	ggcagtaacc	ttactcctaa											605
cagtatttgg	tgaagatgat	cagtctcagg	atgttctgag	attgcatcag	gatattaatg											665
attataaccg	gagattctca	gggcaaccca	gatctgtaag	taatgctaaa	gcatgttcaa											725
agtttagagga	agacacattt	cttctctttt	gtaaaagtga	gtttaccaac	aagtattcct											785
tgactatgag	aaatcttggc	caggcacagt	agctaacgcc	tataatccta	gcactttggg											845
aggccaaggc	aggtggatca	cttgagccca	ggagtttgag	accagccttg	gaaacatgat											905
gaaaccccat	ctctagaaaa	aacaccaaaa	aattggacaa	gagtgttggc	acatgcctgt											965
agtccttgct	tcttgggagg	ctgaaatggg	aggatcacct	gagcccagga	ggttgaggct											1025
atagttagcc	atgatcgcac	tattgcactc	ccacctgggt	ggcagtgaga	cccttctcct											1085
aaaaacaaga	aaagaaaaaa	aaaaaaaaaa	a													1116
<210> 32																
<211> 1114																
<212> DNA																
<213> Homo sapiens																
<220>																
<221> CDS																
<222> 117..362																
<400> 32																
ataagggggac	gtctagtggg	ttgcccggga	gggggtggcg	gagcggtcct	ggaaataatc											60
tgctctctgt	cgccgggaac	tggcgaggta	gttccttcgc	ggtggagaga	cctgga atg											119
					Met											
					1											
gcc aaa tat	caa ggt gaa	gtt caa agt	ttg aaa ctg	gat gat gat	tca											167
Ala Lys Tyr	Gln Gly Glu	Val Gln Ser	Leu Lys Leu	Asp Asp Asp	Ser											
	5		10		15											
gtt ata gaa	gga gta agc	gac caa gta	ctt gtg gca	gtt gtg gtc	agt											215
Val Ile Glu	Gly Val Ser	Asp Gln Val	Leu Val Ala	Val Val Val	Ser											
	20		25		30											
ttc gct ttg	att gct acc	ctg gta tat	gca ctt ttc	aga aat gta	cat											263
Phe Ala Leu	Ile Ala Thr	Leu Val Tyr	Ala Leu Phe	Arg Asn Val	His											
	35		40		45											
caa aac att	cac cca gaa	aac cag gag	cta gta agg	gta ctt cga	gaa											311
Gln Asn Ile	His Pro Glu	Asn Gln Glu	Leu Val Arg	Val Leu Arg	Glu											
	50		55		60											
cag ctt caa	aca gaa cag	gat gca cct	gct gac tcg	aca gca gtt	cta											359
Gln Leu Gln	Thr Glu Gln	Asp Ala Pro	Ala Asp Ser	Thr Ala Val	Leu											
	70		75		80											
cac tgacatgtac	tgccccatct	gcctgcacca	agcctccttc	ccggtggaga												412
His																
ccaactgtgg	acatcttttt	tgtggtgcct	gcattattgc	ttactggcga	tatggttcat											472
ggcttggggc	aatcagttgt	ccaatctgta	gacaaacgag	acatggccac	attgcattgt											532
ccagaacagc	ttagaccatg	acagtttagca	tcgaagccac	ctgaggaggg	aggcagtaac											592
cttactccta	acagtatttg	gtgaagatga	tcagtctcag	gatgttctga	gattgcatca											652
ggatattaat	gattataacc	ggagattctc	agggcaaccc	agatctgtaa	gtaatgctaa											712
agcatgttca	aagtttagagg	aagacacatt	tcttctcttt	tgtaaagtga	ggtttaccac											772
caagtattct	ttgactatga	gaaatcttgg	ccaggcacag	tagctaacgc	ctataatcct											832
agcacttttg	gaggccaagg	caggtggatc	acttgagccc	aggagtttga	gaccagcctt											892
ggaaacatga	tgaaacccca	tctctagaaa	aaacacaaaa	aaattggaca	agagtgttgg											952
cacatgcctg	tagtccctgc	ttcttgggag	gctgaaatgg	gaggatcacc	tgagcccagg											1012
agggttaggc	tatagttagc	catgatcgca	ctattgcact	cccacctggg	tggcagttag											1072



Lys	Ile	Lys	Arg	Ile	Arg	Gly	Met	Ala	Tyr	Ser	Val	Arg	Val	Ser	Pro		
160					165					170					175		
cag	atg	gcg	aac	cgg	att	gtg	gat	tct	gca	agg	agc	atc	ctc	aac	aag		797
Gln	Met	Ala	Asn	Arg	Ile	Val	Asp	Ser	Ala	Arg	Ser	Ile	Leu	Asn	Lys		
				180					185					190			
ttc	ata	cct	gat	atc	tat	att	tac	aca	gat	cac	att	aaa	gga	gtc	aac		845
Phe	Ile	Pro	Asp	Ile	Tyr	Ile	Tyr	Thr	Asp	His	Ile	Lys	Gly	Val	Asn		
				195				200					205				
tct	ggg	aag	tct	cgg	ggc	ttt	ggg	ttg	tca	ctg	ggt	gct	gag	acc	acc		893
Ser	Gly	Lys	Ser	Pro	Gly	Phe	Gly	Leu	Ser	Leu	Val	Ala	Glu	Thr	Thr		
		210					215					220					
agt	ggc	acc	ttc	ctc	agt	gct	gaa	ctg	gcc	tcc	aac	ccc	cag	ggc	cag		941
Ser	Gly	Thr	Phe	Leu	Ser	Ala	Glu	Leu	Ala	Ser	Asn	Pro	Gln	Gly	Gln		
		225				230					235						
gga	gca	gca	gta	ctt	cca	gag	gac	ctt	ggc	agg	aac	tgt	gcc	cgg	ctg		989
Gly	Ala	Ala	Val	Leu	Pro	Glu	Asp	Leu	Gly	Arg	Asn	Cys	Ala	Arg	Leu		
240					245					250				255			
ctg	ctg	gag	gaa	atc	tac	agg	ggt	gga	tgc	gta	gac	tcg	acc	aac	caa		1037
Leu	Leu	Glu	Glu	Ile	Tyr	Arg	Gly	Gly	Cys	Val	Asp	Ser	Thr	Asn	Gln		
				260					265					270			
agc	ctg	gcg	cta	ctc	atg	acc	ctt	gga	cag	cag	gat	gtt	tcc	aaa			1085
Ser	Leu	Ala	Leu	Leu	Met	Thr	Leu	Gly	Gln	Gln	Asp	Val	Ser	Lys			
			275				280					285					
gtc	ctg	cta	ggc	cct	ctc	tct	ccc	tac	acg	ata	gaa	ttt	ttg	cgg	cat		1133
Val	Leu	Leu	Gly	Pro	Leu	Ser	Pro	Tyr	Thr	Ile	Glu	Phe	Leu	Arg	His		
			290				295					300					
ttg	aag	agc	ttt	ttc	cag	att	atg	ttt	aaa	att	gaa	acc	aag	cca	tgt		1181
Leu	Lys	Ser	Phe	Phe	Gln	Ile	Met	Phe	Lys	Ile	Glu	Thr	Lys	Pro	Cys		
		305			310						315						
ggt	gaa	gaa	ctc	aag	ggt	ggg	gat	aaa	gtg	ctg	atg	acc	tgt	gtt	ggc		1229
Gly	Glu	Glu	Leu	Lys	Gly	Gly	Asp	Lys	Val	Leu	Met	Thr	Cys	Val	Gly		
320					325					330				335			
att	ggt	ttc	tcc	aac	ctt	agc	agg	acc	ctc	aag	tgataacccat	cacaagataa					1282
Ile	Gly	Phe	Ser	Asn	Leu	Ser	Arg	Thr	Leu	Lys							
				340					345								
ggccccagtg	cctacagaca	aagcagaagc	tgccacggac	accaatggga	ccaagtccaa												1342
atggattaat	ccaggacaga	atagccactt	gcttaatttt	ctgtgaagaa	atatcaatat												1402
acaaataaaa	gacatccctg	tagcatatgg	tttccagctg	tttctccagt	ggcattgcc												1462
ttgcccagga	ggggcccgat	caccatgaga	gctcccttgc	cttacctgga	ggaagaatgt												1522
gccttcaggc	cacagtcgtg	ctgctagaac	agtctcgtag	ctgcagttca	gctgtgcttc												1582
ctcagcctac	tatcataggc	ttcctcagcc	ctctgtcata	tggctgtttt	gcaaacctgt												1642
ggagtctgtt	actgttcttt	ctgcaaggac	tcacctctt	gagccttggg	ttttgttgta												1702
gggattaaat	gagataatat	gagtggcagc	tcttcatgag	tcctgcagt	ctaagcaa												1762
gtcagaaaatt	ggtgtattag	actatttatc	tttgatcttc	tgaatggatt	gctgtcatgg												1822
acacggacac	ggatcttcat	ctggttcatt	gtattttatat	gtgagggatg	gatggctgcg												1882
gggctccaag	taagttattg	ggatgttttt	atattccagg	tgtgctgtac	gttcttattt												1942
tattttcaca	atagctctgt	gatgtaagt	ctatctccat	gagaaaattc	ataaagggtg												2002
ttttgttcac	ttgaaatgta	taatgtaaag	acattaaatc	tcctcattta	aggaaaaaaa												2062
aaaaaaaaaa																	2072

<210> 34  
 <211> 409  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 35..316

<220>  
 <221> sig\_peptide  
 <222> 35..109  
 <223> Von Heijne matrix  
 score 5.38058532480537  
 seq AVTSLLSPTPATA/LA

<400> 34  
 ttttttttcca gaccggaagt gactgatcga aagc atg gcg tcg gtg gtg ttg gcg 55  
 Met Ala Ser Val Val Leu Ala  
 -25 -20  
 ctg agg acc cgg aca gcc gtt aca tcc ttg cta agc ccc act ccg gct 103  
 Leu Arg Thr Arg Thr Ala Val Thr Ser Leu Leu Ser Pro Thr Pro Ala  
 -15 -10 -5  
 aca gct ctt gct gtc aga tac gca tcc aag aag tcg ggt ggt agc tcc 151  
 Thr Ala Leu Ala Val Arg Tyr Ala Ser Lys Lys Ser Gly Gly Ser Ser  
 1 5 10  
 aaa aac ctc ggt gga aag tca tca ggc aga cgc caa ggc att aag aaa 199  
 Lys Asn Leu Gly Gly Lys Ser Ser Gly Arg Arg Gln Gly Ile Lys Lys  
 15 20 25 30  
 atg gaa ggt cac tat gtt cat gct ggg aac atc att gca aca cag cgc 247  
 Met Glu Gly His Tyr Val His Ala Gly Asn Ile Ile Ala Thr Gln Arg  
 35 40 45  
 cat ttc cgc tgg cac cca ggt gcc cat gtg agt tgc tcc gtt gct gcc 295  
 His Phe Arg Trp His Pro Gly Ala His Val Ser Cys Ser Val Ala Ala  
 50 55 60  
 ccc ctt ttt cct ttt cta ggt tgacctctcc ttgcccctaa gcatggtaat 346  
 Pro Leu Phe Pro Phe Leu Gly  
 65  
 aacagttgca tgtattgagt gcttaccaaaa tggcaagcat tgtgccaaaa aaaaaaaaaa 406  
 aaa 409

<210> 35  
 <211> 836  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 177..767  
 <220>  
 <221> sig\_peptide  
 <222> 177..236  
 <223> Von Heijne matrix  
 score 6.51720597568932  
 seq LAVILTLLGLAIL/AI

<400> 35  
 aatctgctcc acgcaatttc tcagtgatcc tctgcatctc tgcctacaag ggcctccctg 60  
 acacccaagt tcatattgct cagaaacagt gaacttgagt ttttcatttt accttgatct 120  
 ctctctgaca aagaaatcca gatgatgcga gacctgatga agacaatata tggaaa atg 179  
 Met  
 -20  
 aca gtc ttg gaa ata act ttg gct gtc atc ctg act cta ctg gga ctt 227  
 Thr Val Leu Glu Ile Thr Leu Ala Val Ile Leu Thr Leu Leu Gly Leu  
 -15 -10 -5

```

gcc atc ctg gct att ttg tta aca aga tgg gca cga cgt aag caa agt      275
Ala Ile Leu Ala Ile Leu Leu Thr Arg Trp Ala Arg Arg Lys Gln Ser
      1      5      10
gaa atg tat atc tcc aga tac agt tca gaa caa agt gct aga ctt ctg      323
Glu Met Tyr Ile Ser Arg Tyr Ser Ser Glu Gln Ser Ala Arg Leu Leu
      15      20      25
gac tat gag gat ggt aga gga tcc cga cat gca tat tca aca caa agt      371
Asp Tyr Glu Asp Gly Arg Gly Ser Arg His Ala Tyr Ser Thr Gln Ser
      30      35      40      45
gag aga tcc aaa aga gat tac aca cca tca acc aac tct cta gca ctg      419
Glu Arg Ser Lys Arg Asp Tyr Thr Pro Ser Thr Asn Ser Leu Ala Leu
      50      55      60
tct cga tca agt att gct tta cct caa gga tcc atg agt agt ata aaa      467
Ser Arg Ser Ser Ile Ala Leu Pro Gln Gly Ser Met Ser Ser Ile Lys
      65      70      75
tgt tta caa aca act gaa gaa cct cct tcc aga act gca gga gcc atg      515
Cys Leu Gln Thr Thr Glu Glu Pro Pro Ser Arg Thr Ala Gly Ala Met
      80      85      90
atg caa ttc aca gcc cct att ccc gga gct aca gga cct atc aag ctc      563
Met Gln Phe Thr Ala Pro Ile Pro Gly Ala Thr Gly Pro Ile Lys Leu
      95      100      105
tct caa aaa acc att gtg caa act cta gga cct att gta caa tat cct      611
Ser Gln Lys Thr Ile Val Gln Thr Leu Gly Pro Ile Val Gln Tyr Pro
      110      115      120      125
gga tcc aat ggg agg ata aac ata agc cag ctc acc tca gag gat ctc      659
Gly Ser Asn Gly Arg Ile Asn Ile Ser Gln Leu Thr Ser Glu Asp Leu
      130      135      140
act ggg gct aaa gga agg gtc aca tct ggt cca cag ttc cct aat agc      707
Thr Gly Ala Lys Gly Arg Val Thr Ser Gly Pro Gln Phe Pro Asn Ser
      145      150      155
cac cat gtg cca gag aat cta cat gga tac atg aat tcc ctt tcc ctt      755
His His Val Pro Glu Asn Leu His Gly Tyr Met Asn Ser Leu Ser Leu
      160      165      170
ttc tcc cct gct tgactccctc tcccttatgt gtaaacaatt taaaaatatg      807
Phe Ser Pro Ala
      175
atagtgtata aatgaaaaaa aaaaaaaaaa      836

```

<210> 36  
 <211> 1323  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 208..1239

<220>  
 <221> sig\_peptide  
 <222> 208..294  
 <223> Von Heijne matrix  
 score 5.73027134157378  
 seq GLVLICVSKTHS/LK

```

<400> 36
agtctcgtat cgcgccccggg aggcgcgcgga gccagcggc tggcgccaga tccaggctcc      60
tggaagaacc atgtccggca gctactggtc atgccaggca cacactgctg cccaagagga      120
gctgctgttt gaattatctg tgaatgttgg gaagaggaat gccagagctg ccggctgaaa      180

```

attacccaac caagagaaat ctgcagg atg gac ttt ctg gtc ctc ttc ttg ttc	234
Met Asp Phe Leu Val Leu Phe Leu Phe	
-25	
tac ctg gct tgc gtg ctg atg ggt ctt gtt ctt atc tgc gtc tgc tgc	282
Tyr Leu Ala Ser Val Leu Met Gly Leu Val Leu Ile Cys Val Cys Ser	
-20 -15 -10 -5	
aaa acc cat agc ttg aaa ggc ctg gcc agg gga gga gca cag ata ttt	330
Lys Thr His Ser Leu Lys Gly Leu Ala Arg Gly Gly Ala Gln Ile Phe	
1 5 10	
tcc tgt ata att cca gaa tgt ctt cag aga gcc gtg cat gga ttg ctt	378
Ser Cys Ile Ile Pro Glu Cys Leu Gln Arg Ala Val His Gly Leu Leu	
15 20 25	
cat tac ctt ttc cat acg aga aac cac acc ttc att gtc ctg cac ctg	426
His Tyr Leu Phe His Thr Arg Asn His Thr Phe Ile Val Leu His Leu	
30 35 40	
gtc ttg caa ggg atg gtt tat act gag tac acc tgg gaa gta ttt ggc	474
Val Leu Gln Gly Met Val Tyr Thr Glu Tyr Thr Trp Glu Val Phe Gly	
45 50 55 60	
tac tgt cag gag ctg gag ttg tcc ttg cat tac ctt ctt ctg ccc tat	522
Tyr Cys Gln Glu Leu Glu Leu Ser Leu His Tyr Leu Leu Leu Pro Tyr	
65 70 75	
ctg ctg cta ggt gta aac ctg ttt ttt ttc acc ctg act tgt gga acc	570
Leu Leu Leu Gly Val Asn Leu Phe Phe Phe Thr Leu Thr Cys Gly Thr	
80 85 90	
aat cct ggc att ata aca aaa gca aat gaa tta tta ttt ctt cat gtt	618
Asn Pro Gly Ile Ile Thr Lys Ala Asn Glu Leu Leu Phe Leu His Val	
95 100 105	
tat gaa ttt gat gaa gtg atg ttt cca aag aac gtg agg tgc tct act	666
Tyr Glu Phe Asp Glu Val Met Phe Pro Lys Asn Val Arg Cys Ser Thr	
110 115 120	
tgt gat tta agg aaa cca gct cga tcc aag cac tgc agt gtg tgt aac	714
Cys Asp Leu Arg Lys Pro Ala Arg Ser Lys His Cys Ser Val Cys Asn	
125 130 135 140	
tgg tgt gtg cac cgt ttc gac cat cac tgt gtt tgg gtg aac aac tgc	762
Trp Cys Val His Arg Phe Asp His His Cys Val Trp Val Asn Asn Cys	
145 150 155	
atc ggg gcc tgg aac atc agg tac ttc ctc atc tac gtc ttg acc ttg	810
Ile Gly Ala Trp Asn Ile Arg Tyr Phe Leu Ile Tyr Val Leu Thr Leu	
160 165 170	
acg gcc tgc gct gcc acc gtc gcc att gtg agc acc act ttt ctg gtc	858
Thr Ala Ser Ala Ala Thr Val Ala Ile Val Ser Thr Thr Phe Leu Val	
175 180 185	
cac ttg gtg gtg atg tca gat tta tac cag gag act tac atc gat gac	906
His Leu Val Val Met Ser Asp Leu Tyr Gln Glu Thr Tyr Ile Asp Asp	
190 195 200	
ctt gga cac ctc cat gtt atg gac acg gtc ttt ctt att cag tac ctg	954
Leu Gly His Leu His Val Met Asp Thr Val Phe Leu Ile Gln Tyr Leu	
205 210 215 220	
ttc ctg act ttt cca cgg att gtc ttc atg ctg ggc ttt gtc gtg gtt	1002
Phe Leu Thr Phe Pro Arg Ile Val Phe Met Leu Gly Phe Val Val Val	
225 230 235	
ctg agc ttc ctc ctg ggt ggc tac ctg ttg ttt gtc ctg tat ctg gcg	1050
Leu Ser Phe Leu Leu Gly Gly Tyr Leu Leu Phe Val Leu Tyr Leu Ala	
240 245 250	
gcc acc aac cag act act aac gag tgg tac aga ggt gac tgg gcc tgg	1098
Ala Thr Asn Gln Thr Thr Asn Glu Trp Tyr Arg Gly Asp Trp Ala Trp	
255 260 265	
tgc cag cgt tgt ccc ctt gtg gcc tgg cct ccg tca gca gag ccc caa	1146



Cys	Gln	Arg	Cys	Pro	Leu	Val	Ala	Trp	Pro	Pro	Ser	Ala	Glu	Pro	Gln		
270						275					280						
gtc	cac	cgg	aac	att	cac	tcc	cat	ggg	ctt	cgg	agc	aac	ctt	caa	gag	1194	
Val	His	Arg	Asn	Ile	His	Ser	His	Gly	Leu	Arg	Ser	Asn	Leu	Gln	Glu		
285					290					295					300		
atc	ttt	cta	cct	gcc	ttt	cca	tgt	cat	gag	agg	aag	aaa	caa	gaa		1239	
Ile	Phe	Leu	Pro	Ala	Phe	Pro	Cys	His	Glu	Arg	Lys	Lys	Gln	Glu			
				305					310					315			
tgacaagtgt	atgactgcct	ttgagctgta	gttcccgttt	atttacacat	gtggatcctc											1299	
gttttccaaa	aaaaaaaaaaaa	aaaa														1323	

<210> 37  
 <211> 1945  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 60..1682

<220>  
 <221> sig\_peptide  
 <222> 60..143  
 <223> Von Heijne matrix  
 score 3.75144398608723  
 seq SGLLLQVLFRLIT/FV

<400> 37																	
atcgcgacta	aacggagtg	cggcggcatt	tcctggtgtc	tgagcctggc	gcggaggct											59	
atg ggc agc	cag gag gtg	ctg ggc	cac gcg gcc	cgg ctg tcc	tcc tcc											107	
Met Gly Ser	Gln Glu Val	Leu Gly	His Ala Ala	Arg Leu Ser	Ser Ser												
	-25		-20		-15												
ggt ctc ctc	ctg cag gtg	ttg ttt	cgg ttg atc	acc ttt gtc	ttg aat											155	
Gly Leu Leu	Leu Gln Val	Leu Phe	Arg Leu Ile	Thr Phe Val	Leu Asn												
	-10		-5		1												
gca ttt att	ctt cgc ttc	ctg tca aag	gaa atc gtt	ggc gta gta	aat											203	
Ala Phe Ile	Leu Arg Phe	Leu Ser Lys	Glu Ile Val	Gly Val Val	Asn												
5		10		15	20												
gta aga cta	acg ctg ctt	tac tca acc	acc ctc ttc	ctg gcc aga	gag											251	
Val Arg Leu	Thr Leu Tyr	Ser Thr Thr	Leu Phe Leu	Ala Arg Glu													
	25		30		35												
gcc ttc cgc	aga gca tgt	ctc agt ggg	ggc acc cag	cga gac tgg	agc											299	
Ala Phe Arg	Arg Ala Cys	Leu Ser Gly	Gly Gly Thr	Gln Arg Asp	Trp Ser												
	40		45		50												
cag acc ctc	aac ctg ctg	tgg cta aca	gtc ccc ctg	ggt gtg ttt	tgg											347	
Gln Thr Leu	Asn Leu Leu	Trp Leu Thr	Val Pro Leu	Gly Val Phe	Trp												
	55		60		65												
tcc tta ttc	ctg ggc tgg	atc tgg ttg	cag ctg ctt	gaa gtg cct	gat											395	
Ser Leu Phe	Leu Gly Trp	Ile Trp Leu	Gln Leu Leu	Glu Val Pro	Asp												
	70		75		80												
cct aat gtt	gtc cct cac	tat gca act	gga gtg gtg	ctg ttt ggt	ctc											443	
Pro Asn Val	Val Pro His	Tyr Ala Thr	Gly Val Val	Leu Phe Gly	Leu												
85		90		95	100												
tcg gca gtg	gtg gag ctt	cta gga gag	ccc ttt tgg	gtc ttg gca	caa											491	
Ser Ala Val	Val Glu Leu	Leu Leu Gly	Glu Pro Phe	Trp Val Leu	Ala Gln												
	105		110		115												
gca cat atg	ttt gtg aag	ctc aag gtg	att gca gag	agc ctg tcg	gta											539	
Ala His Met	Phe Val Lys	Leu Lys Val	Ile Ala Glu	Ser Leu Ser	Val												

att	ctt	aag	acc	ggt	ctg	aca	gct	ttt	ctc	gtg	ctg	tgg	ttg	cct	cac	587
Ile	Leu	Lys	Thr	Val	Leu	Thr	Ala	Phe	Leu	Val	Leu	Trp	Leu	Pro	His	
		135					140					145				
tgg	gga	ttg	tac	att	ttc	tct	ttg	gcc	cag	ctt	ttc	tat	acc	aca	ggt	635
Trp	Gly	Leu	Tyr	Ile	Phe	Ser	Leu	Ala	Gln	Leu	Phe	Tyr	Thr	Thr	Val	
	150					155				160						
ctg	gtg	ctc	tgc	tat	ggt	att	tat	ttc	aca	aag	tta	ctg	ggt	tcc	cca	683
Leu	Val	Leu	Cys	Tyr	Val	Ile	Tyr	Phe	Thr	Lys	Leu	Leu	Gly	Ser	Pro	
165					170					175					180	
gaa	tca	acc	aag	ctt	caa	act	ctt	cct	gtc	tcc	aga	ata	aca	gat	ctg	731
Glu	Ser	Thr	Lys	Leu	Gln	Thr	Leu	Pro	Val	Ser	Arg	Ile	Thr	Asp	Leu	
				185					190					195		
tta	ccc	aat	att	aca	aga	aat	gga	gcg	ttt	ata	aac	tgg	aaa	gag	gct	779
Leu	Pro	Asn	Ile	Thr	Arg	Asn	Gly	Ala	Phe	Ile	Asn	Trp	Lys	Glu	Ala	
		200					205						210			
aaa	ctg	act	tgg	agt	ttt	ttc	aaa	cag	tct	ttc	ttg	aaa	cag	att	ttg	827
Lys	Leu	Thr	Trp	Ser	Phe	Phe	Lys	Gln	Ser	Phe	Leu	Lys	Gln	Ile	Leu	
		215					220					225				
aca	gaa	ggc	gag	cga	tat	gtg	atg	aca	ttt	ttg	aat	gta	ttg	aac	ttt	875
Thr	Glu	Gly	Glu	Arg	Tyr	Val	Met	Thr	Phe	Leu	Asn	Val	Leu	Asn	Phe	
	230					235					240					
ggt	gat	cag	ggt	gtg	tat	gat	ata	gtg	aat	aat	ctt	ggc	tcc	ctt	gtg	923
Gly	Asp	Gln	Gly	Val	Tyr	Asp	Ile	Val	Asn	Asn	Leu	Gly	Ser	Leu	Val	
245					250				255						260	
gcc	aga	tta	att	ttc	cag	cca	ata	gag	gaa	agt	ttt	tat	ata	ttt	ttt	971
Ala	Arg	Leu	Ile	Phe	Gln	Pro	Ile	Glu	Glu	Ser	Phe	Tyr	Ile	Phe	Phe	
				265				270						275		
gct	aag	gtg	ctg	gag	agg	gga	aag	gat	gcc	aca	ctt	cag	aag	cag	gag	1019
Ala	Lys	Val	Leu	Glu	Arg	Gly	Lys	Asp	Ala	Thr	Leu	Gln	Lys	Gln	Glu	
		280					285					290				
gac	ggt	gct	gtg	gct	gct	gca	gtc	ttg	gag	tcc	ctg	ctc	aag	ctg	gcc	1067
Asp	Val	Ala	Val	Ala	Ala	Ala	Val	Leu	Glu	Ser	Leu	Leu	Lys	Leu	Ala	
		295				300						305				
ctg	ctg	gcc	ggc	ctg	acc	atc	act	ggt	ttt	ggc	ttt	gcc	tat	tct	cag	1115
Leu	Leu	Ala	Gly	Leu	Thr	Ile	Thr	Val	Phe	Gly	Phe	Ala	Tyr	Ser	Gln	
		310				315				320						
ctg	gct	ctg	gat	atc	tac	gga	ggg	acc	atg	ctt	agc	tca	gga	tcc	ggt	1163
Leu	Ala	Leu	Asp	Ile	Tyr	Gly	Gly	Thr	Met	Leu	Ser	Ser	Gly	Ser	Gly	
325					330					335					340	
cct	ggt	ttg	ctg	cgt	tcc	tac	tgt	ctc	tat	ggt	ctc	ctg	ctt	gcc	atc	1211
Pro	Val	Leu	Leu	Arg	Ser	Tyr	Cys	Leu	Tyr	Val	Leu	Leu	Leu	Ala	Ile	
				345				350						355		
aat	gga	gtg	aca	gag	tgt	ttc	aca	ttt	gct	gcc	atg	agc	aaa	gag	gag	1259
Asn	Gly	Val	Thr	Glu	Cys	Phe	Thr	Phe	Ala	Ala	Met	Ser	Lys	Glu	Glu	
		360					365						370			
gtc	gac	agg	tac	aat	ttt	gtg	atg	ctg	gcc	ctg	tcc	tcc	tca	ttc	ctg	1307
Val	Asp	Arg	Tyr	Asn	Phe	Val	Met	Leu	Ala	Leu	Ser	Ser	Ser	Phe	Leu	
		375				380						385				
gtg	tta	tcc	tat	ctc	ttg	acc	cgt	tgg	tgt	ggc	agc	gtg	ggc	ttc	atc	1355
Val	Leu	Ser	Tyr	Leu	Leu	Thr	Arg	Trp	Cys	Gly	Ser	Val	Gly	Phe	Ile	
		390				395				400						
ttg	gcc	aac	tgc	ttt	aac	atg	ggc	att	cgg	atc	acg	cag	agc	ctt	tgc	1403
Leu	Ala	Asn	Cys	Phe	Asn	Met	Gly	Ile	Arg	Ile	Thr	Gln	Ser	Leu	Cys	
405					410					415					420	
ttc	atc	cac	cgc	tac	cga	agg	agc	ccc	cac	agg	ccc	ctg	gct	ggc		1451
Phe	Ile	His	Arg	Tyr	Tyr	Arg	Arg	Ser	Pro	His	Arg	Pro	Leu	Ala	Gly	
				425				430						435		

```

ctg cac cta tcg cca gtc ctg ctc ggg aca ttt gcc ctc agt ggt ggg      1499
Leu His Leu Ser Pro Val Leu Leu Gly Thr Phe Ala Leu Ser Gly Gly
                                440                445                450
gtt act gct gtt tcg gag gta ttc ctc tgc tgt gag cag ggc tgg cca      1547
Val Thr Ala Val Ser Glu Val Phe Leu Cys Cys Glu Gln Gly Trp Pro
                                455                460                465
gcc aga ctg gca cac att gct gtg ggg gcc ttc tgt ctg gga gca act      1595
Ala Arg Leu Ala His Ile Ala Val Gly Ala Phe Cys Leu Gly Ala Thr
                                470                475                480
ctc ggg aca gca ttc ctc aca gag acc aag ctg atc cat ttc ctc agg      1643
Leu Gly Thr Ala Phe Leu Thr Glu Thr Lys Leu Ile His Phe Leu Arg
                                485                490                495                500
act cag tta ggt gtg ccc aga cgc act gac aaa atg aca tgacttcagg      1692
Thr Gln Leu Gly Val Pro Arg Arg Thr Asp Lys Met Thr
                                505                510
gaagcctgga caccgcaggc acctggacca gctatgggta gttctgtggg tggaacacat      1752
tctgtgtaag agcccaactg agggctctgc agcggagtga cagcaacccc agagatgagg      1812
caccagagag tgccactgca tgagacacct gtgaccattc gaagtctgaa atgcgggggg      1872
ggagtttcat ttttaagtga agaccaaag ccctttaaaa ataatagttt tttatcaaaa      1932
aaaaaaaaaa aaa                                                         1945

<210> 38
<211> 1330
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 198..998

<220>
<221> sig_peptide
<222> 198..269
<223> Von Heijne matrix
      score 9.08017839002281
      seq LLLGPGLLATVRA/EC

<400> 38
agaaatcagc cctttgcaga gggcgagag ggcctggaaa cctctgggac cttttcccag      60
gaactgttta tggtttcccc ctaggcttag gagacgtaga tgcataggtg gattggatac      120
atcgatggta gctataagag tcgtgtctga acccggtttt tccaattggc ctgctccatc      180
cgaacagcgt caactcc atg gcg cgg ttc ctg aca ctt tgc act tgg ctg      230
      Met Ala Arg Phe Leu Thr Leu Cys Thr Trp Leu
                                -20                -15

ctg ttg ctc ggc ccc ggg ctc ctg gcg acc gtg cgg gcc gaa tgc agc      278
Leu Leu Leu Gly Pro Gly Leu Leu Ala Thr Val Arg Ala Glu Cys Ser
                                -10                -5                1

cag gat tgc gcg acg tgc agc tac cgc cta gtg cgc ccg gcc gac atc      326
Gln Asp Cys Ala Thr Cys Ser Tyr Arg Leu Val Arg Pro Ala Asp Ile
                                5                10                15

aac ttc ctg gct tgc gta atg gaa tgt gaa ggt aaa ctg cct tct ctg      374
Asn Phe Leu Ala Cys Val Met Glu Cys Glu Gly Lys Leu Pro Ser Leu
                                20                25                30                35

aaa att tgg gaa acc tgc aag gag ctc ctg cag ctg tcc aaa cca gat      422
Lys Ile Trp Glu Thr Cys Lys Glu Leu Leu Gln Leu Ser Lys Pro Asp
                                40                45                50

ctt cct caa gat ggc acc agc acc ctc aga gaa aat agc aaa ccg gaa      470
Leu Pro Gln Asp Gly Thr Ser Thr Leu Arg Glu Asn Ser Lys Pro Glu

```

	55		60		65		
gaa agc cat ttg cta gcc aaa agg tat ggg ggc ttc atg aaa agg tat							518
Glu Ser His Leu Leu Ala Lys Arg Tyr Gly Gly Phe Met Lys Arg Tyr							
	70		75		80		
gga ggc ttc atg aag aaa atg gat gag ctt tat ccc atg gag cca gaa							566
Gly Gly Phe Met Lys Lys Met Asp Glu Leu Tyr Pro Met Glu Pro Glu							
	85		90		95		
gaa gag gcc aat gga agt gag atc ctc gcc aag cgg tat ggg ggc ttc							614
Glu Glu Ala Asn Gly Ser Glu Ile Leu Ala Lys Arg Tyr Gly Gly Phe							
	100		105		110		115
atg aag aag gat gca gag gag gac gac tcg ctg gcc aat tcc tca gac							662
Met Lys Lys Asp Ala Glu Glu Asp Asp Ser Leu Ala Asn Ser Ser Asp							
	120		125		130		
ctg cta aaa gag ctt ctg gaa aca ggg gac aac cga gag cgt agc cac							710
Leu Leu Lys Glu Leu Leu Glu Thr Gly Asp Asn Arg Glu Arg Ser His							
	135		140		145		
cac cag gat ggc agt gat aat gag gaa gaa gtg agc aag aga tat ggg							758
His Gln Asp Gly Ser Asp Asn Glu Glu Glu Val Ser Lys Arg Tyr Gly							
	150		155		160		
ggc ttc atg aga ggc tta aag aga agc ccc caa ctg gaa gat gaa gcc							806
Gly Phe Met Arg Gly Leu Lys Arg Ser Pro Gln Leu Glu Asp Glu Ala							
	165		170		175		
aaa gag ctg cag aag cga tat ggg ggc ttc atg aga aga gta ggt cgc							854
Lys Glu Leu Gln Lys Arg Tyr Gly Gly Phe Met Arg Arg Val Gly Arg							
	180		185		190		195
cca gag tgg tgg atg gac tac cag aaa cgg tat gga ggt ttc ctg aag							902
Pro Glu Trp Trp Met Asp Tyr Gln Lys Arg Tyr Gly Gly Phe Leu Lys							
	200		205		210		
cgc ttt gcc gag gct ctg ccc tcc gac gaa gaa ggc gaa agt tac tcc							950
Arg Phe Ala Glu Ala Leu Pro Ser Asp Glu Glu Gly Glu Ser Tyr Ser							
	215		220		225		
aaa gaa gtt cct gaa atg gaa aaa aga tac gga gga ttt atg aga ttt							998
Lys Glu Val Pro Glu Met Glu Lys Arg Tyr Gly Gly Phe Met Arg Phe							
	230		235		240		
taatattttt cccactagt gccccaggcc ccagcaagcc tccctccatc ctccagtggg							1058
aaactgttga tgggtgttta ttgtcatgtg ttgcttgccct tgtatagtgt acttcattgt							1118
ctggataact atacaacctg aaaactgtca ttccaggttc tgtgctcttt ttggagtctt							1178
taagctcagt attagtctat tgcagctatc tcgttttcat gctaaaatag tttttgttat							1238
cttgtctctt atttttgaca aacatcaata aatgcttact tgtatataga gataataaac							1298
ctattacccc aagtgcacaaa aaaaaaaaaa aa							1330

<210> 39  
 <211> 2124  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 505..1590

<220>  
 <221> sig\_peptide  
 <222> 505..624  
 <223> Von Heijne matrix  
 score 8.5056444915604  
 seq VVMLMLLTLLVLG/MV

<400> 39

cctggcataa	ctgataggca	tgtatgggag	gaccacattc	ctggggacag	cctgggtatg	60
tgacatggca	ggtgaccagg	ttcccatgaa	tgcccagaggc	tgtgcccatac	ccatgagctg	120
gggcttccct	ggaggtaaag	agctaggggtg	gggtggcagt	gggtagaacc	ccagctggac	180
agctccttcc	ttagctctgt	gattgctaca	gctggttctg	gaagccacag	gcgccctcag	240
gacaaatggg	gcttcttcag	cacagggtag	tgagtgtctga	gctaagcaag	gacactgtcc	300
ccttctctgc	ccaggctcga	gctgtgcacc	tttaccctgg	caattgccct	gggtgctgtc	360
ctgctcctgc	ccttctccat	catcagcaat	gaggtgtctgc	tctccctgcc	tcggaactac	420
tacatccagt	ggctcaacgg	ctccctcatc	catggcctct	ggaaccttgt	ttttctcttc	480
tccaacctgt	ccctcatctt	cctc	atg ccc ttt gca tat ttc ttc act gag			531
		Met Pro Phe Ala Tyr Phe Phe Thr Glu				
		-40		-35		
tct gag ggc ttt gct ggc tcc aga aag ggt gtc ctg ggc cgg gtc tat						579
Ser Glu Gly Phe Ala Gly Ser Arg Lys Gly Val Leu Gly Arg Val Tyr						
-30		-25		-20		
gag aca gtg gtg atg ttg atg ctc ctc act ctg ctg gtg cta ggt atg						627
Glu Thr Val Val Met Leu Met Leu Leu Thr Leu Leu Val Leu Gly Met						
-15		-10		-5		1
gtg tgg gtg gca tca gcc att gtg gac aag aac aag gcc aac aga gag						675
Val Trp Val Ala Ser Ala Ile Val Asp Lys Asn Lys Ala Asn Arg Glu						
5		10		15		
tca ctc tat gac ttt tgg gag tac tat ctc ccc tac ctc tac tca tgc						723
Ser Leu Tyr Asp Phe Trp Glu Tyr Tyr Leu Pro Tyr Leu Tyr Ser Cys						
20		25		30		
atc tcc ttc ctt ggg gtt ctg ctg ctc ctg gtg tgt act cca ctg ggt						771
Ile Ser Phe Leu Gly Val Leu Leu Leu Leu Val Cys Thr Pro Leu Gly						
35		40		45		
ctc gcc cgc atg ttc tcc gtc act ggg aag ctg cta gtc aag ccc cgg						819
Leu Ala Arg Met Phe Ser Val Thr Gly Lys Leu Leu Val Lys Pro Arg						
50		55		60		65
ctg ctg gaa gac ctg gag gag cag ctg tac tgc tca gcc ttt gag gag						867
Leu Leu Glu Asp Leu Glu Glu Gln Leu Tyr Cys Ser Ala Phe Glu Glu						
70		75		80		
gca gcc ctg acc cgc agg atc tgt aat cct act tcc tgc tgg ctg cct						915
Ala Ala Leu Thr Arg Arg Ile Cys Asn Pro Thr Ser Cys Trp Leu Pro						
85		90		95		
tta gac atg gag ctg cta cac aga cag gtc ctg gct ctg cag aca cag						963
Leu Asp Met Glu Leu Leu His Arg Gln Val Leu Ala Leu Gln Thr Gln						
100		105		110		
agg gtc ctg ctg gag aag agg cgg aag gct tca gcc tgg caa cgg aac						1011
Arg Val Leu Leu Glu Lys Arg Arg Lys Ala Ser Ala Trp Gln Arg Asn						
115		120		125		
ctg ggc tac ccc ctg gct atg ctg tgc ttg ctg gtg ctg acg ggc ctg						1059
Leu Gly Tyr Pro Leu Ala Met Leu Cys Leu Leu Val Leu Thr Gly Leu						
130		135		140		145
tct gtg ctc att gtg gcc atc cac atc ctg gag ctg ctc atc gat gag						1107
Ser Val Leu Ile Val Ala Ile His Ile Leu Glu Leu Leu Ile Asp Glu						
150		155		160		
gct gcc atg ccc cga ggc atg cag ggt acc tcc tta ggc cag gtc tcc						1155
Ala Ala Met Pro Arg Gly Met Gln Gly Thr Ser Leu Gly Gln Val Ser						
165		170		175		
ttc tcc aag ctg ggc tcc ttt ggt gcc gtc att cag gtt gta ctc atc						1203
Phe Ser Lys Leu Gly Ser Phe Gly Ala Val Ile Gln Val Val Leu Ile						
180		185		190		
ttt tac cta atg gtg tcc tca gtt gtg ggc ttc tat agc tct cca ctc						1251
Phe Tyr Leu Met Val Ser Ser Val Val Gly Phe Tyr Ser Ser Pro Leu						
195		200		205		
ttc cgg agc ctg cgg ccc aga tgg cac gac act gcc atg acg cag ata						1299
Phe Arg Ser Leu Arg Pro Arg Trp His Asp Thr Ala Met Thr Gln Ile						

```

210          215          220          225
att ggg aac tgt gtc tgt ctc ctg gtc cta agc tca gca ctt cct gtc      1347
Ile Gly Asn Cys Val Cys Leu Leu Val Leu Ser Ser Ala Leu Pro Val
          230          235          240
ttc tct cga acc ctg ggg ctc act cgc ttt gac ctg ctg ggt gac ttt      1395
Phe Ser Arg Thr Leu Gly Leu Thr Arg Phe Asp Leu Leu Gly Asp Phe
          245          250          255
gga cgc ttc aac tgg ctg ggc aat ttc tac att gtg ttc ctc tac aac      1443
Gly Arg Phe Asn Trp Leu Gly Asn Phe Tyr Ile Val Phe Leu Tyr Asn
          260          265          270
gca gcc ttt gca ggc ctc acc aca ctc tat ctg gtg aag acc ttc act      1491
Ala Ala Phe Ala Gly Leu Thr Thr Leu Tyr Leu Val Lys Thr Phe Thr
          275          280          285
gca gct gtg cgg gca gag ctg atc cgg gcc ttt ggg ctg gac aga ctg      1539
Ala Ala Val Arg Ala Glu Leu Ile Arg Ala Phe Gly Leu Asp Arg Leu
290          295          300          305
ccg ctg ccc gtc tcc ggt ttc ccc cag gca tct agg aag acc cag cac      1587
Pro Leu Pro Val Ser Gly Phe Pro Gln Ala Ser Arg Lys Thr Gln His
          310          315          320
cag tgacctccag ctgggggtgg gaagaaaaaa actggacact gccatctgct      1640
Gln
gcctaggcct ggagggaagc ccaaggctac ttggacctca ggacctggaa tctgagaggg      1700
tgggtggcag aggggagcag agccatctgc actattgcat aatctgagcc agagtttggg      1760
accaggacct cctgcttttc cataacttaac tgtggcctca gcatggggta gggctgggtg      1820
actgggtcta gccctgatc ccaaactctgt ttacacatca atctgcctca ctgctgttct      1880
gggccatccc catagccatg tttacatgat ttgatgtgca ataggggtggg gtaggggcag      1940
ggaaaggact gggccagggc aggctcggga gatagattgt ctcccttgcc tctggcccag      2000
cagagcctaa gcaactgtgt atcctggagg ggctttggac cacctgaaag accaagggga      2060
tagggaggag gaggttcag ccatcagcaa taaagttgat cccaggcaaa aaaaaaaaaa      2120
aaaa      2124

```

<210> 40  
 <211> 1159  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 84..326

<220>  
 <221> sig\_peptide  
 <222> 84..146  
 <223> Von Heijne matrix  
 score 6.39000252120129  
 seq LGLSVLLTAATVA/GV

```

<400> 40
agtacaggcg gcggtgcgca ctctgcggcg gcctctgcgc ctcgggcggg cgggagagag      60
aggccgcggc cgccagcgtg ggg atg tct agg agc tcg aag gtg gtg ctg ggc      113
          Met Ser Arg Ser Ser Lys Val Val Leu Gly
          -20          -15
ctc tcg gtg ctg ctg acg gcg gcc aca gtg gcc ggc gta cat gtg aag      161
Leu Ser Val Leu Leu Thr Ala Ala Thr Val Ala Gly Val His Val Lys
          -10          -5          1          5
cag cag tgg gac cag cag agg ctt cgt gac gga gtt atc aga gac att      209
Gln Gln Trp Asp Gln Gln Arg Leu Arg Asp Gly Val Ile Arg Asp Ile
          10          15          20

```

```

gag agg caa att cgg aaa aaa gaa aac att cgt ctt ttg gga gaa cag      257
Glu Arg Gln Ile Arg Lys Lys Glu Asn Ile Arg Leu Leu Gly Glu Gln
      25              30              35
att att ttg act gag caa ctt gaa gca gaa aga gag aag atg tta ttg      305
Ile Ile Leu Thr Glu Gln Leu Glu Ala Glu Arg Glu Lys Met Leu Leu
      40              45              50
gca aaa gga tct caa aaa tca tgacttgaat gtgaaatatc tggtggacag      356
Ala Lys Gly Ser Gln Lys Ser
      55              60
acaacacgag tttgtgtgtg tgtgttgatg gagagtagct tagtagtatac ttcattctttt      416
tttttgggtca ctgtcctttt aaacttgatc aaataaagga cagtgggtca tataagttac      476
tgctttcagg gtcccttata tctgaataaa ggagtgtggg cagacacttt ttggaagagt      536
ctgtctgggt gatcctggta gaagcccatc tagggtcact gtccagtgtc tagggttgtt      596
actgagaagc actgccgagc ttgtgagaag gaagggatgg atagtagcat ccacctgagt      656
agtctgatca gtccgcatga tgacgaagcc acgagaacat cgacctcaga aggactggag      716
gaaggtgaaa gtggaggagg agacgctcct gatcgtcgaa tyccgaggat caggkcatca      776
gtggacttat cgcacgacca gagggtggat tccctcaaca gtgatgaagg agacgtgtct      836
tggtatggagg agcagctgtc ctacttctgt gacaagtgcc aaaaatggat accagccagt      896
aaggagcttc tcaattcctt tgatttgtca attcctgtgt gaaggtttgt ttttccaacc      956
tgtgaaagaa acgtgaatgt aaaagagacc taaataaaaag gataattata tttattctct      1016
agttgatcag ctataaattt atataaaaca taggcattgtt tgtactaatg aaacgtactg      1076
tcaacctcta tcacattgtt aaattaacac ttttgggtgg aactcaataa aattgagaaa      1136
attgcaaaaa aaaaaaaaaa aaa      1159

<210> 41
<211> 1953
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 56..1678

<220>
<221> sig_peptide
<222> 56..139
<223> Von Heijne matrix
      score 3.75144398608723
      seq SGLLLQVLFRLIT/FV

<400> 41
agactaaacg gaggggcggc ggcatttcct ggtgtctgag cctggcgcgagg aggct atg      58
                                     Met
ggc agc cag gag gtg ctg ggc cac gcg gcc cgg ctg gcc tcc tcc ggt      106
Gly Ser Gln Glu Val Leu Gly His Ala Ala Arg Leu Ala Ser Ser Gly
      -25              -20              -15
ctc ctc ctg cag gtg ttg ttt cgg ttg atc acc ttt gtc ttg aat gca      154
Leu Leu Leu Gln Val Leu Phe Arg Leu Ile Thr Phe Val Leu Asn Ala
      -10              -5              1              5
ttt att ctt cgc ttc ctg tca aag gaa atc gtt ggc gta gta aat gta      202
Phe Ile Leu Arg Phe Leu Ser Lys Glu Ile Val Gly Val Val Asn Val
      10              15              20
aga cta acg ctg ctt tac tca acc acc ctc ttc ctg gcc aga gag gcc      250
Arg Leu Thr Leu Leu Tyr Ser Thr Thr Leu Phe Leu Ala Arg Glu Ala
      25              30              35
ttc cgc aga gca tgt ctc agt ggg ggc acc cag cga gac tgg agc cag      298
Phe Arg Arg Ala Cys Leu Ser Gly Gly Thr Gln Arg Asp Trp Ser Gln
      40              45              50

```

acc	ctc	aac	ctg	ctg	tgg	cta	aca	gtc	ccc	ctg	ggt	gtg	ttt	tgg	tcc	346
Thr	Leu	Asn	Leu	Leu	Trp	Leu	Thr	Val	Pro	Leu	Gly	Val	Phe	Trp	Ser	
55						60					65					
tta	ttc	ctg	ggc	tgg	atc	tgg	ttg	cag	ctg	ctt	gaa	gtg	cct	gat	cct	394
Leu	Phe	Leu	Gly	Trp	Ile	Trp	Leu	Gln	Leu	Leu	Glu	Val	Pro	Asp	Pro	
70					75					80					85	
aat	gtt	gtc	cct	cac	tat	gca	act	gga	gtg	gtg	ctg	ttt	ggt	ctc	tcg	442
Asn	Val	Val	Pro	His	Tyr	Ala	Thr	Gly	Val	Val	Leu	Phe	Gly	Leu	Ser	
				90					95					100		
gca	gtg	gtg	gag	ctt	cta	gga	gag	ccc	ttt	tgg	gtc	ttg	gca	caa	gca	490
Ala	Val	Val	Glu	Leu	Leu	Gly	Glu	Pro	Phe	Trp	Val	Leu	Ala	Gln	Ala	
			105					110					115			
cat	atg	ttt	gtg	aag	ctc	aag	gtg	att	gca	gag	agc	ctg	tcg	gta	att	538
His	Met	Phe	Val	Lys	Leu	Lys	Val	Ile	Ala	Glu	Ser	Leu	Ser	Val	Ile	
		120					125					130				
ctt	aag	agc	gtt	ctg	aca	gct	ttt	ctc	gtg	ctg	tgg	ttg	cct	cac	tgg	586
Leu	Lys	Ser	Val	Leu	Thr	Ala	Phe	Leu	Val	Leu	Trp	Leu	Pro	His	Trp	
	135					140					145					
gga	ttg	tac	att	ttc	tct	ttg	gcc	cag	ctt	ttc	tat	acc	aca	gtt	ctg	634
Gly	Leu	Tyr	Ile	Phe	Ser	Leu	Ala	Gln	Leu	Phe	Tyr	Thr	Thr	Val	Leu	
150					155					160					165	
gtg	ctc	tgc	tat	gtt	att	tat	ttc	aca	aag	tta	ctg	ggt	tcc	cca	gaa	682
Val	Leu	Cys	Tyr	Val	Ile	Tyr	Phe	Thr	Lys	Leu	Leu	Gly	Ser	Pro	Glu	
				170					175					180		
tca	acc	aag	ctt	caa	act	ctt	cct	gtc	tcc	aga	ata	aca	gat	ctg	tta	730
Ser	Thr	Lys	Leu	Gln	Thr	Leu	Pro	Val	Ser	Arg	Ile	Thr	Asp	Leu	Leu	
		185					190						195			
ccc	aat	att	aca	aga	aat	gga	gcg	ttt	ata	aac	tgg	aaa	gag	gct	aaa	778
Pro	Asn	Ile	Thr	Arg	Asn	Gly	Ala	Phe	Ile	Asn	Trp	Lys	Glu	Ala	Lys	
	200					205						210				
ctg	act	tgg	agt	ttt	ttc	aaa	cag	tct	ttc	ttg	aaa	cag	att	ttg	aca	826
Leu	Thr	Trp	Ser	Phe	Phe	Lys	Gln	Ser	Phe	Leu	Lys	Gln	Ile	Leu	Thr	
	215					220					225					
gaa	ggc	gag	cga	tat	gtg	atg	aca	ttt	ttg	aat	gta	ttg	aac	ttt	ggt	874
Glu	Gly	Glu	Arg	Tyr	Val	Met	Thr	Phe	Leu	Asn	Val	Leu	Asn	Phe	Gly	
230					235					240					245	
gat	cag	ggt	gtg	tat	gat	ata	gtg	aat	aat	ctt	ggc	tcc	ctt	gtg	gcc	922
Asp	Gln	Gly	Val	Tyr	Asp	Ile	Val	Asn	Leu	Gly	Ser	Leu	Val	Ala		
				250				255						260		
aga	tta	att	ttc	cag	cca	ata	gag	gaa	agt	ttt	tat	ata	ttt	ttt	gct	970
Arg	Leu	Ile	Phe	Gln	Pro	Ile	Glu	Glu	Ser	Phe	Tyr	Ile	Phe	Phe	Ala	
		265					270						275			
aag	gtg	ctg	gag	agg	gga	aag	gat	gcc	aca	ctt	cag	aag	cag	gag	gac	1018
Lys	Val	Leu	Glu	Arg	Gly	Lys	Asp	Ala	Thr	Leu	Gln	Lys	Gln	Glu	Asp	
		280				285						290				
gtt	gct	gtg	gct	gct	gca	gtc	ttg	gag	tcc	ctg	ctc	aag	ctg	gcc	ctg	1066
Val	Ala	Val	Ala	Ala	Ala	Val	Leu	Glu	Ser	Leu	Leu	Lys	Leu	Ala	Leu	
		295				300					305					
ctg	gcc	ggc	ctg	acc	atc	act	gtt	ttt	ggc	ttt	gcc	tat	tct	cag	ctg	1114
Leu	Ala	Gly	Leu	Thr	Ile	Thr	Val	Phe	Gly	Phe	Ala	Tyr	Ser	Gln	Leu	
				315					320					325		
gct	ctg	gat	atc	aac	gga	ggg	acc	atg	ctt	agc	tca	gga	tcc	ggt	cct	1162
Ala	Leu	Asp	Ile	Asn	Gly	Gly	Thr	Met	Leu	Ser	Ser	Gly	Ser	Gly	Pro	
				330				335						340		
gtt	ttg	ctg	cgt	tcc	tac	tgt	ctc	tat	gtt	ctc	ctg	ctt	gcc	atc	aat	1210
Val	Leu	Leu	Arg	Ser	Tyr	Cys	Leu	Tyr	Val	Leu	Leu	Leu	Ala	Ile	Asn	
			345					350					355			
gga	gtg	aca	gag	tgt	ttc	aca	ttt	gct	gcc	atg	agc	aaa	gag	gag	gtc	1258



Gly	Val	Thr	Glu	Cys	Phe	Thr	Phe	Ala	Ala	Met	Ser	Lys	Glu	Glu	Val	
		360					365					370				
gac	agg	tac	aat	ttt	gtg	atg	ctg	gcc	ctg	tcc	tcc	tca	ttc	ctg	gtg	1306
Asp	Arg	Tyr	Asn	Phe	Val	Met	Leu	Ala	Leu	Ser	Ser	Ser	Phe	Leu	Val	
		375					380					385				
tta	tcc	tat	ctc	ttg	acc	cgt	tgg	tgt	ggc	agc	gtg	ggc	ttc	atc	ttg	1354
Leu	Ser	Tyr	Leu	Leu	Thr	Arg	Trp	Cys	Gly	Ser	Val	Gly	Phe	Ile	Leu	
		390				395				400					405	
gcc	aac	tgc	ttt	aac	atg	ggc	att	cgg	atc	acg	cag	agc	ctt	tgc	ttc	1402
Ala	Asn	Cys	Phe	Asn	Met	Gly	Ile	Arg	Ile	Thr	Gln	Ser	Leu	Cys	Phe	
				410					415					420		
atc	cac	cgc	tac	tac	cga	agg	agc	ccc	cac	agg	ccc	ctg	gct	ggc	ctg	1450
Ile	His	Arg	Tyr	Arg	Arg	Ser	Pro	His	Arg	Pro	Leu	Ala	Gly	Leu		
			425					430				435				
cac	cta	tcg	cca	gtc	ctg	ctc	ggg	aca	ttt	gcc	ctc	agt	ggt	ggg	gtt	1498
His	Leu	Ser	Pro	Val	Leu	Leu	Gly	Thr	Phe	Ala	Leu	Ser	Gly	Gly	Val	
		440					445					450				
act	gct	ggt	tcg	gag	gta	ttc	ctc	tgc	tgt	gag	cag	ggc	tgg	cca	gcc	1546
Thr	Ala	Val	Ser	Glu	Val	Phe	Leu	Cys	Cys	Glu	Gln	Gly	Trp	Pro	Ala	
		455				460					465					
aga	ctg	gca	cac	att	gct	gtg	ggg	gcc	ttc	tgt	ctg	gga	gca	act	ctc	1594
Arg	Leu	Ala	His	Ile	Ala	Val	Gly	Ala	Phe	Cys	Leu	Gly	Ala	Thr	Leu	
		470				475				480					485	
ggg	aca	gca	ttc	ctc	aca	gag	acc	aag	ctg	atc	cat	ttc	ctc	agg	act	1642
Gly	Thr	Ala	Phe	Leu	Thr	Glu	Thr	Lys	Leu	Ile	His	Phe	Leu	Arg	Thr	
				490					495					500		
cag	tta	ggt	gtg	ccc	aga	cgc	act	gac	aaa	atg	acg	tgacttcagg				1688
Gln	Leu	Gly	Val	Pro	Arg	Arg	Thr	Asp	Lys	Met	Thr					
			505					510								
gaagcctgga	cacccgagggc	acctggacca	gctatgggta	gttctgtggg	tggaacacat											1748
tctgtgtaag	agccccactg	agggctctgc	agcggagtga	cagcaacccc	agagatgagg											1808
caccagagag	tgccactgca	tgagacacct	gtgaccattc	gaagtctgaa	atgcgggggg											1868
ggagtttcat	ttttaagtga	agaccaaaag	cccttttaaaa	ataatagttt	tttatcattt											1928
tatagtga	aaaaa	aaaaa	aaaaa													1953

<210> 42  
 <211> 1688  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 119..1522

<220>  
 <221> sig\_peptide  
 <222> 119..181  
 <223> Von Heijne matrix  
 score 11.6921972463885  
 seq LLLCLALSGAET/KP

<400>	42															
aaaaggctgc	aggctgccag	gtgtgcttgg	agagccccct	tcttccgccg	ggcctcgcaa											60
gcagcgtagg	actgtggaga	agggcggtgg	gcaaggaggg	aactcgagag	cagcctcc											118
atg ggc aca	cag gag ggc	tgg tgc ctg	ctg ctc tgc	ctg gct cta	tct											166
Met Gly Thr	Gln Glu Gly	Trp Cys Leu	Leu Leu Leu	Cys Leu Ala	Leu Ser											
	-20		-15		-10											
gga gca gca	gaa acc aag	ccc cac cca	gca gag ggg	cag tgg	cgg gca											214

Gly	Ala	Ala	Glu	Thr	Lys	Pro	His	Pro	Ala	Glu	Gly	Gln	Trp	Arg	Ala		
-5					1				5					10			
gtg	gac	gtg	gtc	cta	gac	tgt	ttc	ctg	gtg	aag	gac	ggg	gag	cac	cgt		262
Val	Asp	Val	Val	Leu	Asp	Cys	Phe	Leu	Val	Lys	Asp	Gly	Ala	His	Arg		
			15					20					25				
gga	gct	ctc	gcc	agc	agt	gag	gac	agg	gca	agg	gcc	tcc	ctt	gtg	ctg		310
Gly	Ala	Leu	Ala	Ser	Ser	Glu	Asp	Arg	Ala	Arg	Ala	Ser	Leu	Val	Leu		
		30					35					40					
aag	cag	gtg	cca	gtg	ctg	gac	gat	ggc	tcc	ctg	gag	gac	ttc	acc	gat		358
Lys	Gln	Val	Pro	Val	Leu	Asp	Asp	Gly	Ser	Leu	Glu	Asp	Phe	Thr	Asp		
	45					50					55						
ttc	caa	ggg	ggc	aca	ctg	gcc	caa	gat	gac	cca	cct	att	atc	ttt	gag		406
Phe	Gln	Gly	Gly	Thr	Leu	Ala	Gln	Asp	Asp	Pro	Pro	Ile	Ile	Phe	Glu		
60					65					70					75		
gcc	tca	gtg	gac	ctg	gtc	cag	att	ccc	cag	gcc	gag	gcc	ttg	ctc	cat		454
Ala	Ser	Val	Asp	Leu	Val	Gln	Ile	Pro	Gln	Ala	Glu	Ala	Leu	Leu	His		
				80					85					90			
gct	gac	tgc	agt	ggg	aag	gag	gtg	acc	tgt	gag	atc	tcc	cgc	tac	ttt		502
Ala	Asp	Cys	Ser	Gly	Lys	Glu	Val	Thr	Cys	Glu	Ile	Ser	Arg	Tyr	Phe		
			95					100					105				
ctc	cag	atg	aca	gag	acc	act	gtt	aag	aca	gca	gct	tgg	ttc	atg	gcc		550
Leu	Gln	Met	Thr	Glu	Thr	Thr	Val	Lys	Thr	Ala	Ala	Trp	Phe	Met	Ala		
		110					115					120					
aac	gtg	cag	gtc	tct	gga	ggg	gga	cct	agc	atc	tcc	ttg	gtg	atg	aag		598
Asn	Val	Gln	Val	Ser	Gly	Gly	Gly	Pro	Ser	Ile	Ser	Leu	Val	Met	Lys		
	125					130					135						
act	ccc	agg	gtc	gcc	aag	aat	gag	gtg	ctc	tgg	cac	cca	acg	ctg	aac		646
Thr	Pro	Arg	Val	Ala	Lys	Asn	Glu	Val	Leu	Trp	His	Pro	Thr	Leu	Asn		
140					145					150				155			
ttg	cca	ctg	agc	ccc	cag	ggg	act	gtg	cga	act	gca	gtg	gag	ttc	cag		694
Leu	Pro	Leu	Ser	Pro	Gln	Gly	Thr	Val	Arg	Thr	Ala	Val	Glu	Phe	Gln		
				160					165					170			
gtg	atg	aca	cag	acc	caa	tcc	ctg	agc	ttc	ctg	ctg	ggg	tcc	tca	gcc		742
Val	Met	Thr	Gln	Thr	Gln	Ser	Leu	Ser	Phe	Leu	Leu	Gly	Ser	Ser	Ala		
			175					180					185				
tcc	ttg	gac	tgt	ggc	ttc	tcc	atg	gca	ccg	ggc	ttg	gac	ctc	atc	agt		790
Ser	Leu	Asp	Cys	Gly	Phe	Ser	Met	Ala	Pro	Gly	Leu	Asp	Leu	Ile	Ser		
		190					195					200					
gtg	gag	tgg	cga	ctg	cag	cac	aag	ggc	agg	ggg	cag	ttg	gtg	tac	agc		838
Val	Glu	Trp	Arg	Leu	Gln	His	Lys	Gly	Arg	Gly	Gln	Leu	Val	Tyr	Ser		
	205					210					215						
tgg	acc	gca	ggg	cag	ggg	cag	gct	gtg	cgg	aag	ggc	gct	acc	ctg	gag		886
Trp	Thr	Ala	Gly	Gln	Gly	Gln	Ala	Val	Arg	Lys	Gly	Ala	Thr	Leu	Glu		
220					225				230					235			
cct	gca	caa	ctg	ggc	atg	gcc	agg	gat	gcc	tcc	ctc	acc	ctg	ccc	ggc		934
Pro	Ala	Gln	Leu	Gly	Met	Ala	Arg	Asp	Ala	Ser	Leu	Thr	Leu	Pro	Gly		
				240					245					250			
ctc	act	ata	cag	gac	gag	ggg	acc	tac	att	tgc	cag	atc	acc	acc	tct		982
Leu	Thr	Ile	Gln	Asp	Glu	Gly	Thr	Tyr	Ile	Cys	Gln	Ile	Thr	Thr	Ser		
		255						260					265				
ctg	tac	cga	gct	cag	cag	atc	atc	cag	ctc	aac	atc	caa	gct	tcc	cct		1030
Leu	Tyr	Arg	Ala	Gln	Gln	Ile	Ile	Gln	Leu	Asn	Ile	Gln	Ala	Ser	Pro		
		270				275						280					
aaa	gta	cga	ctg	agc	ttg	gca	aac	gaa	gct	ctg	ctg	ccc	acc	ctc	atc		1078
Lys	Val	Arg	Leu	Ser	Leu	Ala	Asn	Glu	Ala	Leu	Leu	Pro	Thr	Leu	Ile		
	285					290					295						
tgc	gac	att	gct	ggc	tat	tac	cct	ctg	gat	gtg	gtg	gtg	acg	tgg	acc		1126
Cys	Asp	Ile	Ala	Gly	Tyr	Tyr	Pro	Leu	Asp	Val	Val	Val	Thr	Trp	Thr		

```

300          305          310          315
cga gag gag ctg ggt gga tcc cca gcc caa gtc tct ggt gcc tcc ttc 1174
Arg Glu Glu Leu Gly Gly Ser Pro Ala Gln Val Ser Gly Ala Ser Phe
          320          325          330
tcc agc ctg agg caa agc gtg gca ggc acc tac agc atc tcc tcc tct 1222
Ser Ser Leu Arg Gln Ser Val Ala Gly Thr Tyr Ser Ile Ser Ser Ser
          335          340          345
ctc acc gca gaa cct ggc tct gca ggt gcc act tac acc tgc cag gtc 1270
Leu Thr Ala Glu Pro Gly Ser Ala Gly Ala Thr Tyr Thr Cys Gln Val
          350          355          360
aca cac atc tct ctg gag gag ccc ctt ggg gcc agc acc cag gtt gtc 1318
Thr His Ile Ser Leu Glu Glu Pro Leu Gly Ala Ser Thr Gln Val Val
          365          370          375
cca cca gag cgg aga aca gcc ttg gga gtc atc ttt gcc agc agt ctc 1366
Pro Pro Glu Arg Arg Thr Ala Leu Gly Val Ile Phe Ala Ser Ser Leu
380          385          390          395
ttc ctt ctt gca ctg atg ttc ctg ggg ctt cag aga cgg caa gca cct 1414
Phe Leu Leu Ala Leu Met Phe Leu Gly Leu Gln Arg Arg Gln Ala Pro
          400          405          410
aca gga ctt ggg ctg ctt cag gct gaa cgc tgg gag acc act tcc tgt 1462
Thr Gly Leu Gly Leu Leu Gln Ala Glu Arg Trp Glu Thr Thr Ser Cys
          415          420          425
gct gac aca cag agc tcc cat ctc cat gaa gac cgc aca gcg cgt gta 1510
Ala Asp Thr Gln Ser Ser His Leu His Glu Asp Arg Thr Ala Arg Val
          430          435          440
agc cag ccc agc tgacctaaag cgacatgaga ctactagaaa gaaacgacac 1562
Ser Gln Pro Ser
445
ccttccccaa gccccacag ctactccaac ccaaacaaca accaagccag tttaatggta 1622
ggaatttgta ttttttgct ttgttcagaa tacatgacat tggtaaataa aaaaaaaaaa 1682
aaaaaa 1688

```

<210> 43  
 <211> 1942  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 334..1551

<220>  
 <221> sig\_peptide  
 <222> 334..426  
 <223> Von Heijne matrix  
 score 4.0554926521937  
 seq TVFLLVTLQALDT/VE

```

<400> 43
gctcataggg agaaaggaag ctgcgctgcg ttctgcggga cgaaccctgc tccgcgcgag 60
aatttttttg attccttctt atttgagaa atctccagct gctctgatca tagcctaaga 120
agactgcacg ctgcttcctc tcgatgccaa gccagaccct ctcaaacct cggatctcag 180
tccttcacgg agacctgggc ccagcaggaa tggcagtgca ggaaattggc gccagatgg 240
ttcttccatg tgaagttgtc tcgggctctg ggctgacgag agaacacctg gtaaccaggt 300
tagccctctg tcagtcaccc agggcagggc agc atg gtg cgg att cag agg agg 354
Met Val Arg Ile Gln Arg Arg
          -30          -25
aag ctt ttg gca tct tgc ctg tgc gtc aca gcc acc gtc ttt ctg ctt 402

```

Lys	Leu	Leu	Ala	Ser	Cys	Leu	Cys	Val	Thr	Ala	Thr	Val	Phe	Leu	Leu	
				-20					-15					-10		
gtc	aca	ctc	cag	gcc	ttg	gat	acc	gtt	gag	aat	cta	atg	aaa	gtc	acg	450
Val	Thr	Leu	Gln	Ala	Leu	Asp	Thr	Val	Glu	Asn	Leu	Met	Lys	Val	Thr	
			-5					1			5					
ggc	cct	ccc	cag	gga	gtt	aca	gac	tcc	atg	caa	tgc	ttc	aat	gat	cag	498
Gly	Pro	Pro	Gln	Gly	Val	Thr	Asp	Ser	Met	Gln	Cys	Phe	Asn	Asp	Gln	
	10					15				20						
tgg	cct	tta	tct	aac	acc	agg	agc	agc	gag	cac	ata	aaa	gag	gtc	atg	546
Trp	Pro	Leu	Ser	Asn	Thr	Arg	Ser	Ser	Glu	His	Ile	Lys	Glu	Val	Met	
	25				30				35						40	
gtt	gag	ctg	ggg	aag	ttt	gaa	agg	aag	gag	ttt	aaa	agt	tcc	agt	ttg	594
Val	Glu	Leu	Gly	Lys	Phe	Glu	Arg	Lys	Glu	Phe	Lys	Ser	Ser	Ser	Leu	
				45					50					55		
caa	gat	gga	cat	aca	aaa	atg	gag	gaa	gca	cct	acg	cat	ctt	aat	tca	642
Gln	Asp	Gly	His	Thr	Lys	Met	Glu	Glu	Ala	Pro	Thr	His	Leu	Asn	Ser	
			60					65					70			
ttt	ctt	aag	aaa	gaa	gga	ttg	acc	ttc	aac	agg	aaa	aga	aaa	tgg	gaa	690
Phe	Leu	Lys	Lys	Glu	Gly	Leu	Thr	Phe	Asn	Arg	Lys	Arg	Lys	Trp	Glu	
		75				80					85					
ttg	gac	agc	tac	ccc	att	atg	ctc	tgg	tgg	tcc	ccg	ctg	acg	ggg	gag	738
Leu	Asp	Ser	Tyr	Pro	Ile	Met	Leu	Trp	Trp	Ser	Pro	Leu	Thr	Gly	Glu	
	90					95					100					
act	ggg	agg	tta	ggc	caa	tgt	gga	gca	gat	gct	tgt	ttc	ttc	acc	atc	786
Thr	Gly	Arg	Leu	Gly	Gln	Cys	Gly	Ala	Asp	Ala	Cys	Phe	Phe	Thr	Ile	
	105				110					115					120	
aac	cgg	acc	tac	ctc	cat	cat	cac	atg	acc	aaa	gca	ttc	ctc	ttc	tat	834
Asn	Arg	Thr	Tyr	Leu	His	His	His	Met	Thr	Lys	Ala	Phe	Leu	Phe	Tyr	
				125					130					135		
ggt	act	gac	ttt	aac	ata	gat	agc	tta	cct	ctg	cct	cgg	aaa	gcc	cat	882
Gly	Thr	Asp	Phe	Asn	Ile	Asp	Ser	Leu	Pro	Leu	Pro	Arg	Lys	Ala	His	
			140					145					150			
cat	gac	tgg	gct	gtt	ttt	cat	gaa	gag	tcc	ccg	aaa	aac	aat	tat	aag	930
His	Asp	Trp	Ala	Val	Phe	His	Glu	Glu	Ser	Pro	Lys	Asn	Asn	Tyr	Lys	
		155				160						165				
ctc	ttt	cat	aaa	cca	gtg	atc	acc	ttg	ttc	aac	tac	act	gcc	acg	ttc	978
Leu	Phe	His	Lys	Pro	Val	Ile	Thr	Leu	Phe	Asn	Tyr	Thr	Ala	Thr	Phe	
		170				175					180					
agc	agg	cat	tcc	cac	ttg	cca	cta	act	acc	caa	tac	ttg	gag	agc	att	1026
Ser	Arg	His	Ser	His	Leu	Pro	Leu	Thr	Thr	Gln	Tyr	Leu	Glu	Ser	Ile	
	185				190					195					200	
gaa	gtc	ctg	aag	tca	ctc	cga	tac	cta	gtt	cct	ttg	cag	tcc	aaa	aac	1074
Glu	Val	Leu	Lys	Ser	Leu	Arg	Tyr	Leu	Val	Pro	Leu	Gln	Ser	Lys	Asn	
				205					210					215		
aag	ctt	aga	aaa	aga	ctt	gct	ccg	ctg	gtg	tat	gta	cag	tca	tac	tgt	1122
Lys	Leu	Arg	Lys	Arg	Leu	Ala	Pro	Leu	Val	Tyr	Val	Gln	Ser	Tyr	Cys	
			220					225					230			
gac	cca	cca	tca	gac	agg	gac	agc	tat	gtt	cgc	gag	ctg	atg	act	tac	1170
Asp	Pro	Pro	Ser	Asp	Arg	Asp	Ser	Tyr	Val	Arg	Glu	Leu	Met	Thr	Tyr	
		235				240						245				
atc	gag	gtc	gat	tcc	tat	ggt	gaa	tgt	tta	cga	aac	aaa	gac	ctc	cct	1218
Ile	Glu	Val	Asp	Ser	Tyr	Gly	Glu	Cys	Leu	Arg	Asn	Lys	Asp	Leu	Pro	
		250				255					260					
cag	cag	ctg	aaa	aat	cca	gcc	tct	atg	gat	gcc	gat	ggc	ttt	tat	agg	1266
Gln	Gln	Leu	Lys	Asn	Pro	Ala	Ser	Met	Asp	Ala	Asp	Gly	Phe	Tyr	Arg	
		265			270					275					280	
atc	att	gca	cag	tat	aag	ttt	atc	cta	gct	ttt	gag	aat	gca	gtt	tgt	1314
Ile	Ile	Ala	Gln	Tyr	Lys	Phe	Ile	Leu	Ala	Phe	Glu	Asn	Ala	Val	Cys	

																285																	290																	295																																	
gat	gac	tac	atc	act	gag	aag	ttc	tgg	agg	cca	ctg	aaa	ctg	ggg	gta																	1362																																																			
Asp	Asp	Tyr	Ile	Thr	Glu	Lys	Phe	Trp	Arg	Pro	Leu	Lys	Leu	Gly	Val																																																																				
																300																	305																	310																																	
gtc	cct	gta	tat	tac	gga	tcc	ccc	agc	atc	aca	gac	tgg	ctt	cca	agt																	1410																																																			
Val	Pro	Val	Tyr	Tyr	Gly	Ser	Pro	Ser	Ile	Thr	Asp	Trp	Leu	Pro	Ser																																																																				
																315																	320																	325																																	
aac	aaa	agt	gct	att	ctt	gta	tca	gaa	ttt	tct	cac	ccc	agg	gaa	ctg																	1458																																																			
Asn	Lys	Ser	Ala	Ile	Leu	Val	Ser	Glu	Phe	Ser	His	Pro	Arg	Glu	Leu																																																																				
																330																	335																	340																																	
gca	agt	tac	atc	aga	cga	ctg	gat	tct	gat	gac	aga	ttg	tat	gag	gcc																	1506																																																			
Ala	Ser	Tyr	Ile	Arg	Arg	Leu	Asp	Ser	Asp	Asp	Arg	Leu	Tyr	Glu	Ala																																																																				
																345																	350																	355																	360																
tat	gta	gaa	tgg	aag	ctg	aag	ggt	aga	tct	cta	acc	agc	gac	ttc																	1551																																																				
Tyr	Val	Glu	Trp	Lys	Leu	Lys	Gly	Arg	Ser	Leu	Thr	Ser	Asp	Phe																																																																					
																365																	370																	375																																	
tgacagctct	caggggaacgg				aaatgggggag				tgcaagacgt				caaccaggac				aattacatcg																				1611																																														
atgcattttga	gtgtatggtg				tgcaccaagg				tgtgggctaa				tatcaggctt				caggaaaagg																				1671																																														
gcttaccacc	caaaagatgg				gaggcagaag				ataccacact				gagttgccca				gagcccacag																				1731																																														
tgtttgcttt	ctcaccactc				cggactccac				ctttgagctc				tttgcgagag				atgtggattt																				1791																																														
ccagcttttga	acaatcaag				aaagaagccc				aggcactaag				gtggctgggt				gataggaatc																				1851																																														
aaaactttttc	atctcaagag				ttttggggcc				tgattattcaa				ggactgattt				caaaaatgat																				1911																																														
caqaatqaaa	caqaaaaaaa				aaaaaaaaa				a																				1942																																																						

```
<210> 44
<211> 1657
<212> DNA
<213> Homo sapiens
```

```
<220>
<221> CDS
<222> 72..986
```

```
<220>
<221> sig_peptide
<222> 72..149
<223> Von Heijne matrix
score 6.33091407142367
seq GVGLVTLGLAVG/SY
```

[illegible]

Pro	Val	Gly	Lys	His	Ile	Tyr	Leu	Ser	Thr	Arg	Ile	Asp	Gly	Ser	Leu	
			55					60					65			
gtc	atc	agg	cca	tac	act	cct	gtc	acc	agt	gat	gag	gat	caa	ggc	tat	398
Val	Ile	Arg	Pro	Tyr	Thr	Pro	Val	Thr	Ser	Asp	Glu	Asp	Gln	Gly	Tyr	
		70					75					80				
gtg	gat	ctt	gtc	atc	aag	gtc	tac	ctg	aag	ggg	gtg	cac	ccc	aaa	ttt	446
Val	Asp	Leu	Val	Ile	Lys	Val	Tyr	Leu	Lys	Gly	Val	His	Pro	Lys	Phe	
	85					90					95					
cct	gag	gga	ggg	aag	atg	tct	cag	tac	ctg	gat	agc	ctg	aag	ggt	ggg	494
Pro	Glu	Gly	Gly	Lys	Met	Ser	Gln	Tyr	Leu	Asp	Ser	Leu	Lys	Val	Gly	
	100			105						110					115	
gat	gtg	gtg	gag	ttt	cgg	ggg	cca	agc	ggg	ttg	ctc	act	tac	act	gga	542
Asp	Val	Val	Glu	Phe	Arg	Gly	Pro	Ser	Gly	Leu	Leu	Thr	Tyr	Thr	Gly	
				120					125					130		
aaa	ggg	cat	ttt	aac	att	cag	ccc	aac	aag	aaa	tct	cca	cca	gaa	ccc	590
Lys	Gly	His	Phe	Asn	Ile	Gln	Pro	Asn	Lys	Lys	Ser	Pro	Pro	Glu	Pro	
		135						140					145			
cga	gtg	gcg	aag	aaa	ctg	gga	atg	att	gcc	ggc	ggg	aca	gga	atc	acc	638
Arg	Val	Ala	Lys	Lys	Leu	Gly	Met	Ile	Ala	Gly	Gly	Thr	Gly	Ile	Thr	
		150					155					160				
cca	atg	cta	cag	ctg	atc	cgg	gcc	atc	ctg	aaa	gtc	cct	gaa	gat	cca	686
Pro	Met	Leu	Gln	Leu	Ile	Arg	Ala	Ile	Leu	Lys	Val	Pro	Glu	Asp	Pro	
		165				170					175					
acc	cag	tgc	ttt	ctg	ctt	ttt	gcc	aac	cag	aca	gaa	aag	gat	atc	atc	734
Thr	Gln	Cys	Phe	Leu	Leu	Phe	Ala	Asn	Gln	Thr	Glu	Lys	Asp	Ile	Ile	
	180				185				190						195	
ttg	cgg	gag	gac	tta	gag	gaa	ctg	cag	gcc	cgc	tat	ccc	aat	cgc	ttt	782
Leu	Arg	Glu	Asp	Leu	Glu	Glu	Leu	Gln	Ala	Arg	Tyr	Pro	Asn	Arg	Phe	
				200					205					210		
aag	ctc	tgg	ttc	act	ctg	gat	cat	ccc	cca	aaa	gat	tgg	gcc	tac	agc	830
Lys	Leu	Trp	Phe	Thr	Leu	Asp	His	Pro	Pro	Lys	Asp	Trp	Ala	Tyr	Ser	
			215					220					225			
aag	ggc	ttt	gtg	act	gcc	gac	atg	atc	cgg	gaa	cac	ctg	ccc	gct	cca	878
Lys	Gly	Phe	Val	Thr	Ala	Asp	Met	Ile	Arg	Glu	His	Leu	Pro	Ala	Pro	
		230				235						240				
ggg	gat	gat	gtg	ctg	gta	ctg	ctt	tgt	ggg	cca	ccc	cca	atg	gtg	cag	926
Gly	Asp	Asp	Val	Leu	Val	Leu	Leu	Cys	Gly	Pro	Pro	Pro	Met	Val	Gln	
		245				250					255					
ctg	gcc	tgc	cat	ccc	aac	ttg	gac	aaa	ctg	ggc	tac	tca	caa	aag	atg	974
Leu	Ala	Cys	His	Pro	Asn	Leu	Asp	Lys	Leu	Gly	Tyr	Ser	Gln	Lys	Met	
	260				265				270						275	
cga	ttc	acc	tac	tgagc	atcct	ccagcttccc	tggtgctggt	cgctgcagtt								1026
Arg	Phe	Thr	Tyr													
gttccccatc	agtactcaag	cactataagc	cttagattcc	tttcctcaga	gtttcagggt											1086
ttttcagtta	catctagagc	tgaaatctgg	atagtagctg	caggaacaat	attcctgtag											1146
ccatggaaga	gggccaaggc	tcagtcactc	cttgatggc	ctcctaaatc	tccccgtggc											1206
aacagggtcca	ggagaggccc	atggagcagt	ctcttccatg	gagtaagaag	gaaggagca											1266
tgtacgcttg	gtccaagatt	ggctagttcc	ttgatagcat	cttactctca	ccttcttgtg											1326
gtctgtgatg	aaaggaacag	tctgtgcaat	gggttttact	taaacttcac	tgttcaacct											1386
atgagcaaat	ctgtatgtgt	gagtataagt	tgagcatagc	atacttccag	aggtggtctt											1446
atggagatgg	caagaaagga	ggaaatgatt	tcttcagatc	tcaaaggagt	ctgaaatatc											1506
atattttctgt	gtgtgtctct	ctcagcccct	gcccaggcta	gagggaaaca	gctactgata											1566
atcgaaaact	gctgtttgtg	gcaggaaccc	ctggctgtgc	aaataaatgg	ggctgaggcc											1626
cctgtgtgat	attaaaaaaaa	aaaaaaaaaa	a													1657

<210> 45  
 <211> 1733  
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 157..1482

<220>

<221> sig\_peptide

<222> 157..219

<223> Von Heijne matrix

score 11.6921972463885

seq LLLCLALSGAAET/KP

<400> 45

aaagaaaagt	cggcagcaga	gggaacaggg	aagaaaccta	aaggctgcag	gctgccaggt	60
gtgcttggag	agcccccttc	ttccgccggg	cctcgcaagc	agcgtaggac	tgtggagaag	120
ggcgggtgggc	aaggagggaa	ctcgagagca	gcctcc atg	ggc aca cag	gag ggc	174
			Met Gly Thr	Gln Glu Gly		
			-20			
tgg tgc ctg	ctg ctc tgc	ctg gct cta	tct gga gca	gca gaa acc	aag	222
Trp Cys Leu	Leu Leu Cys	Leu Ala Leu	Ser Gly Ala	Ala Glu Thr	Lys	
-15	-10	-5	1			
ccc cac cca	gca gag ggg	cag ttg cgg	gca gtg gac	gtg gtc cta	gac	270
Pro His Pro	Ala Glu Gly	Gln Leu Arg	Ala Val Asp	Val Val Leu	Asp	
	5	10	15			
tgc ttc ctg	gcg aag gac	ggt gcg cac	cgt gga gct	ctc gcc agc	agt	318
Cys Phe Leu	Ala Lys Asp	Gly Ala His	Arg Gly Ala	Leu Ala Ser	Ser	
	20	25	30			
gag gac agg	gca agg gcc	tcc ctt gtg	ctg aag cag	gtg cca gtg	ctg	366
Glu Asp Arg	Ala Arg Ala	Ser Leu Val	Leu Lys Gln	Val Pro Val	Leu	
	35	40	45			
gac gat ggc	tcc ctg gag	gac ttc acc	gat ttc caa	ggg ggc aca	ctg	414
Asp Asp Gly	Ser Leu Glu	Asp Phe Thr	Asp Phe Gln	Gly Gly Thr	Leu	
	50	55	60		65	
gcc caa gat	gac cca cct	att atc ttt	gag gcc tca	gtg gac ctg	gtc	462
Ala Gln Asp	Asp Pro Pro	Ile Ile Phe	Glu Ala Ser	Val Asp Leu	Val	
	70	75	80			
cag att ccc	cag gcc gag	gcc ttg ctc	cat gct gac	tgc agt ggg	aag	510
Gln Ile Pro	Gln Ala Glu	Ala Leu His	Ala Asp Cys	Ser Gly Lys		
	85	90	95			
gag gtg acc	tgt gag atc	tcc cgc tac	ttt ctc cag	atg aca gag	acc	558
Glu Val Thr	Cys Glu Ile	Ser Arg Tyr	Phe Leu Gln	Met Thr Glu	Thr	
	100	105	110			
act gtt aag	aca gca gct	tgg ttc atg	gcc aac atg	cag gtc tct	gga	606
Thr Val Lys	Thr Ala Ala	Trp Phe Met	Ala Asn Met	Gln Val Ser	Gly	
	115	120	125			
ggg gga cst	agc atc tcc	ttg gtg atg	aag act ccc	agg gtc acc	aag	654
Gly Gly Xaa	Ser Ile Ser	Leu Val Met	Lys Thr Pro	Arg Val Thr	Lys	
	130	135	140		145	
aat gag gcg	ctc tgg cac	ccg acg ctg	aac ttg cca	ctg agc ccc	cag	702
Asn Glu Ala	Leu Trp His	Pro Thr Leu	Asn Leu Pro	Leu Ser Pro	Gln	
	150	155	160			
ggg act gtg	cga act gca	gtg gag ttc	cag gtg atg	aca cag acc	caa	750
Gly Thr Val	Arg Thr Ala	Val Glu Phe	Gln Val Met	Thr Gln Thr	Gln	
	165	170	175			
tcc ctg agc	ttc ctg ctg	ggg tcc tca	gcc tcc ttg	gac tgt ggc	ttc	798
Ser Leu Ser	Phe Leu Leu	Gly Ser Ser	Ala Ser Leu	Asp Cys Gly	Phe	
	180	185	190			

tcc atg gca ccg ggc ttg gac ctc atc agt gtg gag tgg cga ctg cag	846
Ser Met Ala Pro Gly Leu Asp Leu Ile Ser Val Glu Trp Arg Leu Gln	
195 200 205	
cac aag ggc agg ggt cag ttg gtg tac agc tgg acc gca ggg cag ggg	894
His Lys Gly Arg Gly Gln Leu Val Tyr Ser Trp Thr Ala Gly Gln Gly	
210 215 220 225	
cag gct gtg cgg aag ggc gct acc ctg gag cct gca caa ctg ggc atg	942
Gln Ala Val Arg Lys Gly Ala Thr Leu Glu Pro Ala Gln Leu Gly Met	
230 235 240	
gcc agg gat gcc tcc ctc acc ctg ccc ggc ctc act ata cag gac gag	990
Ala Arg Asp Ala Ser Leu Thr Leu Pro Gly Leu Thr Ile Gln Asp Glu	
245 250 255	
ggg acc tac att tgc cag atc acc acc tct ctg tac cga gct cag cag	1038
Gly Thr Tyr Ile Cys Gln Ile Thr Thr Ser Leu Tyr Arg Ala Gln Gln	
260 265 270	
atc atc cag ctc aac atc caa gct tcc cct aaa gta cga ctg agc ttg	1086
Ile Ile Gln Leu Asn Ile Gln Ala Ser Pro Lys Val Arg Leu Ser Leu	
275 280 285	
gca aac gaa gct ctg ctg ccc acc ctc atc tgc gac att gct ggc tat	1134
Ala Asn Glu Ala Leu Leu Pro Thr Leu Ile Cys Asp Ile Ala Gly Tyr	
290 295 300 305	
tac cct ctg gat gtg gtg gtg acg tgg acc cga gag gag ctg ggt gga	1182
Tyr Pro Leu Asp Val Val Val Thr Trp Thr Arg Glu Glu Leu Gly Gly	
310 315 320	
tcc cca gcc caa gtc tct ggt gcc tcc ttc tcc agc ctc agg caa agc	1230
Ser Pro Ala Gln Val Ser Gly Ala Ser Phe Ser Ser Leu Arg Gln Ser	
325 330 335	
gtg gca ggc acc tac agc atc tcc tcc tct ctc acc gca gaa cct ggc	1278
Val Ala Gly Thr Tyr Ser Ile Ser Ser Ser Leu Thr Ala Glu Pro Gly	
340 345 350	
tct gca ggt gcc act tac acc tgc cag gtc aca cac atc tct ctg gag	1326
Ser Ala Gly Ala Thr Tyr Thr Cys Gln Val Thr His Ile Ser Leu Glu	
355 360 365	
gag ccc ctt ggg gcc agc acc cag gtt gtc cca cca gag cgg aga aca	1374
Glu Pro Leu Gly Ala Ser Thr Gln Val Val Pro Pro Glu Arg Arg Thr	
370 375 380 385	
gcc ttg gga gtc atc ttt gcc agc agt ctc ttc ctt ctt gca ctg atg	1422
Ala Leu Gly Val Ile Phe Ala Ser Ser Leu Phe Leu Leu Ala Leu Met	
390 395 400	
ttc ctg ggg ctt cag aga cgg caa gca cct aca gga ctt ggg ctg ctt	1470
Phe Leu Gly Leu Gln Arg Arg Gln Ala Pro Thr Gly Leu Gly Leu Leu	
405 410 415	
cag gct gaa cgc taggagacca cttcctgtgc tgacacacag agctcccatc	1522
Gln Ala Glu Arg	
420	
tccatgaaga ccgcacagcg cgtgtaagcc agcccagctg acctaaagcg acatgagact	1582
actagaaaga aacgacacccc ttccccaagc ccccacagct actccaaccc aaacaacaac	1642
caagccagtt taatggtagg aatttgatt ttttgcttt gttcagaata catgacattg	1702
gtaaatatgc cacaaaaaaaa aaaaaaaaaa a	1733

<210> 46  
 <211> 1871  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 195..1052



```

<220>
<221> sig_peptide
<222> 195..338
<223> Von Heijne matrix
      score 3.50178852790004
      seq LGVFFVCHQLSSS/LN

<400> 46
agtgactgcc gggagtcctg cagggggcggg gcggcgccaa gcgcagggag cccggctgag      60
tggcagccca gattgaagat ggatacgtga caatcccagg gaccgctgca ctgacttcat      120
ttccttagac aagacacagt gtagggcccg gcccggtgtg gcccaggac tcctttggaa      180
tatagctgtg gaca atg aat cct gcg agc gat ggg ggc aca tca gag agc      230
              Met Asn Pro Ala Ser Asp Gly Gly Thr Ser Glu Ser
              -45              -40

att ttt gac ctg gac tat gca tcc tgg ggg atc cgc tcc acg ctg atg      278
Ile Phe Asp Leu Asp Tyr Ala Ser Trp Gly Ile Arg Ser Thr Leu Met
      -35              -30              -25

gtc gct ggc ttt gtc ttc tac ttg ggc gtc ttt gtg gtc tgc cac cag      326
Val Ala Gly Phe Val Phe Tyr Leu Gly Val Phe Val Val Cys His Gln
      -20              -15              -10              -5

ctg tcc tct tcc ctg aat gcc act tac cgt tct ttg gtg gcc aga gag      374
Leu Ser Ser Ser Leu Asn Ala Thr Tyr Arg Ser Leu Val Ala Arg Glu
              1              5              10

aag gtc ttc tgg gac ctg gcg gcc acg cgt gca gtc ttt ggt gtt cag      422
Lys Val Phe Trp Asp Leu Ala Ala Thr Arg Ala Val Phe Gly Val Gln
              15              20              25

agc aca gcc gca ggc ctg tgg gct ctg ctg ggg gac cct gtg ctg cat      470
Ser Thr Ala Ala Gly Leu Trp Ala Leu Leu Gly Asp Pro Val Leu His
              30              35              40

gcc gac aag gcg cgt ggc cag cag aac tgg tgc tgg ttt cac atc acg      518
Ala Asp Lys Ala Arg Gly Gln Gln Asn Trp Cys Trp Phe His Ile Thr
      45              50              55              60

aca gca acg gga ttc ttt tgc ttt gaa aat gtt gca gtc cac ctg tcc      566
Thr Ala Thr Gly Phe Phe Cys Phe Glu Asn Val Ala Val His Leu Ser
              65              70              75

aac ttg atc ttc cgg aca ttt gac ttg ttt ctg gtt atc cac cat ctc      614
Asn Leu Ile Phe Arg Thr Phe Asp Leu Phe Leu Val Ile His His Leu
              80              85              90

ttt gcc ttt ctt ggg ttt ctt ggc tgc ttg gtc aat ctc caa gct ggc      662
Phe Ala Phe Leu Gly Phe Leu Gly Cys Leu Val Asn Leu Gln Ala Gly
              95              100              105

cac tat cta gct atg acc acg ttg ctc ctg gag atg agc acg ccc ttt      710
His Tyr Leu Ala Met Thr Thr Leu Leu Leu Glu Met Ser Thr Pro Phe
              110              115              120

acc tgc gtt tcc tgg atg ctc tta aag gcg ggc tgg tcc gag tct ctg      758
Thr Cys Val Ser Trp Met Leu Leu Lys Ala Gly Trp Ser Glu Ser Leu
      125              130              135              140

ttt tgg aag ctc aac cag tgg ctg atg att cac atg ttt cac tgc cgc      806
Phe Trp Lys Leu Asn Gln Trp Leu Met Ile His Met Phe His Cys Arg
              145              150              155

atg gtt cta acc tac cac atg tgg tgg gtg tgt ttc tgg cac tgg gac      854
Met Val Leu Thr Tyr His Met Trp Trp Val Cys Phe Trp His Trp Asp
              160              165              170

ggc ctg gtc agc agc ctg tat ctg cct cat ttg aca ctg ttc ctt gtc      902
Gly Leu Val Ser Ser Leu Tyr Leu Pro His Leu Thr Leu Phe Leu Val
              175              180              185

gga ctg gct ctg ctt acg cta atc att aat cca tat tgg acc cat aag      950

```

```

Gly Leu Ala Leu Leu Thr Leu Ile Ile Asn Pro Tyr Trp Thr His Lys
190 195 200
aag act cag cag ctt ctc aat ccg gtg gac tgg aac ttc gca cag cca 998
Lys Thr Gln Gln Leu Leu Asn Pro Val Asp Trp Asn Phe Ala Gln Pro
205 210 215 220
gaa gcc aag agc agg cca gaa ggc aac ggg cag ctg ctg cgg aag aag 1046
Glu Ala Lys Ser Arg Pro Glu Gly Asn Gly Gln Leu Leu Arg Lys Lys
225 230 235
agg cca tagctgctcc agccgggggct ccgggggcggc agcagagctg gcacaccgat 1102
Arg Pro
tctgggaagc cccgcgaatg atggctttttg aattaatgag gcagtgaatg ttttgtgttt 1162
acttctaagg gaaatactaa ctttctttcg cattagtatt aattttgaag tagctacaaa 1222
gtattttttaa gaaattataa ttttatgact gtctggcagg ctctgtcagt ttagccgcgc 1282
cggaccgtgt caagcatcta ggagaggagt ccatgggtgtc caggcatcgg ggcgtcacac 1342
ctgttgagga gtgggggtggc tttgaatgct ggaaatggct tcatagttaa gtgcctccca 1402
cagggcggggt gggtcagcgt tgactctttc cagctgcaca ctcatatgcc gtgtgtctta 1462
ttcagaagtc acattctttt cagttggaga gaattgggct aagatagaaa ataacatgat 1522
ttgttcctta ttaaagtttc ccagcgtatg aaattctaag ctgggtggggg tggctcacac 1582
ccgacgtaat cccagcacgt tgggaggccg aggcagggtg atcacttgag gccaggagtt 1642
cgagaccagc ctggtcaaga tggtgaaacc ccattctctac taaaattaca aaaattagcc 1702
gggtgtcgtg gcacacacct gtaatcccag ctatttgga ggccaaggca ggagaattgc 1762
ctgaacccgg gaggcggagg ttgcagttag ctgagatcgc accactgcac tccagcactc 1822
cagcctgggt gacggagcaa cactctctcg caaaaaaaaa aaaaaaaaaa 1871

<210> 47
<211> 1523
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 217..1410

<220>
<221> sig_peptide
<222> 217..279
<223> Von Heijne matrix
score 5.8172934575094
seq ALLWAQEVGQVLA/GR

<400> 47
acttccccgg gagccggaag tcccgtctca cggttgccct ggcagcgcgc gaggctgggtg 60
agtcggcagc cctgtggcag ccggcgggct ggtttccatg gttgcacgat taggaaccac 120
cagctgctgc atcccatggc caggggtggc gtccagggtg cagagcagct aggaacgcaa 180
ggcctgaacc tggggccaga caccctctc cgggcc atg gtc aac gac cct cca 234
Met Val Asn Asp Pro Pro
-20
gta cct gcc tta ctg tgg gcc cag gag gtg ggc caa gtc ttg gca ggc 282
Val Pro Ala Leu Leu Trp Ala Gln Glu Val Gly Gln Val Leu Ala Gly
-15 -10 -5 1
cgt gcc cgc agg ctg ctg ctg cag ttt ggg gtg ctc ttc tgc acc atc 330
Arg Ala Arg Arg Leu Leu Leu Gln Phe Gly Val Leu Phe Cys Thr Ile
5 10 15
ctc ctt ttg ctc tgg gtg tct gtc ttc ctc tat ggc tcc ttc tac tat 378
Leu Leu Leu Leu Trp Val Ser Val Phe Leu Tyr Gly Ser Phe Tyr Tyr
20 25 30
tcc tat atg ccg aca gtc agc cac ctc agc cct gtg cat ttc tac tac 426
Ser Tyr Met Pro Thr Val Ser His Leu Ser Pro Val His Phe Tyr Tyr

```

35	agg	acc	gac	tgt	gat	tcc	tcc	acc	acc	tca	ctc	tgc	tcc	ttc	cct	gtt	474
Arg	Thr	Asp	Cys	Asp	Ser	Ser	Thr	Thr	Ser	Leu	Cys	Ser	Phe	Pro	Val		
50					55					60					65		
gcc	aat	gtc	tcg	ctg	act	aag	ggg	gga	cgt	gat	cgg	gtg	ctg	atg	tat	522	
Ala	Asn	Val	Ser	Leu	Thr	Lys	Gly	Gly	Arg	Asp	Arg	Val	Leu	Met	Tyr		
				70					75					80			
gga	cag	ccg	tat	cgt	gtt	acc	tta	gag	ctt	gag	ctg	cca	gag	tcc	cct	570	
Gly	Gln	Pro	Tyr	Arg	Val	Thr	Leu	Glu	Leu	Glu	Leu	Pro	Glu	Ser	Pro		
			85					90					95				
gtg	aat	caa	gat	ttg	ggc	atg	ttc	ttg	gtc	acc	att	tcc	tgc	tac	acc	618	
Val	Asn	Gln	Asp	Leu	Gly	Met	Phe	Leu	Val	Thr	Ile	Ser	Cys	Tyr	Thr		
			100				105						110				
aga	ggg	ggc	cga	atc	atc	tcc	act	tct	tcg	cgt	tcg	gtg	atg	ctg	cat	666	
Arg	Gly	Gly	Arg	Ile	Ile	Ser	Thr	Ser	Ser	Arg	Ser	Val	Met	Leu	His		
			115			120							125				
tac	cgc	tca	gac	ctg	ctc	cag	atg	ctg	gac	aca	ctg	gtc	ttc	tct	agc	714	
Tyr	Arg	Ser	Asp	Leu	Leu	Gln	Met	Leu	Asp	Thr	Leu	Val	Phe	Ser	Ser		
				130		135				140					145		
ctc	ctg	cta	ttt	ggc	ttt	gca	gag	cag	aag	cag	ctg	ctg	gag	gtg	gaa	762	
Leu	Leu	Leu	Phe	Gly	Phe	Ala	Glu	Gln	Lys	Gln	Leu	Leu	Glu	Val	Glu		
				150					155					160			
ctc	tac	gca	gac	tat	aga	gag	aac	tcg	tac	gtg	ccg	acc	act	gga	gcg	810	
Leu	Tyr	Ala	Asp	Tyr	Arg	Glu	Asn	Ser	Tyr	Val	Pro	Thr	Thr	Gly	Ala		
			165					170					175				
atc	att	gag	atc	cac	agc	aag	cgc	atc	cag	ctg	tat	gga	gcc	tac	ctc	858	
Ile	Ile	Glu	Ile	His	Ser	Lys	Arg	Ile	Gln	Leu	Tyr	Gly	Ala	Tyr	Leu		
			180				185						190				
cgc	atc	cac	gcg	cac	ttc	act	ggg	ctc	aga	tac	ctg	cta	tac	aac	ttc	906	
Arg	Ile	His	Ala	His	Phe	Thr	Gly	Leu	Arg	Tyr	Leu	Leu	Tyr	Asn	Phe		
			195			200						205					
ccg	atg	acc	tgc	gcc	ttc	ata	ggg	gtt	gcc	agc	aac	ttc	acc	ttc	ctc	954	
Pro	Met	Thr	Cys	Ala	Phe	Ile	Gly	Val	Ala	Ser	Asn	Phe	Thr	Phe	Leu		
				210		215				220					225		
agc	gtc	atc	gtg	ctc	ttc	agc	tac	atg	cag	tgg	gtg	tgg	ggg	ggc	atc	1002	
Ser	Val	Ile	Val	Leu	Phe	Ser	Tyr	Met	Gln	Trp	Val	Trp	Gly	Gly	Ile		
				230					235					240			
tgg	ccc	cga	cac	cgc	ttc	tct	ttg	cag	gtt	aac	atc	cga	aaa	aga	gac	1050	
Trp	Pro	Arg	His	Arg	Phe	Ser	Leu	Gln	Val	Asn	Ile	Arg	Lys	Arg	Asp		
			245					250					255				
aat	tcc	cgg	aag	gaa	gtc	caa	cga	agg	atc	tct	gct	cat	cag	cca	ggg	1098	
Asn	Ser	Arg	Lys	Glu	Val	Gln	Arg	Arg	Ile	Ser	Ala	His	Gln	Pro	Gly		
			260				265						270				
cct	gaa	ggc	cag	gag	gag	tca	act	ccg	caa	tca	gat	gtt	aca	gag	gat	1146	
Pro	Glu	Gly	Gln	Glu	Glu	Ser	Thr	Pro	Gln	Ser	Asp	Val	Thr	Glu	Asp		
			275			280					285						
ggg	gag	agc	cct	gaa	gat	ccc	tca	ggg	aca	gag	ggg	cag	ctg	tcc	gag	1194	
Gly	Glu	Ser	Pro	Glu	Asp	Pro	Ser	Gly	Thr	Glu	Gly	Gln	Leu	Ser	Glu		
			290			295				300					305		
gag	gag	aaa	cca	gat	cag	cag	ccc	ctg	agc	gga	gaa	gag	gag	cta	gag	1242	
Glu	Glu	Lys	Pro	Asp	Gln	Gln	Pro	Leu	Ser	Gly	Glu	Glu	Glu	Leu	Glu		
			310						315					320			
cct	gag	gcc	agt	gat	ggg	tca	ggc	tcc	tgg	gaa	gat	gca	gct	ttg	ctg	1290	
Pro	Glu	Ala	Ser	Asp	Gly	Ser	Gly	Ser	Trp	Glu	Asp	Ala	Ala	Leu	Leu		
			325					330					335				
acg	gag	gcc	aac	ctg	cct	gct	cct	gct	cct	gct	tct	gct	tct	gcc	cct	1338	
Thr	Glu	Ala	Asn	Leu	Pro	Ala	Pro	Ala	Pro	Ala	Ser	Ala	Ser	Ala	Pro		
			340				345						350				



cgatgcccag aatccagaac tttgtctatc actctcccca acaacctaga tgtgaaaaca 792  
gaataaaactt cacccagaaa gcaaaaaaaaa aaaaaaaaaa 832

<210> 49  
<211> 831  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 234..491

<220>  
<221> sig\_peptide  
<222> 234..293  
<223> Von Heijne matrix  
score 4.85037394589162  
seq AVAGLPALGFTGA/GI

<400> 49  
gtttactcgc tgctgtgccc atctatcagc aggctccggg ctgaagattg cttctcttct 60  
ctcctccaag gtctagtac ggagcccgcg cgcggcgcca ccatgcggca gaaggcggtta 120  
tcgcttttct ctgctacctg ctgctcttca cttgcagtgg ggtggaggca ggtaagaaaa 180  
agtgtctgga gagctcggac agcggctccg ggttctggaa ggccctgacc ttc atg 236  
Met  
-20  
gcc gtc gga gga gga ctc gca gtc gcc ggg ctg ccc gcg ctg ggc ttc 284  
Ala Val Gly Gly Gly Leu Ala Val Ala Gly Leu Pro Ala Leu Gly Phe  
-15 -10 -5  
acc ggc gcc ggc atc gcg gcc aac tcg gtg gct gcc tcg ctg atg agc 332  
Thr Gly Ala Gly Ile Ala Ala Asn Ser Val Ala Ala Ser Leu Met Ser  
1 5 10  
tgg tct gcg atc ctg aat ggg ggc ggc gtg ccc gcc ggg ggg cta gtg 380  
Trp Ser Ala Ile Leu Asn Gly Gly Gly Val Pro Ala Gly Gly Leu Val  
15 20 25  
gcc acg ctg cag agc ctc ggg gct ggt ggc agc agc gtc gtc ata ggt 428  
Ala Thr Leu Gln Ser Leu Gly Ala Gly Gly Ser Ser Val Val Ile Gly  
30 35 40 45  
aat att ggt gcc ctg atg ggc tac gcc acc cac aag tat ctc gat agt 476  
Asn Ile Gly Ala Leu Met Gly Tyr Ala Thr His Lys Tyr Leu Asp Ser  
50 55 60  
gag gag gat gag gag tagccagcag ctcccagaac ctcttcttcc ttcttggcct 531  
Glu Glu Asp Glu Glu  
65  
aactcttcca gttaggatct agaactttgc cttttttttt tttttttttt tttttttgag 591  
atgggttctc actatattgt ccaggctaga gtgcagtggc tattcacaga tgcgaacata 651  
gtacactgca gcctccaact cctagcctca agtgatcctc ctgtctcaac ctcccaagta 711  
ggattacaag catgcgccga cgatgcccag aatccagaac tttgtctatc actctcccca 771  
acaacctaga tgtgaaaaca gaataaactt cacccagaaa gcaaaaaaaaa aaaaaaaaaa 831

<210> 50  
<211> 917  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 180..800

```

<220>
<221> sig_peptide
<222> 180..248
<223> Von Heijne matrix
      score 14.6828672385356
      seq ILLLLWLIAPSRA/CT

<400> 50
acccttggt tctgcactga tgggtgggtgg atgagtaatg catccaggaa gcctggaggc      60
ctgtgggttc cgcacccgct gccacccccg cccctagcgt ggacatttat cctctagcgc      120
tcaggccctg ccgccatcgc cgcagatcca gcgccagag agacaccaga gaaccacc      179
atg gcc ccc ttt gag ccc ctg gct tct ggc atc ctg ttg ttg ctg tgg      227
Met Ala Pro Phe Glu Pro Leu Ala Ser Gly Ile Leu Leu Leu Leu Trp
      -20      -15      -10
ctg ata gcc ccc agc agg gcc tgc acc tgt gtc cca ccc cac cca cag      275
Leu Ile Ala Pro Ser Arg Ala Cys Thr Cys Val Pro Pro His Pro Gln
      -5      1      5
acg gcc ttc tgc aat tcc gac ctc gtc atc agg gcc aag ttc gtg ggg      323
Thr Ala Phe Cys Asn Ser Asp Leu Val Ile Arg Ala Lys Phe Val Gly
10      15      20      25
aca cca gaa gtc aac cag acc acc tta tac cag cgt tat gag atc aag      371
Thr Pro Glu Val Asn Gln Thr Thr Leu Tyr Gln Arg Tyr Glu Ile Lys
      30      35      40
atg acc aag atg tat aaa ggg ttc caa gcc tta ggg gat gcc gct gac      419
Met Thr Lys Met Tyr Lys Gly Phe Gln Ala Leu Gly Asp Ala Ala Asp
      45      50      55
atc cgg ttc gtc tac acc ccc gcc atg gag agt gtc tgc gga tac ttc      467
Ile Arg Phe Val Tyr Thr Pro Ala Met Glu Ser Val Cys Gly Tyr Phe
      60      65      70
cac agg tcc cac aac cgc agc gag gag ttt ctc att gct gga aaa ctg      515
His Arg Ser His Asn Arg Ser Glu Glu Phe Leu Ile Ala Gly Lys Leu
      75      80      85
cag gat gga ctc ttg cac atc act acc tgc agt ttt gtg gct ccc tgg      563
Gln Asp Gly Leu Leu His Ile Thr Thr Cys Ser Phe Val Ala Pro Trp
90      95      100      105
aac agc ctg agc tta gct cag cgc cgg ggc ttc acc aag acc tac act      611
Asn Ser Leu Ser Leu Ala Gln Arg Arg Gly Phe Thr Lys Thr Tyr Thr
      110      115      120
gtt ggc tgt gag gaa tgc aca gtg ttt ccc tgt tta tcc ttc ccc tgc      659
Val Gly Cys Glu Glu Cys Thr Val Phe Pro Cys Leu Ser Phe Pro Cys
      125      130      135
aaa ctg cag agt ggc act cat tgc ttg tgg acg gac cag ctc ctc caa      707
Lys Leu Gln Ser Gly Thr His Cys Leu Trp Thr Asp Gln Leu Leu Gln
      140      145      150
ggc tct gaa aag ggc ttc cag tcc cgt cac ctt gcc tgc ctg cct cgg      755
Gly Ser Glu Lys Gly Phe Gln Ser Arg His Leu Ala Cys Leu Pro Arg
      155      160      165
gag cca ggg ctg tgc acc tgg cag tcc ctg cgg tcc cag ata gcc      800
Glu Pro Gly Leu Cys Thr Trp Gln Ser Leu Arg Ser Gln Ile Ala
170      175      180
tgaatcctgc ccggagtgga agctgaagcc tgcacagtgt ccaccctgtt cccactccca      860
tctttcttcc ggacaatgaa ataaagagtt accaccacagc aaaaaaaaaa aaaaaaa      917

<210> 51
<211> 621
<212> DNA
<213> Homo sapiens

```

<220>  
<221> CDS  
<222> 140..472

<220>  
<221> sig\_peptide  
<222> 140..211  
<223> Von Heijne matrix  
score 8.44884907465122  
seq FVVFSLFILICAMA/GD

<400> 51  
atatttttttt catatctgac atttctatgt cctatgacgg tttcacagct atcctacttt 60  
ggagaagatg ctggaaaattc agagtttccg ccagagaata tatgcctgaa ctaaaagagg 120  
aagtggctta taggagaaaa atg aaa tat gat tgt ccc ttc agt ggg aca tca 172  
Met Lys Tyr Asp Cys Pro Phe Ser Gly Thr Ser  
-20 -15  
ttt gtg gtc ttc tct ctc ttt ttg atc tgt gca atg gct gga gat gta 220  
Phe Val Val Phe Ser Leu Phe Leu Ile Cys Ala Met Ala Gly Asp Val  
-10 -5 1  
gtc tac gct gac atc aaa act gtt cgg act tcc ccg tta gaa ctc gcg 268  
Val Tyr Ala Asp Ile Lys Thr Val Arg Thr Ser Pro Leu Glu Leu Ala  
5 10 15  
ttt cca ctt cag aga tct gtt tct ttc aac ttt tct act gtc cat aaa 316  
Phe Pro Leu Gln Arg Ser Val Ser Phe Asn Phe Ser Thr Val His Lys  
20 25 30 35  
tca tgt cct gcc aaa gac tgg aag gtg cat aag gga aaa tgt tac tgg 364  
Ser Cys Pro Ala Lys Asp Trp Lys Val His Lys Gly Lys Cys Tyr Trp  
40 45 50  
att gct gaa act aag aaa tct tgg aac aaa agt caa aat gac tgt gcc 412  
Ile Ala Glu Thr Lys Lys Ser Trp Asn Lys Ser Gln Asn Asp Cys Ala  
55 60 65  
ata aac aat tca tat ctc atg gtg att caa gac att act gct atg gtg 460  
Ile Asn Asn Ser Tyr Leu Met Val Ile Gln Asp Ile Thr Ala Met Val  
70 75 80  
aga ttt aac att tagaggtgac agcatccccc acactggcag ttaatttttt 512  
Arg Phe Asn Ile  
85  
gtctacaaac ttggcaaaaag tctgtgaaaa gaagtttcaa cttcatgtgt tattaactat 572  
acaaatatta gttgaatgaa ttgttgaatt acaaaaaaaaa aaaaaaaaaa 621

<210> 52  
<211> 673  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 68..484

<220>  
<221> sig\_peptide  
<222> 68..112  
<223> Von Heijne matrix  
score 4.93618539864455  
seq AVVFVFSLLDCCA/LI

<400> 52															
ctatcagggg tgggtcgggg catccgagcg ggtttgacgg aaggagcggc ggcgacggag															60
gaggagg atg gag gcg gtg gtg ttc gtc ttc tct ctc ctc gat tgt tgc															109
Met Glu Ala Val Val Phe Val Phe Ser Leu Leu Asp Cys Cys															
-15 -10 -5															
gcg ctc atc ttc ctc tcg gtc tac ttc ata att aca ttg tct gat tta															157
Ala Leu Ile Phe Leu Ser Val Tyr Phe Ile Ile Thr Leu Ser Asp Leu															
1 5 10 15															
gaa tgt gat tac att aat gct aga tca tgt tgc tca aaa tta aac aag															205
Glu Cys Asp Tyr Ile Asn Ala Arg Ser Cys Cys Ser Lys Leu Asn Lys															
20 25 30															
tgg gta att cca gaa ttg att ggc cat acc att gtc act gta tta ctg															253
Trp Val Ile Pro Glu Leu Ile Gly His Thr Ile Val Thr Val Leu Leu															
35 40 45															
ctc atg tca ttg cac tgg ttc atc ttc ctt ctc aac tta cct gtt gcc															301
Leu Met Ser Leu His Trp Phe Ile Phe Leu Leu Asn Leu Pro Val Ala															
50 55 60															
act tgg aat ata tat cga tac att atg gtg ccg agt ggt aac atg gga															349
Thr Trp Asn Ile Tyr Arg Tyr Ile Met Val Pro Ser Gly Asn Met Gly															
65 70 75															
gtg ttt gat cca aca gaa ata cac aat cga ggg cag ctg aag tca cac															397
Val Phe Asp Pro Thr Glu Ile His Asn Arg Gly Gln Leu Lys Ser His															
80 85 90 95															
atg aaa gaa gcc atg atc aag ctt ggt ttc cac ttg ctc tgc ttc ttc															445
Met Lys Glu Ala Met Ile Lys Leu Gly Phe His Leu Leu Cys Phe Phe															
100 105 110															
atg tat ctt tat agt atg atc tta gct ttg ata aat gac tgaagctgga															494
Met Tyr Leu Tyr Ser Met Ile Leu Ala Leu Ile Asn Asp															
115 120															
gaagccgtgg ttgaagtcag cctacactac agtgcacagt tgaggagcca gagacttctt															554
aaatcatcct tagaaccgtg accatagcag tatatatattt cctcttgga caaaaaacta															614
tttttgctgt atttttacca tataaaqtat ttaaaaaaca cqaaaaaaaa aaaaaaaaaa															673

```
<210> 53
<211> 897
<212> DNA
<213> Homo sapiens
```

```
<220>  
<221> CDS  
<222> 38..517
```

```
<220>
<221> sig_peptide
<222> 38..118
<223> Von Heijne matrix
score 7.20400999800742
seq VLWLSGLSEPGAA/RQ
```

```

<400> 53
agattggggac agtcgccagg gatggctgag cgtgaag atg cag cgg gtg tcc ggg      55
                                     Met Gln Arg Val Ser Gly
                                     -25
ctg ctc tcc tgg acg ctg agc aga gtc ctg tgg ctc tcc ggc ctc tct      103
Leu Leu Ser Trp Thr Leu Ser Arg Val Leu Trp Leu Ser Gly Leu Ser
-20                               -15                               -10
gag ccg gga gct gcc cgg cag ccc cgg atc atg gaa gag aaa gcg cta      151
Glu Pro Gly Ala Ala Arg Gln Pro Arg Ile Met Glu Glu Lys Ala Leu

```



```

-5          1          5          10
gag gtt tat gat ttg att aga act atc cgg gac cca gaa aag ccc aat      199
Glu Val Tyr Asp Leu Ile Arg Thr Ile Arg Asp Pro Glu Lys Pro Asn
          15          20          25
act tta gaa gaa ctg gaa gtg gtc tcg gaa agt tgt gtg gaa gtt cag      247
Thr Leu Glu Glu Leu Glu Val Val Ser Glu Ser Cys Val Glu Val Gln
          30          35          40
gag ata aat gaa gaa gaa tat ctg gtt att atc agg ttc acg cca aca      295
Glu Ile Asn Glu Glu Glu Tyr Leu Val Ile Ile Arg Phe Thr Pro Thr
          45          50          55
gta cct cat tgc tct ttg gcg act ctt att ggg ctg tgc tta aga gta      343
Val Pro His Cys Ser Leu Ala Thr Leu Ile Gly Leu Cys Leu Arg Val
          60          65          70          75
aaa ctt cag cga tgt tta cca ttt aaa cat aag ttg gaa atc tac att      391
Lys Leu Gln Arg Cys Leu Pro Phe Lys His Lys Leu Glu Ile Tyr Ile
          80          85          90
tct gaa gga acc cac tca aca gaa gaa gac atc aat aag cag ata aat      439
Ser Glu Gly Thr His Ser Thr Glu Glu Asp Ile Asn Lys Gln Ile Asn
          95          100          105
gac aaa gag cga gtg gca gct gca atg gaa aac ccc aac tta cgg gaa      487
Asp Lys Glu Arg Val Ala Ala Ala Met Glu Asn Pro Asn Leu Arg Glu
          110          115          120
att gtg gaa cag tgt gtc ctt gaa cct gac tgatagctgt tttaagagcc      537
Ile Val Glu Gln Cys Val Leu Glu Pro Asp
          125          130
actggcctgt aattgtttga tatatttgta actctttgta taatgtcaga gactcatgtt      597
taatacatag gtgatttgta cctcagagca ttttttaaag gattctttcc aagcgagatt      657
taattataag gtagtaccta atttgttcaa tgtataacat tctcaggatt tgtaacactt      717
aaatgatcag acagaataat attttctagt tattatgtgt aagatgagtt gctatttttc      777
tgatgctcat tctgatacaa ctatttttcg tgtcaaatat ctactgtgcc caaatgtact      837
caatttaaatt cattactctg taaaataaat aagcagatga ttcttataaa aaaaaaaaaa      897

<210> 54
<211> 1101
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 92..634

<220>
<221> sig_peptide
<222> 92..139
<223> Von Heijne matrix
      score 7.36306712986597
      seq FLLLTCLFITGTS/VS

<400> 54
cttaaaaaaaaa aaagtgcttg aaagagaagg ggacaaagga acaccagtat taagaggatt      60
ttccagtgtt tctggcagtt ggtccagaag g atg cct cca ttc ctg ctt ctc      112
                               Met Pro Pro Phe Leu Leu Leu
                               -15                               -10
acc tgc ctc ttc atc aca ggc acc tcc gtg tca ccc gtg gcc cta gat      160
Thr Cys Leu Phe Ile Thr Gly Thr Ser Val Ser Pro Val Ala Leu Asp
          -5          1          5
cct tgt tct gct tac atc agc ctg aat gag ccc tgg agg aac act gac      208
Pro Cys Ser Ala Tyr Ile Ser Leu Asn Glu Pro Trp Arg Asn Thr Asp

```

[illegible]

```
<210> 55
<211> 1047
<212> DNA
<213> Homo sapiens
```

```
<220>  
<221> CDS  
<222> 27..767
```

```
<220>
<221> sig_peptide
<222> 27..80
<223> Von Heijne matrix
      score 8.96664802487992
      seq LFCLAVLAASSFS/KA
```

```

<400> 55
agcagaggcc ctacaccac cgaggc atg ggg ctc cct ggg ctg ttc tgc ttg      53
                               Met Gly Leu Pro Gly Leu Phe Cys Leu
                               -15                               -10
qcc qtg ctg gct gcc agc agc ttc tcc aag gca cgg gag gaa gaa att      101

```

Ala	Val	Leu	Ala	Ala	Ser	Ser	Phe	Ser	Lys	Ala	Arg	Glu	Glu	Glu	Ile	
				-5					1				5			
acc	cct	gtg	gtc	tcc	att	gcc	tac	aaa	gtc	ctg	gaa	gtt	ttc	ccc	aaa	149
Thr	Pro	Val	Val	Ser	Ile	Ala	Tyr	Lys	Val	Leu	Glu	Val	Phe	Pro	Lys	
		10					15					20				
ggc	cgc	tgg	gtg	ctc	ata	acc	tgc	tgt	gca	ccc	cag	cca	cca	ccg	ccc	197
Gly	Arg	Trp	Val	Leu	Ile	Thr	Cys	Cys	Ala	Pro	Gln	Pro	Pro	Pro	Pro	
	25					30					35					
atc	acc	tat	tcc	ctc	tgt	gga	acc	aag	aac	atc	aag	gtg	gcc	aag	aag	245
Ile	Thr	Tyr	Ser	Leu	Cys	Gly	Thr	Lys	Asn	Ile	Lys	Val	Ala	Lys	Lys	
	40				45					50					55	
gtg	gtg	aag	acc	cac	gag	ccg	gcc	tcc	ttc	aac	ctc	aac	gtc	aca	ctc	293
Val	Val	Lys	Thr	His	Glu	Pro	Ala	Ser	Phe	Asn	Leu	Asn	Val	Thr	Leu	
				60					65					70		
aag	tcc	agt	cca	gac	ctg	ctc	acc	tac	ttc	tgc	cgg	gcg	tcc	tcc	acc	341
Lys	Ser	Ser	Pro	Asp	Leu	Leu	Thr	Tyr	Phe	Cys	Arg	Ala	Ser	Ser	Thr	
		75						80					85			
tca	ggt	gcc	cat	gtg	gac	agt	gcc	agg	cta	cag	atg	cac	tgg	gag	ctg	389
Ser	Gly	Ala	His	Val	Asp	Ser	Ala	Arg	Leu	Gln	Met	His	Trp	Glu	Leu	
		90					95					100				
tgg	tcc	aag	cca	gtg	tct	gag	ctg	cgg	gcc	aac	ttc	act	ctg	cag	gac	437
Trp	Ser	Lys	Pro	Val	Ser	Glu	Leu	Arg	Ala	Asn	Phe	Thr	Leu	Gln	Asp	
	105					110					115					
aga	ggg	gca	ggc	ccc	agg	gtg	gag	atg	atc	tgc	cag	gcg	tcc	tcg	ggc	485
Arg	Gly	Ala	Gly	Pro	Arg	Val	Glu	Met	Ile	Cys	Gln	Ala	Ser	Ser	Gly	
	120				125					130					135	
agc	cca	cct	atc	acc	aac	agc	ctg	atc	ggg	aag	gat	ggg	cag	gtc	cac	533
Ser	Pro	Pro	Ile	Thr	Asn	Ser	Leu	Ile	Gly	Lys	Asp	Gly	Gln	Val	His	
				140					145					150		
ctg	cag	cag	aga	cca	tgc	cac	agg	cag	cct	gcc	aac	ttc	tcc	ttc	ctg	581
Leu	Gln	Gln	Arg	Pro	Cys	His	Arg	Gln	Pro	Ala	Asn	Phe	Ser	Phe	Leu	
			155					160					165			
ccg	agc	cag	aca	tcg	gac	tgg	ttc	tgg	tgc	cag	gct	gca	aac	aac	gcc	629
Pro	Ser	Gln	Thr	Ser	Asp	Trp	Phe	Trp	Cys	Gln	Ala	Ala	Asn	Asn	Ala	
		170					175					180				
aat	gtc	cag	cac	agc	gcc	ctc	aca	gtg	gtg	ccc	cca	gga	ggg	ttg	ccc	677
Asn	Val	Gln	His	Ser	Ala	Leu	Thr	Val	Val	Pro	Pro	Gly	Gly	Leu	Pro	
	185					190					195					
agg	gca	ccc	acc	atc	gtg	ctg	gtt	ggc	agc	ctt	gcc	tcc	act	gcg	gcc	725
Arg	Ala	Pro	Thr	Ile	Val	Leu	Val	Gly	Ser	Leu	Ala	Ser	Thr	Ala	Ala	
	200				205					210					215	
atc	acc	tcc	agg	atg	ctg	ggc	tgg	acc	acg	tgg	gcc	agg	tgg			767
Ile	Thr	Ser	Arg	Met	Leu	Gly	Trp	Thr	Trp	Trp	Ala	Arg	Trp			
				220					225							
tgaccagaag	atggaggact	ggcaggggtcc	cctggagagc	cccatccttg	ccttgccgct											827
ctacaggagc	acccgccgtc	tgagtgaaga	ggagtttggg	gggttcagga	tagggaatgg											887
ggaggtcaga	ggacgcaaag	cagcagccat	gtagaatgaa	ccgtccagag	agccaagcac											947
ggcagaggac	tcgaggccat	cagcgtgcac	tgcttcgtatt	tgaggttcat	gcaaaatgag											1007
tgtgttttag	ctgctcttgc	cacaaaaaaaa	aaaaaaaaaaa													1047

<210> 56  
 <211> 925  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 4..399

```

<220>
<221> sig_peptide
<222> 4..126
<223> Von Heijne matrix
      score 4.34454795165846
      seq RVVSWLFSIVVFG/SI

<400> 56
acg atg gaa ggg ggt gcg tac gga gcg ggc aaa gcc ggg ggc gcc ttc      48
  Met Glu Gly Gly Ala Tyr Gly Ala Gly Lys Ala Gly Gly Ala Phe
      -40                      -35                      -30

gac ccc tac acc ctg gtc cgg cag ccg cac acc atc ctg cgc gtc gtg      96
Asp Pro Tyr Thr Leu Val Arg Gln Pro His Thr Ile Leu Arg Val Val
      -25                      -20                      -15

tct tgg ctg ttc tcc ata gtg gtg ttc ggc tcc atc gtg aac gag ggc      144
Ser Trp Leu Phe Ser Ile Val Val Phe Gly Ser Ile Val Asn Glu Gly
      -10                      -5                      1                      5

tac ctc aac agc gcc tcc gag ggg gag cag ttc tgc atc tac aac cgc      192
Tyr Leu Asn Ser Ala Ser Glu Gly Glu Gln Phe Cys Ile Tyr Asn Arg
      10                      15                      20

aac ccc aac gcc tgc agc tat ggc gtg gcc gtg ggc gtg ctc gcc ttc      240
Asn Pro Asn Ala Cys Ser Tyr Gly Val Ala Val Gly Val Leu Ala Phe
      25                      30                      35

ctc acc tgc ctg ctg tac ctg gcc ctg gac gtg tac ttc ccg cag atc      288
Leu Thr Cys Leu Leu Tyr Leu Ala Leu Asp Val Tyr Phe Pro Gln Ile
      40                      45                      50

agc agc gtc aag gac cgc aag aaa gcc gtc ctg tcc gac atc ggt gtc      336
Ser Ser Val Lys Asp Arg Lys Lys Ala Val Leu Ser Asp Ile Gly Val
      55                      60                      65                      70

tcg ggt gag ccc cac cca gca ggt acc ccc tgc aca gag tct aca gag      384
Ser Gly Glu Pro His Pro Ala Gly Thr Pro Cys Thr Glu Ser Thr Glu
      75                      80                      85

ggc tgt ccc ggg cca taggaggcgg ctgccaccct tcttcccatg tttcagatga      439
Gly Cys Pro Gly Pro
      90

gggaaatgag ccttctgggc tttcctctgg ttcgtgggat tctgctacct ggccaaccag      499
tggcaggtct ccaagcccaa ggacaaccca ctgaacgaag ggacggacgc agcccgggcc      559
gccatcgccct tctccttttt ctccatcttc acctggagcc tgaccgcagc cctggccgtg      619
cggagattca aggacctaa cttccaggag gactacagca cactgttccc tgcttcggca      679
cagccgtagg cctccccggc ttgcagaggc cggcagccct gtatcacccc tggcagttag      739
gtggcaggag cagcctagt ccagaaatgt ccaagatgcc agggcatgca gggcagtgga      799
aggctggctt gaggaaccaa ttcaggttct ccactgactc attcattcct tcaccgcctc      859
cttcattgat tcttcattgcg ttcattcatt cagtaaacad ttattgagta aaaaaaaaaa      919
aaaaaa                                           925

<210> 57
<211> 1240
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 127..879

<220>
<221> sig_peptide
<222> 127..198

```

<223> Von Heijne matrix  
score 5.38660866264012  
seq ALCSVCSMSVLRA/YP

<400> 57

```

agtctaggat cctcacacca gctacttgca agggagaagg aaaaggccag taaggcctgg      60
gccaggagag tcccgacagg agtgtcaggt ttcaatctca gcaccagcca ctcagagcag      120
ggcacg atg ttg ggg gcc cgc ctc agg ctc tgg gtc tgt gcc ttg tgc      168
      Met Leu Gly Ala Arg Leu Arg Leu Trp Val Cys Ala Leu Cys
                    -20                    -15
agc gtc tgc agc atg agc gtc ctc aga gcc tat ccc aat gcc tcc cca      216
Ser Val Cys Ser Met Ser Val Leu Arg Ala Tyr Pro Asn Ala Ser Pro
-10                    -5                    1                    5
ctg ctc ggc tcc agc tgg ggt ggc ctg atc cac ctg tac aca gcc aca      264
Leu Leu Gly Ser Ser Trp Gly Gly Leu Ile His Leu Tyr Thr Ala Thr
      10                    15                    20
gcc agg aac agc tac cac ctg cag atc cac aag aat ggc cat gtg gat      312
Ala Arg Asn Ser Tyr His Leu Gln Ile His Lys Asn Gly His Val Asp
      25                    30                    35
ggc gca ccc cat cag acc atc tac agt gcc ctg atg atc aga tca gag      360
Gly Ala Pro His Gln Thr Ile Tyr Ser Ala Leu Met Ile Arg Ser Glu
      40                    45                    50
gat gct ggc ttt gtg gtg att aca ggt gtg atg agc aga aga tac ctc      408
Asp Ala Gly Phe Val Val Ile Thr Gly Val Met Ser Arg Arg Tyr Leu
      55                    60                    65                    70
tgc atg gat ttc aga ggc aac att ttt gga tca cac tat ttc gac ccg      456
Cys Met Asp Phe Arg Gly Asn Ile Phe Gly Ser His Tyr Phe Asp Pro
      75                    80                    85
gag aac tgc agg ttc caa cac cag acg ctg gaa aac ggg tac gac gtc      504
Glu Asn Cys Arg Phe Gln His Gln Thr Leu Glu Asn Gly Tyr Asp Val
      90                    95                    100
tac cac tct cct cag tat cac ttc ctg gtc agt ctg ggc cgg gcg aag      552
Tyr His Ser Pro Gln Tyr His Phe Leu Val Ser Leu Gly Arg Ala Lys
      105                    110                    115
aga gcc ttc ctg cca ggc atg aac cca ccc ccg tac tcc cag ttc ctg      600
Arg Ala Phe Leu Pro Gly Met Asn Pro Pro Pro Tyr Ser Gln Phe Leu
      120                    125                    130
tcc cgg agg aac gag atc ccc cta att cac ttc aac acc ccc ata cca      648
Ser Arg Arg Asn Glu Ile Pro Leu Ile His Phe Asn Thr Pro Ile Pro
      135                    140                    145                    150
cgg cgg cac acc cgg agc gcc gag gac gac tcg gag cgg gac ccc ctg      696
Arg Arg His Thr Arg Ser Ala Glu Asp Asp Ser Glu Arg Asp Pro Leu
      155                    160                    165
aac gtg ctg aag ccc cgg gcc cgg atg acc ccg gcc ccg gcc tcc tgt      744
Asn Val Leu Lys Pro Arg Ala Arg Met Thr Pro Ala Pro Ala Ser Cys
      170                    175                    180
tca cag gag ctc ccg agc gcc gag gac aac agc ccg atg gcc agt gac      792
Ser Gln Glu Leu Pro Ser Ala Glu Asp Asn Ser Pro Met Ala Ser Asp
      185                    190                    195
cca tta ggg gtg gtc agg ggc ggt cga gtg aac acg cac gct ggg gga      840
Pro Leu Gly Val Val Arg Gly Gly Arg Val Asn Thr His Ala Gly Gly
      200                    205                    210
acg ggc ccg gaa ggc tgc cgc ccc ttc gcc aag ttc atc tagggctcgct      889
Thr Gly Pro Glu Gly Cys Arg Pro Phe Ala Lys Phe Ile
      215                    220                    225
ggaagggcac cctctttaac ccatccctca gcaaacgcag ctcttcccaa ggaccaggtc      949
ccttgacggtt ccgaggatgg gaaaggtgac aggggcatgt atggaatttg ctgcttctct      1009
gggggtccctt ccacaggagg tcctgtgaga accaaccttt gagggccaag tcatgggggtt      1069

```

```
tcaccgcctt cctcactcca tatagaacac ctttcccaat aggaaacccc aacaggtaaa 1129
ctagaaattt ccccttcatg aaggtagaga gaaggggtct ctcccaacat atttctcttc 1189
cttgtgcctc tcctctttat cacttttaag catgaaaaaa aaaaaaaaaa a 1240
```

<210> 58  
 <211> 902  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 156..566

<220>  
 <221> sig\_peptide  
 <222> 156..221  
 <223> Von Heijne matrix  
 score 5.67458379966095  
 seq LVSMAGRVCLCQG/SA

```
<400> 58
atttcccagc gtgcctcagg aagggcgcca ggactgcatt ttgctccgga gcgtccagag 60
tcctggccct gagcgggaat cgcagtggcc gaggctgagc ggcaggcgga tcgccccgac 120
cctcactcct ggcgtctgag tctctggcgt agccc atg ctg agt ggg cgg ctg 173
                                Met Leu Ser Gly Arg Leu
                                -20
gtc ctg ggt ctg gtc tcc atg gct ggc cgc gtt tgt ttg tgc cag ggc 221
Val Leu Gly Leu Val Ser Met Ala Gly Arg Val Cys Leu Cys Gln Gly
-15 -10 -5
agc gcg gga tcc ggg gcc atc ggt ccg gtg gag gcc gcc att cgc acg 269
Ser Ala Gly Ser Gly Ala Ile Gly Pro Val Glu Ala Ala Ile Arg Thr
1 5 10 15
aag ttg gag gag gcc ctg agc ccc gag gtg cta gag ctt cgc aac gag 317
Lys Leu Glu Glu Ala Leu Ser Pro Glu Val Leu Glu Leu Arg Asn Glu
20 25 30
agc ggt ggc cac gcg gtc ccg cca ggc agt gag act cac ttc cgc gtg 365
Ser Gly Gly His Ala Val Pro Pro Gly Ser Glu Thr His Phe Arg Val
35 40 45
gct gtg gtg agc tct cgt ttc gag gga ctg agc ccc cta caa cga cac 413
Ala Val Val Ser Ser Arg Phe Glu Gly Leu Ser Pro Leu Gln Arg His
50 55 60
cgg ctg gtc cac gca gcg ctg gcc gag gag ctg gga ggt ccg gtc cat 461
Arg Leu Val His Ala Ala Leu Ala Glu Glu Leu Gly Gly Pro Val His
65 70 75 80
gcg ctg gcc atc cag gca cgg acc ccc gcc cag tgg aga gag aac tct 509
Ala Leu Ala Ile Gln Ala Arg Thr Pro Ala Gln Trp Arg Glu Asn Ser
85 90 95
cag ctg gac act agc ccc cca tgc ctg ggt ggg aac aag aaa act cta 557
Gln Leu Asp Thr Ser Pro Pro Cys Leu Gly Gly Asn Lys Lys Thr Leu
100 105 110
gga acc ccc tgaaccccaa gagagggagg accaggatcc gaatgggctg 606
Gly Thr Pro
115
ggtagagcacg aattaccgag gccttccctt tgatacagtc caggatttgt aagggatgaa 666
gacccttggg cccattctg ttgggggtcca tacatactct ccgaagatag caacttgctt 726
cagggtcaaag tgaacccgag aaaagagaag aatcactcac tactgtctctt gccctggact 786
attcaggaag ggcagcccg atgttccatg ttaaactcgtg acagaattgc accagacctg 846
atgagttgga aacaatccta tacatataaa gaaattacac taaaaaaaaa aaaaaa 902
```

[illegible]

```
<220>
<221> sig_peptide
<222> 35..118
<223> Von Heijne matrix
score 3.75144398608723
seq SGLLLQVLFRLLIT/FV
```

75

Tyr	Phe	Thr	Lys	Leu	Leu	Gly	Ser	Pro	Glu	Ser	Thr	Lys	Leu	Gln	Thr	
			175					180					185			
ctt	cct	gtc	tcc	aga	ata	aca	gat	ctg	tta	ccc	aat	att	aca	aga	aat	727
Leu	Pro	Val	Ser	Arg	Ile	Thr	Asp	Leu	Leu	Pro	Asn	Ile	Thr	Arg	Asn	
			190				195					200				
gga	gcg	ttt	ata	aac	tgg	aaa	gag	gct	aaa	ctg	act	tgg	agt	ttt	ttc	775
Gly	Ala	Phe	Ile	Asn	Trp	Lys	Glu	Ala	Lys	Leu	Thr	Trp	Ser	Phe	Phe	
			205				210				215					
aaa	cag	tct	ttc	ttg	aaa	cag	att	ttg	aca	gaa	ggc	gag	cga	tat	gtg	823
Lys	Gln	Ser	Phe	Leu	Lys	Gln	Ile	Leu	Thr	Glu	Gly	Glu	Arg	Tyr	Val	
					225					230					235	
atg	aca	ttt	ttg	aat	gta	ttg	aac	ttt	ggt	gat	cag	ggt	gtg	tat	gat	871
Met	Thr	Phe	Leu	Asn	Val	Leu	Asn	Phe	Gly	Asp	Gln	Gly	Val	Tyr	Asp	
				240					245					250		
ata	gtg	aat	aat	ctt	ggc	tcc	ctt	gtg	gcc	aga	tta	att	ttc	cag	cca	919
Ile	Val	Asn	Asn	Leu	Gly	Ser	Leu	Val	Ala	Arg	Leu	Ile	Phe	Gln	Pro	
				255				260					265			
ata	gag	gaa	agt	ttt	tat	ata	ttt	ttt	gct	aag	gtg	ctg	gag	agg	gga	967
Ile	Glu	Glu	Ser	Phe	Tyr	Ile	Phe	Phe	Ala	Lys	Val	Leu	Glu	Arg	Gly	
			270				275					280				
aag	gat	gcc	aca	ctt	cag	aag	cag	gag	gac	ggt	gct	gtg	gct	gct	gca	1015
Lys	Asp	Ala	Thr	Leu	Gln	Lys	Gln	Glu	Asp	Val	Ala	Val	Ala	Ala	Ala	
			285			290					295					
gtc	ttg	gag	tcc	ctg	ctc	aag	ctg	gcc	ctg	ctg	gcc	ggc	ctg	acc	atc	1063
Val	Leu	Glu	Ser	Leu	Leu	Lys	Leu	Ala	Leu	Leu	Ala	Gly	Leu	Thr	Ile	
					305					310					315	
act	ggt	ttt	ggc	ttt	gcc	tat	tct	cag	ctg	gct	ctg	gat	atc	tac	gga	1111
Thr	Val	Phe	Gly	Phe	Ala	Tyr	Ser	Gln	Leu	Ala	Leu	Asp	Ile	Tyr	Gly	
				320				325						330		
ggg	acc	atg	ctt	agc	tca	gga	tcc	ggt	cct	ggt	ttg	ctg	cgt	tcc	tac	1159
Gly	Thr	Met	Leu	Ser	Ser	Gly	Ser	Gly	Pro	Val	Leu	Leu	Arg	Ser	Tyr	
			335					340					345			
tgt	ctc	tat	ggt	ctc	ctg	ctt	gcc	atc	aat	gga	gtg	aca	gag	tgt	tta	1207
Cys	Leu	Tyr	Val	Leu	Leu	Leu	Ala	Ile	Asn	Gly	Val	Thr	Glu	Cys	Leu	
			350				355					360				
aca	ttt	gct	gcc	atg	agc	aaa	gag	gag	gtc	gac	agg	tac	aat	ttt	gtg	1255
Thr	Phe	Ala	Ala	Met	Ser	Lys	Glu	Glu	Val	Asp	Arg	Tyr	Asn	Phe	Val	
			365			370					375					
atg	ctg	gcc	ctg	tcc	tcc	ctc	ttc	ctg	gtg	tta	tcc	tat	ctc	ttg	acc	1303
Met	Leu	Ala	Leu	Ser	Ser	Ser	Phe	Leu	Val	Leu	Ser	Tyr	Leu	Leu	Thr	
					385					390					395	
cgt	tgg	tgt	ggc	agc	gtg	ggc	ttc	atc	ttg	gcc	aac	tgc	ttt	aac	atg	1351
Arg	Trp	Cys	Gly	Ser	Val	Gly	Phe	Ile	Leu	Ala	Asn	Cys	Phe	Asn	Met	
				400				405						410		
ggc	att	cgg	atc	acg	cag	agc	ctt	tgc	ttc	atc	cac	cgc	tac	tac	cga	1399
Gly	Ile	Arg	Ile	Thr	Gln	Ser	Leu	Cys	Phe	Ile	His	Arg	Tyr	Tyr	Arg	
			415					420					425			
agg	agc	ccc	cac	agg	ccc	ctg	gct	ggc	ctg	cac	cta	tcg	cca	gtc	ctg	1447
Arg	Ser	Pro	His	Arg	Pro	Leu	Ala	Gly	Leu	His	Leu	Ser	Pro	Val	Leu	
			430				435					440				
ctc	ggg	aca	ttt	gcc	ctc	agt	ggt	ggg	ggt	act	gct	ggt	tcg	gag	gta	1495
Leu	Gly	Thr	Phe	Ala	Leu	Ser	Gly	Gly	Val	Thr	Ala	Val	Ser	Glu	Val	
			445			450					455					
ttc	ctc	tgc	tgt	gat	cag	ggc	tgg	cca	gcc	aga	ctg	gca	cac	att	gct	1543
Phe	Leu	Cys	Cys	Asp	Gln	Gly	Trp	Pro	Ala	Arg	Leu	Ala	His	Ile	Ala	
			460		465					470					475	
gtg	ggg	gcc	ttc	tgt	ctg	gga	gca	act	ctc	ggg	aca	gca	ttc	ctc	aca	1591
Val	Gly	Ala	Phe	Cys	Leu	Gly	Ala	Thr	Leu	Gly	Thr	Ala	Phe	Leu	Thr	



09876997.060801

```

                                480                                485                                490
gag acc aag ctg atc cat ttc ctc agg act cag tta ggt gtg ccc aga      1639
Glu Thr Lys Leu Ile His Phe Leu Arg Thr Gln Leu Gly Val Pro Arg
                                495                                500                                505
cgc act gac aaa atg aca tgacttcagg gaagcctgga cacccgaggc      1687
Arg Thr Asp Lys Met Thr
                                510
acctggacca gctatgggta gttctgtggg tggaacacat tctgtgtaag agccccactg      1747
agggctctgc agcggagtga cagcaacccc agagatgagg caccagagag tgccactgca      1807
tgagacacct gtgaccattc gaagtctgaa atgcgggggg ggagtttcat ttttaagtga      1867
agaccaaag ccctttaaaa ataatagttt tttatcattt tatagtaatc agcattttct      1927
cttttactaa tatactcatt ctttttgaaa aaaaaaaaaa aa      1969

<210> 60
<211> 1132
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 77..937

<220>
<221> sig_peptide
<222> 77..127
<223> Von Heijne matrix
      score 3.74817238048175
      seq RIVSAALLAFVQT/HL

<400> 60
gttgggtgggg ctgggggatg agagctgcac cgcgcggggac aagtcgccgg cgccccgacg      60
gagcagaaga gagagc atg gag ctg gag agg atc gtc agt gca gcc ctc ctt      112
      Met Glu Leu Glu Arg Ile Val Ser Ala Ala Leu Leu
                                -15                                -10

gcc ttt gtc cag aca cac ctc ccg gag gcc gac ctc agt ggc ttg gat      160
Ala Phe Val Gln Thr His Leu Pro Glu Ala Asp Leu Ser Gly Leu Asp
-5                                1                                5                                10
gag gtc atc ttc tcc tat gtg ctt ggg gtc ctg gag gac ctg ggc ccc      208
Glu Val Ile Phe Ser Tyr Val Leu Gly Val Leu Glu Asp Leu Gly Pro
      15                                20                                25

tcg ggc cca tca gag gag aac ttc gat atg gag gct ttc act gag atg      256
Ser Gly Pro Ser Glu Glu Asn Phe Asp Met Glu Ala Phe Thr Glu Met
      30                                35                                40

atg gag gcc tat gtg cct ggc ttc gcc cac atc ccc agg ggc aca ata      304
Met Glu Ala Tyr Val Pro Gly Phe Ala His Ile Pro Arg Gly Thr Ile
      45                                50                                55

ggg gac atg atg cag aag ctc tca ggg cag ctg agc gat gcc agg aac      352
Gly Asp Met Met Gln Lys Leu Ser Gly Gln Leu Ser Asp Ala Arg Asn
      60                                65                                70                                75

aaa gag aac ctg caa ccg cag agc tct ggt gtc caa ggt cag gtg ccc      400
Lys Glu Asn Leu Gln Pro Gln Ser Ser Gly Val Gln Gly Gln Val Pro
      80                                85                                90

atc tcc cca gag ccc ctg cag cgg ccc gaa atg ctc aaa gaa gag act      448
Ile Ser Pro Glu Pro Leu Gln Arg Pro Glu Met Leu Lys Glu Glu Thr
      95                                100                                105

agg tct tcg gct gct gct gct gca gac acc caa gat gag gca act ggc      496
Arg Ser Ser Ala Ala Ala Ala Asp Thr Gln Asp Glu Ala Thr Gly
      110                                115                                120

```

```

gct gag gag gag ctt ctg cca ggg gtg gat gta ctc ctg gag gtg ttc      544
Ala Glu Glu Glu Leu Leu Pro Gly Val Asp Val Leu Leu Glu Val Phe
      125                      130                      135
cct acc tgt tgc gtg gag cag gcc cag tgg gtg ctg gcc aaa gct cgg      592
Pro Thr Cys Ser Val Glu Gln Ala Gln Trp Val Leu Ala Lys Ala Arg
      140                      145                      150                      155
ggg gac ttg gaa gaa gct gtg cag atg ctg gta gag gga aag gaa gag      640
Gly Asp Leu Glu Glu Ala Val Gln Met Leu Val Glu Gly Lys Glu Glu
      160                      165                      170
ggg cct gca gcc tgg gag ggc ccc aac cag gac ctg ccc aga cgc ctc      688
Gly Pro Ala Ala Trp Glu Gly Pro Asn Gln Asp Leu Pro Arg Arg Leu
      175                      180                      185
aga ggc ccc caa aag gat gag ctg aag tcc ttc atc ctg cag aag tac      736
Arg Gly Pro Gln Lys Asp Glu Leu Lys Ser Phe Ile Leu Gln Lys Tyr
      190                      195                      200
atg atg gtg gat agc gca gag gat cag aag att cac cgg ccc atg gct      784
Met Met Val Asp Ser Ala Glu Asp Gln Lys Ile His Arg Pro Met Ala
      205                      210                      215
ccc aag gag gcc ccc aag aag ctg atc cga tac atc gac aac cag gta      832
Pro Lys Glu Ala Pro Lys Lys Leu Ile Arg Tyr Ile Asp Asn Gln Val
      220                      225                      230                      235
gtg agc acc aaa ggg gag cga ttc aaa gat gtg cgg aac cct gag gcc      880
Val Ser Thr Lys Gly Glu Arg Phe Lys Asp Val Arg Asn Pro Glu Ala
      240                      245                      250
gag gag atg aag gcc aca tac atc aac ctc aag cca gcc aga aag tac      928
Glu Glu Met Lys Ala Thr Tyr Ile Asn Leu Lys Pro Ala Arg Lys Tyr
      255                      260                      265
cgc ttc cat tgaggcactc gccggactct gcccgagcct tctaggetca      977
Arg Phe His
      270
gatccagag ggatgcagga gccctataacc cctacacagg ggccccctaa ctctgtccc      1037
ccttctctac tcttttgctc catagtgtta acctactctc ggagctgcct ccatggggcac      1097
agtaaagggtg gcccaaggaa aaaaaaaaaa aaaaaa      1132

```

```

<210> 61
<211> 631
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 9..503

```

```

<220>
<221> sig_peptide
<222> 9..113
<223> Von Heijne matrix
      score 10.2506494380376
      seq LLPLVLLPPLAAA/AA

```

```

<400> 61
tgccaggg atg atg cgc tgc tgc cgc cgc cgc tgc tgc tgc cgg caa cca      50
      Met Met Arg Cys Cys Arg Arg Arg Cys Cys Cys Arg Gln Pro
      -35                      -30                      -25
ccc cat gcc ctg agg ccg ttg ctg ttg ctg ccc ctc gtc ctt tta cct      98
Pro His Ala Leu Arg Pro Leu Leu Leu Leu Pro Leu Val Leu Leu Pro
      -20                      -15                      -10
ccc ctg gca gca gct gca gcg ggc cca aac cga tgt gac acc ata tac      146

```

```

Pro Leu Ala Ala Ala Ala Gly Pro Asn Arg Cys Asp Thr Ile Tyr
-5      1      5      10
cag ggc ttc gcc gag tgt ctc atc cgc ttg ggg gac agc atg ggc cgc      194
Gln Gly Phe Ala Glu Cys Leu Ile Arg Leu Gly Asp Ser Met Gly Arg
      15      20      25
gga ggc gag ctg gag acc atc tgc agg tct tgg aat tac ttc cat gcc      242
Gly Gly Glu Leu Glu Thr Ile Cys Arg Ser Trp Asn Tyr Phe His Ala
      30      35      40
tgt gcc tct cag gtc ctg tca ggc tgt ccg gag gag gca gct gca gtg      290
Cys Ala Ser Gln Val Leu Ser Gly Cys Pro Glu Glu Ala Ala Ala Val
      45      50      55
tgg gaa tca cta cag caa gaa gct cgc cag gcc ccc cgt ccg aat aac      338
Trp Glu Ser Leu Gln Gln Glu Ala Arg Gln Ala Pro Arg Pro Asn Asn
      60      65      70      75
ttg cac act ctg tgc ggt gcc ccg gtg cat gtt cgg gag cgc ggc aca      386
Leu His Thr Leu Cys Gly Ala Pro Val His Val Arg Glu Arg Gly Thr
      80      85      90
ggc tcc gaa acc aac cag gag acg ctg cgg gct aca gcg cct gca ctc      434
Gly Ser Glu Thr Asn Gln Glu Thr Leu Arg Ala Thr Ala Pro Ala Leu
      95      100      105
ccc atg gcc cct gcg ccc cca ctg ctg gcg gct gct ctg gct ctg gcc      482
Pro Met Ala Pro Ala Pro Pro Leu Leu Ala Ala Ala Leu Ala Leu Ala
      110      115      120
tac ctc ctg agg cct ctg gcc tagcttggtg gggtgggtag cagcgcccg      533
Tyr Leu Leu Arg Pro Leu Ala
      125      130
acctccagcc ctgctctggc ggtggttgctc caggctctgc agagcgcagc agggccttttc      593
attaaaggta tttatatattg caaaaaaaaa aaaaaaaaa      631

```

<210> 62  
 <211> 722  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 21..464

<220>  
 <221> sig\_peptide  
 <222> 21..95  
 <223> Von Heijne matrix  
       score 5.38058532480537  
       seq AVTSLLSPTPATA/LA

```

<400> 62
ggaagtgagt gatcgaaagc atg gcg tcg gtg gtg ttg gcg ctg agg acc cgg      53
      Met Ala Ser Val Val Leu Ala Leu Arg Thr Arg
      -25      -20      -15
aca gcc gtt aca tcc ttg cta agc ccc act ccg gct aca gct ctt gct      101
Thr Ala Val Thr Ser Leu Leu Ser Pro Thr Pro Ala Thr Ala Leu Ala
      -10      -5      1
gtc aga tac gca tcc aag aag tcg ggt ggt agc tcc aaa aac ctc ggt      149
Val Arg Tyr Ala Ser Lys Lys Ser Gly Gly Ser Ser Lys Asn Leu Gly
      5      10      15
gga aag tca tca ggc aga cgc caa ggc att aag aaa atg gaa ggt cac      197
Gly Lys Ser Ser Gly Arg Arg Gln Gly Ile Lys Lys Met Glu Gly His
      20      25      30

```

tat gtt cat gct ggg aac atc att gca aca cag cgc cat ttc cgc tgg	245
Tyr Val His Ala Gly Asn Ile Ile Ala Thr Gln Arg His Phe Arg Trp	
35 40 45 50	
cac cca ggt gcc cat gtg ggt gtt ggg aag aat aaa tgt ctg tat gcc	293
His Pro Gly Ala His Val Gly Val Gly Lys Asn Lys Cys Leu Tyr Ala	
55 60 65	
ctg gaa gag ggg ata gtc cgc tac act aag gag gtc tac gtg cct cat	341
Leu Glu Glu Gly Ile Val Arg Tyr Thr Lys Glu Val Tyr Val Pro His	
70 75 80	
ccc aga aac acg gag gct gtg gat ctg atc acc agg ctg ccc aag ggt	389
Pro Arg Asn Thr Glu Ala Val Asp Leu Ile Thr Arg Leu Pro Lys Gly	
85 90 95	
gct gtg ctc tac aag act ttt gtc cac gtg gtt cct gcc aag cct gag	437
Ala Val Leu Tyr Lys Thr Phe Val His Val Val Pro Ala Lys Pro Glu	
100 105 110	
ggc acc ttc aaa ctg gta gct atg ctt tgatgtcctg ttgaggccat	484
Gly Thr Phe Lys Leu Val Ala Met Leu	
115 120	
cggacagaga ctggagccca ggtgacagga gatggtgata ccagaagtca aggggttgggg	544
tggcgacacg gcctcccagag gaagaggtct gcttgatggt gactctgcag gagactctga	604
agtgactgct gggaaaccct ttgggagacc tgacctgggg ccaaaaataa agtgagccag	664
cgatcatgaac gcatgctatt tagggacaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaa	722

<210> 63  
 <211> 1442  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 178..1050

<220>  
 <221> sig\_peptide  
 <222> 178..279  
 <223> Von Heijne matrix  
 score 10.0571391689271  
 seq FLCLLSALLLTEG/KK

<400> 63	
agtgcatgtg tggagcgagg agaagctcac gaatcagctg caggtctctg ttttgaaaaa	60
gcagagatac agaggcagag gaaaagggca ctccatgtg acctgttctt agagcaagac	120
aatcaccatc tgaattccag aagccctgtt catgggtggg gatattttct cgactgc	177
atg gaa tca gaa aga agc aaa agg atg gga aat gcc tgc att ccc ctg	225
Met Glu Ser Glu Arg Ser Lys Arg Met Gly Asn Ala Cys Ile Pro Leu	
-30 -25 -20	
aaa aga att gct tat ttc cta tgt ctc tta tct gcg ctt ttg ctg act	273
Lys Arg Ile Ala Tyr Phe Leu Cys Leu Leu Ser Ala Leu Leu Thr	
-15 -10 -5	
gag ggg aag aaa cca gcg aag cca aaa tgc cct gcc gtg tgt act tgt	321
Glu Gly Lys Lys Pro Ala Lys Pro Lys Cys Pro Ala Val Cys Thr Cys	
1 5 10	
acc aaa gat aat gct tta tgt gag aat gcc aga tcc att cca cgc acc	369
Thr Lys Asp Asn Ala Leu Cys Glu Asn Ala Arg Ser Ile Pro Arg Thr	
15 20 25 30	
gtt cct cct gat gtt atc tca tta tcc ttt gtg aga tct ggt ttt act	417
Val Pro Pro Asp Val Ile Ser Leu Ser Phe Val Arg Ser Gly Phe Thr	
35 40 45	

gaa atc tca gaa ggg agt ttt tta ttc acg cca tcg ctg cag ctc ttg	465
Glu Ile Ser Glu Gly Ser Phe Leu Phe Thr Pro Ser Leu Gln Leu Leu	
50 55 60	
tta ttc aca tcg aac tcc ttt gat gtg atc agt gat gat gct ttt att	513
Leu Phe Thr Ser Asn Ser Phe Asp Val Ile Ser Asp Asp Ala Phe Ile	
65 70 75	
ggg ctt cca cat cta gag tat tta ttc ata gaa aac aac aac atc aag	561
Gly Leu Pro His Leu Glu Tyr Leu Phe Ile Glu Asn Asn Asn Ile Lys	
80 85 90	
tca att tca aga cat act ttc cgg gga cta aag tca tta att cac ttg	609
Ser Ile Ser Arg His Thr Phe Arg Gly Leu Lys Ser Leu Ile His Leu	
95 100 105 110	
agc ctt gca aac aac aat ctc cag aca ctc cca aaa gat att ttc aaa	657
Ser Leu Ala Asn Asn Asn Leu Gln Thr Leu Pro Lys Asp Ile Phe Lys	
115 120 125	
ggc ctg gat tct tta aca aat gtg gac ctg agg ggt aat tca ttt aat	705
Gly Leu Asp Ser Leu Thr Asn Val Asp Leu Arg Gly Asn Ser Phe Asn	
130 135 140	
tgt gac tgt aaa ctg aaa tgg cta gtg gaa tgg ctt ggc cac acc aat	753
Cys Asp Cys Lys Leu Lys Trp Leu Val Glu Trp Leu Gly His Thr Asn	
145 150 155	
gca act gtt gaa gac atc tac tgc gaa ggc ccc cca gaa tac aag aag	801
Ala Thr Val Glu Asp Ile Tyr Cys Glu Gly Pro Pro Glu Tyr Lys Lys	
160 165 170	
cgc aaa atc aat agt ctc tcc tcg aag gat ttc gat tgc atc att aca	849
Arg Lys Ile Asn Ser Leu Ser Ser Lys Asp Phe Asp Cys Ile Ile Thr	
175 180 185 190	
gaa ttt gca aag tct caa gac ctg cct tat caa tca ttg tcc ata gac	897
Glu Phe Ala Lys Ser Gln Asp Leu Pro Tyr Gln Ser Leu Ser Ile Asp	
195 200 205	
act ttt tct tat ttg aat gat gag tat gta gtc atc gct cag cct ttt	945
Thr Phe Ser Tyr Leu Asn Asp Glu Tyr Val Val Ile Ala Gln Pro Phe	
210 215 220	
act gga aaa tgc att ttc ctt gaa tgg gac cat gtg gaa aag acc ttc	993
Thr Gly Lys Cys Ile Phe Leu Glu Trp Asp His Val Glu Lys Thr Phe	
225 230 235	
cgg aat tat gac aac att aca gtt tta agg gaa ata cac aga ttt aca	1041
Arg Asn Tyr Asp Asn Ile Thr Val Leu Arg Glu Ile His Arg Phe Thr	
240 245 250	
aac atg tca tagttgactt aagcgcgatga gacaccaaatt tctgtggctg	1090
Asn Met Ser	
255	
ccatcagaaa ttttctacag tacatgaccc ggatgaactc aatgcatgat gactcttctt	1150
atcacacttg caaatgaatg cctttcaaac attgagactg ctagaaccaa gcactaccag	1210
tatctccatc cttaactgtc cagtccagtg atgtgggaag ttacctttta taagacaaaa	1270
tttaattgtg taactgttct ttgcagtga gatgtgtaaa taagcgttta atggtatctg	1330
ttactccaaa aagaaatatt aatatgtact tttccattta tttattcatg tgtacagaaa	1390
caactgccaa ataaaatggtt tacattttct ttcagaaaaa aaaaaaaaaa aa	1442

<210> 64  
 <211> 795  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 32..274

```

<220>
<221> sig_peptide
<222> 32..178
<223> Von Heijne matrix
      score 4.30837886795471
      seq LMVELLLKVFVVEA/AV

<400> 64
gttccggttg gcgcgcgttg aggctgcggt c atg gag gga gca gga gct gga      52
                               Met Glu Gly Ala Gly Ala Gly
                               -45
tcc ggc ttc cgg aag gag ctg gtg agc agg ctg ctg cac ctg cac ttc      100
Ser Gly Phe Arg Lys Glu Leu Val Ser Arg Leu Leu His Leu His Phe
      -40                               -35                               -30
aag gat gac aag acc aaa gtg agc ggg gac gcg ctg cag ctc atg gtg      148
Lys Asp Asp Lys Thr Lys Val Ser Gly Asp Ala Leu Gln Leu Met Val
      -25                               -20                               -15
gag ttg ctg aag gtc ttc gtt gtg gaa gca gca gtc cgc ggc gtg cgg      196
Glu Leu Leu Lys Val Phe Val Val Glu Ala Ala Val Arg Gly Val Arg
      -10                               -5                               1                               5
cag gcc cag gca gaa gac gcg ctc cgt gtg gac gtg gac cag ctg gag      244
Gln Ala Gln Ala Glu Asp Ala Leu Arg Val Asp Val Asp Gln Leu Glu
      10                               15                               20
aag gtg ctt ccg cag ctg ctc ctg gac ttc tagggatctc agccgtggct      294
Lys Val Leu Pro Gln Leu Leu Leu Asp Phe
      25                               30
gaggccaccc ccagaggagc ccctggtcca cagaagcagg ccttgtgttt ccagcggcct      354
ctgataagag gcaggggaagg acctgaagga tttggagttg attcaaacaa gatctctggg      414
agtctccagc ctgtgcagaa ggggcaggac tgcagtgcac tgcgggcctt ggagtgtcca      474
gtggggacac tgggtgtgga aggggcagca cctggggagt cctgcctct cctccctggg      534
acaatagtgt gcatgccacc cggggtccta caggcaggtg ctgggaaagg cctggccagc      594
aggtagcctg tgtgtttgac aaacagcagc tggcagcgct gcctcctgcc cacattcctg      654
ccaccgcaca tcaaagctgg cgtgtgacct ttccagccat gcgatattcc ccttgaaga      714
tgcttcccca ggctataaat ttgttctcac aaagcaacat caataaatca aaactgtctc      774
tctcaaaaaa aaaaaaaaaa a      795

<210> 65
<211> 1236
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 222..920

<220>
<221> sig_peptide
<222> 222..311
<223> Von Heijne matrix
      score 4.35083245061594
      seq VAHALSLPAESYG/ND

<400> 65
accgaaaatt actgacgagt caatcacctc agatctctca agcagtcag cctacgcaac      60
agtactccac ctctgcgcct gtgcggggag ggtaaggcgg ggccagcaac ttcctcagct      120
ggagggagag cgcacggtgg agccgccagt tgagaaggac tctgatccgg ctcagctttc      180
caatcagctg cggaaggagc cacgctttcg ggggttgcaa g atg gcg gcc acc agt      236
                               Met Ala Ala Thr Ser

```

-30

gga act gat gag ccg gtt tcc ggg gag ttg gtg tct gtg gca cat gcg	284
Gly Thr Asp Glu Pro Val Ser Gly Glu Leu Val Ser Val Ala His Ala	
-25 -20 -15 -10	
ctt tct ctc cca gca gag tgc tat ggc aac gat cct gac att gag atg	332
Leu Ser Leu Pro Ala Glu Ser Tyr Gly Asn Asp Pro Asp Ile Glu Met	
-5 1 5	
gct tgg gcc atg aga gca atg cag cat gct gaa gtc tat tac aag ctg	380
Ala Trp Ala Met Arg Ala Met Gln His Ala Glu Val Tyr Tyr Lys Leu	
10 15 20	
att tca tca gtt gac cca cag ttc ctc aaa ctc acc aaa gta gat gac	428
Ile Ser Ser Val Asp Pro Gln Phe Leu Lys Leu Thr Lys Val Asp Asp	
25 30 35	
caa att tac tct gag ttc cgg aaa aat ttt gag acc ctt agg ata gat	476
Gln Ile Tyr Ser Glu Phe Arg Lys Asn Phe Glu Thr Leu Arg Ile Asp	
40 45 50 55	
gtg ttg gac cca gaa gaa ctc aag tca gaa tca gcc aaa gag aag tgg	524
Val Leu Asp Pro Glu Glu Leu Lys Ser Glu Ser Ala Lys Glu Lys Trp	
60 65 70	
agg cca ttc tgc ttg aag ttt aat ggg att gtt gaa gac ttc aac tat	572
Arg Pro Phe Cys Leu Lys Phe Asn Gly Ile Val Glu Asp Phe Asn Tyr	
75 80 85	
ggt act ttg ctg cga cta gat tgt tct cag ggc tac act gag gaa aac	620
Gly Thr Leu Leu Arg Leu Asp Cys Ser Gln Gly Tyr Thr Glu Glu Asn	
90 95 100	
acc atc ttt gcc ccc agg ata caa ttc ttt gcc att gaa att gct cgg	668
Thr Ile Phe Ala Pro Arg Ile Gln Phe Phe Ala Ile Glu Ile Ala Arg	
105 110 115	
aac cgg gaa ggc tat aac aaa gct gtt tat atc agt gtt cag gac aaa	716
Asn Arg Glu Gly Tyr Asn Lys Ala Val Tyr Ile Ser Val Gln Asp Lys	
120 125 130 135	
gaa gga gag aaa gga gtc aac aat gga gga gaa aaa aga gct gac agt	764
Glu Gly Glu Lys Gly Val Asn Asn Gly Gly Glu Lys Arg Ala Asp Ser	
140 145 150	
gga gaa gaa gag aac acc aag aat gga gga gag aaa gga gct gat agt	812
Gly Glu Glu Glu Asn Thr Lys Asn Gly Gly Glu Lys Gly Ala Asp Ser	
155 160 165	
gga gaa gaa aaa gag gaa gga atc aac aga gaa gac aaa act gac aaa	860
Gly Glu Glu Lys Glu Glu Gly Ile Asn Arg Glu Asp Lys Thr Asp Lys	
170 175 180	
gga gga gaa aaa ggg aaa gaa gct gac aaa gaa atc aac aaa agt ggt	908
Gly Gly Glu Lys Gly Lys Glu Ala Asp Lys Glu Ile Asn Lys Ser Gly	
185 190 195	
gaa aaa gct atg taagggtatagc aggggaacagc actctagaag ctatgactca	960
Glu Lys Ala Met	
200	
attgagacta caagtaccac ggtgctactt gcacagacccc ctttggttaa atgtaaattc	1020
ttgtacaatt gaaggatacgc cagaaggaca tctttctagt ctaacagtca ggagctgctc	1080
tggtcattcc cttgtatgaa ctggtctataa gactgttagt ggggtggttag ttgatttttc	1140
ctgggtatact gtttcttggc tgacactact ggtcaagtaa gaaatttgta aataaatttc	1200
ttttggttct tattaaaaaca aaaaaaaaaa aaaaaa	1236

<210> 66  
 <211> 881  
 <212> DNA  
 <213> Homo sapiens

<220>

<221> CDS  
<222> 101..355

<220>  
<221> sig\_peptide  
<222> 101..160  
<223> Von Heijne matrix  
score 9.32665652007071  
seq LFLCYLLLLFTCSG/VE

<400> 66  
ttactcgtc ctgtgcccac ctatcagcag gctccgggct gaagattgct tctcttctct 60  
cctccaaggt ctagtgcagg agcccgcgcg cggcgccacc atg cgg cag aag gcg 115  
Met Arg Gln Lys Ala  
-20  
gta tcg ctt ttc ttg tgc tac ctg ctg ctc ttc act tgc agt ggg gtg 163  
Val Ser Leu Phe Leu Cys Tyr Leu Leu Leu Phe Thr Cys Ser Gly Val  
-15 -10 -5 1  
gag gca ggt aag aaa aag tgc tcg gag agc tcg gac agc ggc tcc ggg 211  
Glu Ala Gly Lys Lys Lys Cys Ser Glu Ser Ser Asp Ser Gly Ser Gly  
5 10 15  
ttc tgg aag gcc ctg acc ttc atg gcc gtc gga gga gga ctc gca gtc 259  
Phe Trp Lys Ala Leu Thr Phe Met Ala Val Gly Gly Gly Leu Ala Val  
20 25 30  
gcc ggg ctg ccc gcg ctg ggc ttc acc ggc gcc ggc atc gcg gcc aac 307  
Ala Gly Leu Pro Ala Leu Gly Phe Thr Gly Ala Gly Ile Ala Ala Asn  
35 40 45  
tcg gtg gct gcc tcg ctg atg agc tgg tct gcg atc ctg aat ggg ggc 355  
Ser Val Ala Ala Ser Leu Met Ser Trp Ser Ala Ile Leu Asn Gly Gly  
50 55 60 65  
tagtggccac gctgcagagc ctccggggctg gtggcagcag cgtcgtcata ggtaatatg 415  
gtgccctgat gggctacgcc acccacaagt atctcgatag tgaggaggat gaggagtagc 475  
cagcagctcc cagaacctct tcttcttct tggcctaact cttccagtta ggatctagaa 535  
ctttgccttt tttttttttt tttttttttt ttgagatggg ttctcactat attgtccagg 595  
ctagagtgca gkggctattc acagatgcga acatagtaca ctgcagcctc caactcctag 655  
cctcaagtga tcctcctgtc tcaacctccc aagtaggatt acaagcatgc gccgacgatg 715  
cccaraatcc araactttgt ctatcactct ccccaacaac ctatgatgtga aaacagaata 775  
aacttcaccc agaaaaaaaa aaammacaar aaaaaaaaaa aaaaaaaaaa aaaaaaaaaam 835  
aaaaaaaaaa rrraaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 881

<210> 67  
<211> 524  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 173..487  
  
<220>  
<221> sig\_peptide  
<222> 173..301  
<223> Von Heijne matrix  
score 4.27484469223909  
seq AGSLVATLQSVGA/AG

<400> 67  
agggcagagt aggcgcgtcc ctactggatg gagggggaag taacacccca agaacgctgt 60



```

catttcctgg gccaaagttgg gacccggacg gcctcaccat gatgaaacgg gcagctgctg 120
ctgcagtgagg aggagccctg gcagtggggg ctgtgccgtg gtgctcagtg cc atg ggc 178
Met Gly
ttc act ggg gca gga atc gcc gcg tcc tcc ata gca gcc aag atg atg 226
Phe Thr Gly Ala Gly Ile Ala Ala Ser Ser Ile Ala Ala Lys Met Met
-40 -35 -30
tcc gca gca gcc att gcc aac ggg ggt ggt gtt tct gcg ggg agc ctg 274
Ser Ala Ala Ala Ile Ala Asn Gly Gly Gly Val Ser Ala Gly Ser Leu
-25 -20 -15 -10
gtg gct act ctg cag tcc gtg ggg gca gct gga ctc tcc aca tca tcc 322
Val Ala Thr Leu Gln Ser Val Gly Ala Ala Gly Leu Ser Thr Ser Ser
-5 1 5
aac atc ctc ctg gcc tct gtt ggg tca gtg ttg ggg gcc tgc ttg ggg 370
Asn Ile Leu Leu Ala Ser Val Gly Ser Val Leu Gly Ala Cys Leu Gly
10 15 20
aat tca cct tct tct tct ctc cca gct gaa ccc gag gct aaa gaa gat 418
Asn Ser Pro Ser Ser Ser Leu Pro Ala Glu Pro Glu Ala Lys Glu Asp
25 30 35
gag gca aga gaa aat gta ccc caa ggt gaa cct cca aaa ccc cca ctc 466
Glu Ala Arg Glu Asn Val Pro Gln Gly Glu Pro Pro Lys Pro Pro Leu
40 45 50 55
aag tca gag aaa cat gag gaa taaaggtcac atgcagatgc aaaaaaaaaa 517
Lys Ser Glu Lys His Glu Glu
60
aaaaaaa 524

<210> 68
<211> 1472
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 210..1082

<220>
<221> sig_peptide
<222> 210..311
<223> Von Heijne matrix
score 10.0571391689271
seq FLCLLSALLLTEG/KK

<400> 68
acagtacctc acaggtctct tcccccgagc agtgcattgc tggagcgagg agaagctcac 60
gaatcagctg caggtctctg ttttgaaaaa gcagagatac agaggcagag gaaaagggtg 120
gactcctatg tgacctgttc ttagagcaag acaatcacca tctgaattcc agaagccctg 180
ttcatgggtg gggatatttt ctgcactgc atg gaa tca gaa aga agc aaa agg 233
Met Glu Ser Glu Arg Ser Lys Arg
-30
atg gga aat gcc tgc att ccc ctg aaa aga att gct tat ttc cta tgt 281
Met Gly Asn Ala Cys Ile Pro Leu Lys Arg Ile Ala Tyr Phe Leu Cys
-25 -20 -15
ctc tta tct gcg ctt ttg ctg act gag ggg aag aaa cca gcg aag cca 329
Leu Leu Ser Ala Leu Leu Thr Glu Gly Lys Lys Pro Ala Lys Pro
-10 -5 1 5
aaa tgc cct gcc gtg tgt act tgt acc aaa gat aat gct tta tgt gag 377
Lys Cys Pro Ala Val Cys Thr Cys Thr Lys Asp Asn Ala Leu Cys Glu
10 15 20

```

aat gcc aga tcc att cca cgc acc gtt cct cct gat gtt atc tca tta	425
Asn Ala Arg Ser Ile Pro Arg Thr Val Pro Pro Asp Val Ile Ser Leu	
25 30 35	
tcc ttt gtg aga tct gtt ttt act gaa atc tca gaa ggg agt ttt tta	473
Ser Phe Val Arg Ser Val Phe Thr Glu Ile Ser Glu Gly Ser Phe Leu	
40 45 50	
ttc acg cca tgc ctg cag ctc ttg tta ttc aca tgc aac tcc ttt gat	521
Phe Thr Pro Ser Leu Gln Leu Leu Leu Phe Thr Ser Asn Ser Phe Asp	
55 60 65 70	
gtg atc agt gat gat gct ttt att ggt ctt cca cat cta gag tat tta	569
Val Ile Ser Asp Ala Phe Ile Gly Leu Pro His Leu Glu Tyr Leu	
75 80 85	
ttc ata gaa aac aac aac atc aag tca att tca aga cat act ttc cgg	617
Phe Ile Glu Asn Asn Asn Ile Lys Ser Ile Ser Arg His Thr Phe Arg	
90 95 100	
gga cta aag tca tta att cac ttg agc ctt gca aac aac aat ctc cag	665
Gly Leu Lys Ser Leu Ile His Leu Ser Leu Ala Asn Asn Asn Leu Gln	
105 110 115	
aca ctc cca aaa gat att ttc aaa ggc ctg gat tct tta aca aat gtg	713
Thr Leu Pro Lys Asp Ile Phe Lys Gly Leu Asp Ser Leu Thr Asn Val	
120 125 130	
gac ctg agg ggt aat tca ttt aat tgt gac tgt aaa ctg aaa tgg cta	761
Asp Leu Arg Gly Asn Ser Phe Asn Cys Asp Cys Lys Leu Lys Trp Leu	
135 140 145 150	
gtg gaa tgg ctt ggc cac acc aat gca act gtt gaa gac atc tac tgc	809
Val Glu Trp Leu Gly His Thr Asn Ala Thr Val Glu Asp Ile Tyr Cys	
155 160 165	
gaa ggc ccc cca gaa tac aag aag cgc aaa atc aat agt ctc tcc tgc	857
Glu Gly Pro Glu Tyr Lys Lys Arg Lys Ile Asn Ser Leu Ser Ser	
170 175 180	
aag gat ttc gat tgc atc att aca gaa ttt gca aag tct caa gac ctg	905
Lys Asp Phe Asp Cys Ile Ile Thr Glu Phe Ala Lys Ser Gln Asp Leu	
185 190 195	
cct tat caa tca ttg tcc ata gac act ttt tct tat ttg aat gat gag	953
Pro Tyr Gln Ser Leu Ser Ile Asp Thr Phe Ser Tyr Leu Asn Asp Glu	
200 205 210	
tat gta gtc atc gct cag cct ttt act gga aaa tgc att ttc ctt gaa	1001
Tyr Val Val Ile Ala Gln Pro Phe Thr Gly Lys Cys Ile Phe Leu Glu	
215 220 225 230	
tgg gac cat gtg gaa aag acc ttc cgg aat tat gac aac att aca gtt	1049
Trp Asp His Val Glu Lys Thr Phe Arg Asn Tyr Asp Asn Ile Thr Val	
235 240 245	
tta agg gaa ata cac aga ttt aca aac atg tca tagttgactt aagcgcata	1102
Leu Arg Glu Ile His Arg Phe Thr Asn Met Ser	
250 255	
gacaccaaatt tctgtggctg ccatcagaaa ttttctacag tacatgaccc ggatgaactc	1162
aatgcacgat gactcttctt atcacacttg caaatgaatg cctttcaaac attgagactg	1222
ctagaaccaa gcactaccag tatctccatc cttaactgtc cagtccagtg atgtgggaag	1282
ttacctttta taagacaaaa tttaattgtg taactgttct ttgcagtga gatgtgtaaa	1342
taagcgttta atggtatctg ttactccaaa aagaaatatt aatatgtact tttccattta	1402
tttattcatg tgtacagaaa caactgccaa ataaaatgtt tacattttct tacaaaaaaa	1462
aaaaaaaaa	1472

<210> 69  
 <211> 1737  
 <212> DNA  
 <213> Homo sapiens

<220>  
<221> CDS  
<222> 172..1449

<220>  
<221> sig\_peptide  
<222> 172..255  
<223> Von Heijne matrix  
score 5.94825670923113  
seq XVLLEPFVHQVGG/HS

```

<400> 69
aaacaatagg acggaaaacgc cgaggaaccc ggctgaggcg gcagagcatc ctggccagaa      60
caagccaagg agccaagacg agagggacac acggacaaac aacagacaga agacgtactg      120
gccgctggac tccgctgcct ccccatctc cccgccatct gcgcccggag g atg agc      177
                                     Met Ser

cca gcc ttc agg gcc atg gat gtg gag ccc cgc gcc aaa ggc gtc ctt      225
Pro Ala Phe Arg Ala Met Asp Val Glu Pro Arg Ala Lys Gly Val Leu
-25 -20 -15
ctg gag ccc ttt gtc cac cag gtc ggg ggg cac tca tgc gtg ctc cgc      273
Leu Glu Pro Phe Val His Gln Val Gly Gly His Ser Cys Val Leu Arg
-10 -5 1 5
ttc aat gag aca acc ctg tgc aag ccc ctg gtc cca agg gaa cat cag      321
Phe Asn Glu Thr Thr Leu Cys Lys Pro Leu Val Pro Arg Glu His Gln
10 15 20
ttc tac gag acc ctc cct gct gag atg cgc aaa ttc act ccc cag tac      369
Phe Tyr Glu Thr Leu Pro Ala Glu Met Arg Lys Phe Thr Pro Gln Tyr
25 30 35
aaa ggt gtg gta tct gtg cgc ttt gaa gaa gat gaa gac agg aac ttg      417
Lys Gly Val Val Ser Val Arg Phe Glu Glu Asp Glu Asp Arg Asn Leu
40 45 50
tgt cta ata gca tat cca ttg aaa ggg gac cat gga att gtg gac att      465
Cys Leu Ile Ala Tyr Pro Leu Lys Gly Asp His Gly Ile Val Asp Ile
55 60 65 70
gta gat aat tca gac tgt gaa cca aaa agt aag ctc cta agg tgg aca      513
Val Asp Asn Ser Asp Cys Glu Pro Lys Ser Lys Leu Leu Arg Trp Thr
75 80 85
aca aac aaa aaa cat cat gtc tta gaa aca gaa aag acc cct aag gac      561
Thr Asn Lys Lys His His Val Leu Glu Thr Glu Lys Thr Pro Lys Asp
90 95 100
tgg gtg cgt cag cac cgt aaa gag gag aaa atg aag agc cat aag tta      609
Trp Val Arg Gln His Arg Lys Glu Glu Lys Met Lys Ser His Lys Leu
105 110 115
gaa gaa gaa ttt gag tgg cta aag aaa tct gaa gtc ttg tac tac act      657
Glu Glu Glu Phe Glu Trp Leu Lys Lys Ser Glu Val Leu Tyr Tyr Thr
120 125 130
gta gag aag aag ggg aat ata agt tcc cag ctt aaa cac tat aac cct      705
Val Glu Lys Lys Gly Asn Ile Ser Ser Gln Leu Lys His Tyr Asn Pro
135 140 145 150
tgg agc atg aaa tgt cac cag caa cag tta cag aga atg aag gag aat      753
Trp Ser Met Lys Cys His Gln Gln Gln Leu Gln Arg Met Lys Glu Asn
155 160 165
gca aag cat cgg aac cag tac aaa ttt atc tta ctg gaa aac ctg act      801
Ala Lys His Arg Asn Gln Tyr Lys Phe Ile Leu Leu Glu Asn Leu Thr
170 175 180
tcc cgc tat gag gtg cct tgt gtc ctt gac ctc aag atg ggc aca cga      849
Ser Arg Tyr Glu Val Pro Cys Val Leu Asp Leu Lys Met Gly Thr Arg
185 190 195

```

caa	cat	ggt	gat	gat	gct	tca	gag	gag	aag	gca	gcc	aac	cag	atc	cga	897
Gln	His	Gly	Asp	Asp	Ala	Ser	Glu	Glu	Lys	Ala	Ala	Asn	Gln	Ile	Arg	
200						205					210					
aaa	tgt	cag	cag	agc	aca	tct	gca	gtc	att	ggt	gtg	cgt	gtg	tgt	ggc	945
Lys	Cys	Gln	Gln	Ser	Thr	Ser	Ala	Val	Ile	Gly	Val	Arg	Val	Cys	Gly	
215					220					225					230	
atg	cag	gtg	tac	caa	gca	ggc	agt	ggg	cag	ctc	atg	ttc	atg	aac	aag	993
Met	Gln	Val	Tyr	Gln	Ala	Gly	Ser	Gly	Gln	Leu	Met	Phe	Met	Asn	Lys	
				235				240						245		
tac	cat	gga	cgg	aag	cta	tcg	atg	cag	ggc	ttc	aag	gag	gca	ctt	ttc	1041
Tyr	His	Gly	Arg	Lys	Leu	Ser	Met	Gln	Gly	Phe	Lys	Glu	Ala	Leu	Phe	
			250					255					260			
cag	ttc	ttc	cac	aat	ggg	cgg	tac	ctg	cgc	cgt	gaa	ctc	ctg	ggc	cct	1089
Gln	Phe	Phe	His	Asn	Gly	Arg	Tyr	Leu	Arg	Arg	Glu	Leu	Leu	Gly	Pro	
		265					270					275				
gtg	ctc	aag	aag	ctg	act	gag	ctc	aag	gca	gtg	ttg	gag	cga	cag	gag	1137
Val	Leu	Lys	Lys	Leu	Thr	Glu	Leu	Lys	Ala	Val	Leu	Glu	Arg	Gln	Glu	
		280				285					290					
tcc	tac	cgc	ttc	tac	tca	agc	tcc	ctg	ctg	gtc	att	tat	gat	ggc	aag	1185
Ser	Tyr	Arg	Phe	Tyr	Ser	Ser	Ser	Leu	Leu	Val	Ile	Tyr	Asp	Gly	Lys	
295					300					305					310	
gag	cgg	ccc	gaa	gtg	gtc	ctg	gac	tca	gat	gct	gag	gat	ttg	gag	gac	1233
Glu	Arg	Pro	Glu	Val	Val	Leu	Asp	Ser	Asp	Ala	Glu	Asp	Leu	Glu	Asp	
			315					320						325		
ctg	tca	gag	gaa	tca	gct	gat	gag	tct	gct	ggg	gcc	tat	gcc	tac	aaa	1281
Leu	Ser	Glu	Glu	Ser	Ala	Asp	Glu	Ser	Ala	Gly	Ala	Tyr	Ala	Tyr	Lys	
			330					335					340			
ccc	atc	ggc	gcc	agc	tct	gta	gat	gtg	cgc	atg	atc	gac	ttt	gca	cac	1329
Pro	Ile	Gly	Ala	Ser	Ser	Val	Asp	Val	Arg	Met	Ile	Asp	Phe	Ala	His	
		345					350					355				
acc	acc	tgc	agg	ctg	tat	ggc	gag	gac	acc	gtg	gtg	cat	gag	ggc	cag	1377
Thr	Thr	Cys	Arg	Leu	Tyr	Gly	Glu	Asp	Thr	Val	Val	His	Glu	Gly	Gln	
		360				365				370						
gat	gct	ggc	tat	atc	ttc	ggg	ctc	cag	agc	ctg	ata	gac	att	gtc	aca	1425
Asp	Ala	Gly	Tyr	Ile	Phe	Gly	Leu	Gln	Ser	Leu	Ile	Asp	Ile	Val	Thr	
		375			380					385					390	
gag	ata	agt	gag	gag	agt	ggg	gag	tgagcttgct	agctgctcca	gtacttgaga						1479
Glu	Ile	Ser	Glu	Glu	Ser	Gly	Glu									
				395												

```
<210> 70
<211> 1637
<212> DNA
<213> Homo sapiens
```

```
<220>  
<221> CDS  
<222> 30..1427
```

```
<220>
<221> sig_peptide
<222> 30..77
<223> Von Heijne matrix
```

score 3.71064775937629  
seq YAAAAGVLAGVES/RQ

<400> 70

cta	atc	gaaa	ag	taa	agg	cgc	cg	gga	aac	atg	ggg	ctg	tat	gct	gca	gct	gca	53
										Met	Gly	Leu	Tyr	Ala	Ala	Ala	Ala	
										-15								-10
ggc	gtg	ttg	gcc	ggc	gtg	gag	agc	cgc	cag	ggc	tct	atc	aag	ggg	ttg			101
Gly	Val	Leu	Ala	Gly	Val	Glu	Ser	Arg	Gln	Gly	Ser	Ile	Lys	Gly	Leu			
			-5					1			5							
gtg	tac	tcc	agc	aac	ttc	cag	aac	gtg	aag	cag	ctg	tac	gcg	ctg	gtg			149
Val	Tyr	Ser	Ser	Asn	Phe	Gln	Asn	Val	Lys	Gln	Leu	Tyr	Ala	Leu	Val			
	10					15				20								
tgc	gaa	acg	cag	cgc	tac	tcc	gcc	gtg	ctg	gat	gct	gtg	atc	gcc	agc			197
Cys	Glu	Thr	Gln	Arg	Tyr	Ser	Ala	Val	Leu	Asp	Ala	Val	Ile	Ala	Ser			
	25				30				35					40				
gcc	ggc	ctc	ctc	cgt	gcg	gag	aag	aag	ctg	cgg	ccg	cac	ctg	gcc	aag			245
Ala	Gly	Leu	Leu	Arg	Ala	Glu	Lys	Lys	Leu	Arg	Pro	His	Leu	Ala	Lys			
				45				50						55				
gtg	cta	gtg	tat	gag	ttg	ttg	ttg	gga	aag	ggc	ttt	cga	ggg	ggg	ggg			293
Val	Leu	Val	Tyr	Glu	Leu	Leu	Leu	Gly	Lys	Gly	Phe	Arg	Gly	Gly	Gly			
			60					65					70					
ggc	cga	tgg	aag	gct	ctg	ttg	ggc	cgg	cac	cag	gcg	agg	ctc	aag	gct			341
Gly	Arg	Trp	Lys	Ala	Leu	Leu	Gly	Arg	His	Gln	Ala	Arg	Leu	Lys	Ala			
	75					80				85								
gag	ttg	gct	cgg	ctc	aag	gtt	cat	cgg	ggg	gtg	agc	cgg	aat	gag	gac			389
Glu	Leu	Ala	Arg	Leu	Lys	Val	His	Arg	Gly	Val	Ser	Arg	Asn	Glu	Asp			
	90				95					100								
ctg	ttg	gaa	gtg	gga	tcc	agg	cct	ggt	cca	gcc	tcc	cag	ctg	cct	cga			437
Leu	Leu	Glu	Val	Gly	Ser	Arg	Pro	Gly	Pro	Ala	Ser	Gln	Leu	Pro	Arg			
	105				110					115				120				
ttt	gtg	cgt	gtg	aac	act	ctc	aag	acc	tgc	tcc	gat	gat	gta	gtt	gat			485
Phe	Val	Arg	Val	Asn	Thr	Leu	Lys	Thr	Cys	Ser	Asp	Asp	Val	Val	Asp			
				125					130					135				
tat	ttc	aag	aga	caa	ggg	ttc	tcc	tat	cag	ggg	cgg	gct	tcc	agc	ctc			533
Tyr	Phe	Lys	Arg	Gln	Gly	Phe	Ser	Tyr	Gln	Gly	Arg	Ala	Ser	Ser	Leu			
			140					145					150					
gat	gac	tta	cga	gcc	ctc	aag	ggg	aag	cat	ttt	ctc	ctg	gac	ccc	ttg			581
Asp	Asp	Leu	Arg	Ala	Leu	Lys	Gly	Lys	His	Phe	Leu	Leu	Asp	Pro	Leu			
		155				160						165						
atg	ccg	gag	ctg	ctg	gtg	ttt	ccc	gcc	cag	aca	gat	ctg	cat	gaa	cac			629
Met	Pro	Glu	Leu	Leu	Val	Phe	Pro	Ala	Gln	Thr	Asp	Leu	His	Glu	His			
	170				175						180							
cca	ctg	tac	cgg	gcc	gga	cac	ctc	att	ctg	cag	gac	agg	gcc	agc	tgt			677
Pro	Leu	Tyr	Arg	Ala	Gly	His	Leu	Ile	Leu	Gln	Asp	Arg	Ala	Ser	Cys			
	185				190					195				200				
ctc	cca	gcc	atg	ctg	gac	ccc	ccg	cca	ggc	tcc	cat	gtc	atc	gat				725
Leu	Pro	Ala	Met	Leu	Leu	Asp	Pro	Pro	Pro	Gly	Ser	His	Val	Ile	Asp			
				205				210					215					
gcc	tgt	gcc	gcc	cca	ggc	aat	aag	acc	agt	cac	ttg	gct	gct	ctt	ctg			773
Ala	Cys	Ala	Ala	Pro	Gly	Asn	Lys	Thr	Ser	His	Leu	Ala	Ala	Leu	Leu			
				220				225					230					
aag	aac	caa	ggg	aag	atc	ttt	gcc	ttt	gac	ctg	gat	gcc	aag	cgg	ctg			821
Lys	Asn	Gln	Gly	Lys	Ile	Phe	Ala	Phe	Asp	Leu	Asp	Ala	Lys	Arg	Leu			
		235				240						245						
gca	tcc	atg	gcc	acg	ctg	ctg	gcc	cgg	gct	ggc	gtc	tct	tgc	tgt	gaa			869
Ala	Ser	Met	Ala	Thr	Leu	Leu	Ala	Arg	Ala	Gly	Val	Ser	Cys	Cys	Glu			
	250				255						260							

```

ctg gct gag gag gac ttc ctg gcg gtc tcc ccc tcg gat cca cgc tac      917
Leu Ala Glu Glu Asp Phe Leu Ala Val Ser Pro Ser Asp Pro Arg Tyr
265                               270                               275                               280
cat gag gtc cac tac atc ctg ctg gat cct tcc tgc agt ggc tcg ggt      965
His Glu Val His Tyr Ile Leu Leu Asp Pro Ser Cys Ser Gly Ser Gly
                               285                               290                               295
atg ccg agc aga cag ctg gag gag ccc ggg gca ggc aca cct agc ccg      1013
Met Pro Ser Arg Gln Leu Glu Glu Pro Gly Ala Gly Thr Pro Ser Pro
                               300                               305                               310
gtg cgt ctg cat gcc ctg gca ggc ttc cag cag cga gcc ctg tgc cac      1061
Val Arg Leu His Ala Leu Ala Gly Phe Gln Gln Arg Ala Leu Cys His
                               315                               320                               325
gcg ctc act ttc cct tcc ctg cag cgg ctc gtc tac tcc acg tgc tcc      1109
Ala Leu Thr Phe Pro Ser Leu Gln Arg Leu Val Tyr Ser Thr Cys Ser
                               330                               335                               340
ctc tgc cag gag gag aat gaa gac gtg gtg cga gat gcg ctg cag cag      1157
Leu Cys Gln Glu Glu Asn Glu Asp Val Val Arg Asp Ala Leu Gln Gln
345                               350                               355                               360
aac ccg ggc gcc ttc agg cta gct ccc gcc ctg cct gcc tgg ccc cac      1205
Asn Pro Gly Ala Phe Arg Leu Ala Pro Ala Leu Pro Ala Trp Pro His
                               365                               370                               375
cga ggc ctg agc acg ttc ccg ggt gcc gag cac tgc ctc egg gcc tcc      1253
Arg Gly Leu Ser Thr Phe Pro Gly Ala Glu His Cys Leu Arg Ala Ser
                               380                               385                               390
cct gag acc aca ctc agc agt ggc ttc ttc gtt gct gta att gaa cgg      1301
Pro Glu Thr Thr Leu Ser Ser Gly Phe Phe Val Ala Val Ile Glu Arg
                               395                               400                               405
gtc gag gtg cca agc tca gcc tca cag gcc aaa gca tca gca cca gaa      1349
Val Glu Val Pro Ser Ser Ala Ser Gln Ala Lys Ala Ser Ala Pro Glu
410                               415                               420
cgc aca ccc agc cca gcc cca aag aga aag aag aga cag caa aga gcc      1397
Arg Thr Pro Ser Pro Ala Pro Lys Arg Lys Lys Arg Gln Gln Arg Ala
425                               430                               435                               440
gca gcc ggt gct tgc aca ccg cct tgc aca tagcagaggc tccgggctga      1447
Ala Ala Gly Ala Cys Thr Pro Pro Cys Thr
                               445                               450
ctccttctctg gtgggaaagg aagatgcctg tcctctccgt ggaggaccct gggccctcac      1507
cgcaggaagc agtttggtt ttgaaaggtt attgggtccc ttccttgggc tgtgttcttg      1567
ctggtgagca aagtgttacc tgcaaaaata aaatgcagaa cgtactctac gacaaaaaaa      1627
aaaaaaaaaa                                1637

```

<210> 71  
 <211> 1636  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 30..1175

<220>  
 <221> sig\_peptide  
 <222> 30..77  
 <223> Von Heijne matrix  
 score 3.71064775937629  
 seq YAAAAGVLAVES/RQ

<400> 71

ctaatacgaaa agtaaaggcg cgcggggaac atg ggg ctg tat gct gca gct gca	53
Met Gly Leu Tyr Ala Ala Ala	
-15 -10	
ggc gtg ttg gcc ggc gtg gag agc cgc cag ggc tct atc aag ggg ttg	101
Gly Val Leu Ala Gly Val Glu Ser Arg Gln Gly Ser Ile Lys Gly Leu	
-5 1 5	
gtg tac tcc agc aac ttc cag aac gtg aag cag ctg tac gcg ctg gtg	149
Val Tyr Ser Ser Asn Phe Gln Asn Val Lys Gln Leu Tyr Ala Leu Val	
10 15 20	
tgc gaa acg cag cgc tac tcc gcc gtg ctg gat gct gtg atc gcc agc	197
Cys Glu Thr Gln Arg Tyr Ser Ala Val Leu Asp Ala Val Ile Ala Ser	
25 30 35 40	
gcc ggc ctc ctc cgt gcg gag aag aag ctg cgg ccg cac ctg gcc aag	245
Ala Gly Leu Leu Arg Ala Glu Lys Lys Leu Arg Pro His Leu Ala Lys	
45 50 55	
gtg cta gtg tat gag ttg ttg ttg gga aag ggc ttt cga ggg ggt ggg	293
Val Leu Val Tyr Glu Leu Leu Leu Gly Lys Gly Phe Arg Gly Gly Gly	
60 65 70	
ggc cga tgg aag gct ctg ttg ggc cgg cac cag gcg agg ctc aag gct	341
Gly Arg Trp Lys Ala Leu Leu Gly Arg His Gln Ala Arg Leu Lys Ala	
75 80 85	
gag ttg gct cgg ctc aag gtt cat cgg ggt gtg agc cgg aat gag gac	389
Glu Leu Ala Arg Leu Lys Val His Arg Gly Val Ser Arg Asn Glu Asp	
90 95 100	
ctg ttg gaa gtg gga tcc agg cct ggt cca gcc tcc cag ctg cct cga	437
Leu Leu Glu Val Gly Ser Arg Pro Gly Pro Ala Ser Gln Leu Pro Arg	
105 110 115 120	
ttt gtg cgt gtg aac act ctc aag acc tgc tcc gat gat gta gtt gat	485
Phe Val Arg Val Asn Thr Leu Lys Thr Cys Ser Asp Asp Val Val Asp	
125 130 135	
tat ttc aag aga caa ggt ttc tcc tat cag ggt cgg gct tcc agc ctc	533
Tyr Phe Lys Arg Gln Gly Phe Ser Tyr Gln Gly Arg Ala Ser Ser Leu	
140 145 150	
gat gac tta cga gcc ctc aag ggg aag cat ttt ctc ctg gac ccc ttg	581
Asp Asp Leu Arg Ala Leu Lys Gly Lys His Phe Leu Leu Asp Pro Leu	
155 160 165	
atg ccg gag ctg ctg gtg ttt ccc gcc cag aca gat ctg cat gaa cac	629
Met Pro Glu Leu Leu Val Phe Pro Ala Gln Thr Asp Leu His Glu His	
170 175 180	
cca ctg tac cgg gcc gga cac ctc att ctg cag gac agg gcc agc tgt	677
Pro Leu Tyr Arg Ala Gly His Leu Ile Leu Gln Asp Arg Ala Ser Cys	
185 190 195 200	
ctc cca gcc atg ctg ctg gac ccc ccg cca ggc tcc cat gtc atc gat	725
Leu Pro Ala Met Leu Leu Asp Pro Pro Gly Ser His Val Ile Asp	
205 210 215	
gcc tgt gcc gcc cca ggc aat aag acc agt cac ttg gct gct ctt ctg	773
Ala Cys Ala Ala Pro Gly Asn Lys Thr Ser His Leu Ala Leu Leu	
220 225 230	
aag aac caa ggg aag atc ttt gcc ttt gac ctg gat gcc aag cgg ctg	821
Lys Asn Gln Gly Lys Ile Phe Ala Phe Asp Leu Asp Ala Lys Arg Leu	
235 240 245	
gca tcc atg gcc acg ctg ctg gcc cgg gct ggc gtc tct tgc tgt gaa	869
Ala Ser Met Ala Thr Leu Leu Ala Arg Ala Gly Val Ser Cys Cys Glu	
250 255 260	
ctg gct gag gag gac ttc ctg gcg gtc tcc ccc tgc gat cca cgc tac	917
Leu Ala Glu Glu Asp Phe Leu Ala Val Ser Pro Ser Asp Pro Arg Tyr	
265 270 275 280	
cat gag gtc cac tac atc ctg ctg gat cct tcc tgc agt ggc tgc ggt	965

```

His Glu Val His Tyr Ile Leu Leu Asp Pro Ser Cys Ser Gly Ser Gly
                285                290                295
atg ccg agc aga cag ctg gag gag ccc ggg gca ggc aca cct agc ccg      1013
Met Pro Ser Arg Gln Leu Glu Glu Pro Gly Ala Gly Thr Pro Ser Pro
                300                305                310
gtg cgt ctg cat gcc ctg gca gct tcc agc agc gag ccc tgt gcc acg      1061
Val Arg Leu His Ala Leu Ala Ala Ser Ser Ser Glu Pro Cys Ala Thr
                315                320                325
cgc tca ctt tcc ctt ccc tgc agc ggc tcg tct act cca cgt gct ccc      1109
Arg Ser Leu Ser Leu Pro Cys Ser Gly Ser Ser Thr Pro Arg Ala Pro
                330                335                340
tct gcc agg agg aga atg aag acg tgg tgc gag atg cgc tgc agc aga      1157
Ser Ala Arg Arg Arg Met Lys Thr Trp Cys Glu Met Arg Cys Ser Arg
345                350                355                360
acc cgg gcg cct tca ggc tagctcccg cctgcctgcc tggccccacc      1205
Thr Arg Ala Pro Ser Gly
                365
gaggcctgag cacgttcccg ggtgccgagc actgcctccg ggccctccct gagaccacac      1265
tcagcagtggt cttcttcgtt gctgtaattg aacgggtcga ggtgcccaagc tcagcctcac      1325
aggccaaaagc atcagcacca gaacgcacac ccagcccagc cccaaagaga aagaagagac      1385
agcaaagagc cgcagccggt gcttgcacac cgccttgac atagcagagg ctccgggctg      1445
actccttctt ggtgggaaag gaagatgcct gtcctctccg tggaggaccc tgggccctca      1505
ccgcaggaag cagtttgggt tttgaaaggt tattgggtcc cttccttggg ctgtgttctt      1565
gctggtgagc aaagtgttac ctgcaaaaat aaaatgcaga acgtactcta cgacaaaaaa      1625
aaaaaaaaaa a      1636

<210> 72
<211> 1758
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 66..839

<220>
<221> sig_peptide
<222> 66..173
<223> Von Heijne matrix
      score 4.89555877630516
      seq LLLLRLNDAALRA/LQ

<400> 72
agaggaggtg gcggtggtgg ccctgccttg tggcccccg gctgcttgca ctggaactcg      60
tcgcc atg gag gag ctc cag gag cct ctg aga gga gag ctc cgg ctc tgc      110
      Met Glu Glu Leu Gln Glu Pro Leu Arg Gly Glu Leu Arg Leu Cys
                -35                -30                -25
ttc acg caa gct gcc cgg act agc ctc tta ctg ctc agg ctc aac gac      158
Phe Thr Gln Ala Ala Arg Thr Ser Leu Leu Leu Leu Arg Leu Asn Asp
                -20                -15                -10
gct gcc ctg cgg gcg ctg caa gag tgt cag cgg caa cag gta cgg ccg      206
Ala Ala Leu Arg Ala Leu Gln Glu Cys Gln Arg Gln Gln Val Arg Pro
                -5                1                5                10
gtg att gct ttc caa ggc cac cga ggg tat ctg aga ctc cca ggc cct      254
Val Ile Ala Phe Gln Gly His Arg Gly Tyr Leu Arg Leu Pro Gly Pro
                15                20                25
ggg tgg tcc tgc ctc ttc tcc ttc ata gtg tcc cag tgt tgt cag gag      302
Gly Trp Ser Cys Leu Phe Ser Phe Ile Val Ser Gln Cys Cys Gln Glu

```



30						35						40						
ggc	gct	ggt	ggt	agc	ttg	gac	ctt	gtg	tgc	caa	cgc	ttc	ctc	agg	tct	350		
Gly	Ala	Gly	Gly	Ser	Leu	Asp	Leu	Val	Cys	Gln	Arg	Phe	Leu	Arg	Ser			
45						50						55						
ggg	cct	aac	agc	ctc	cac	tgc	ctg	ggc	tca	ctc	agg	gag	cgc	ctc	att	398		
Gly	Pro	Asn	Ser	Leu	His	Cys	Leu	Gly	Ser	Leu	Arg	Glu	Arg	Leu	Ile			
60						65						70						
att	tgg	gca	gcc	atg	gat	tct	atc	cca	gcc	cca	tca	tca	gtt	cag	gga	446		
Ile	Trp	Ala	Ala	Met	Asp	Ser	Ile	Pro	Ala	Pro	Ser	Ser	Val	Gln	Gly			
80						85						90						
cac	aac	ctg	act	gaa	gat	gcc	aga	cat	cct	gag	agt	tgg	cag	aac	aca	494		
His	Asn	Leu	Thr	Glu	Asp	Ala	Arg	His	Pro	Glu	Ser	Trp	Gln	Asn	Thr			
95						100						105						
gga	ggc	tat	tct	gaa	gga	gat	gca	gta	tca	cag	cca	cag	atg	gca	cta	542		
Gly	Gly	Tyr	Ser	Glu	Gly	Asp	Ala	Val	Ser	Gln	Pro	Gln	Met	Ala	Leu			
110						115						120						
gag	gag	gtg	tca	gtg	tca	gat	cca	ctg	gca	agc	aac	caa	gga	cag	tca	590		
Glu	Glu	Val	Ser	Val	Ser	Asp	Pro	Leu	Ala	Ser	Asn	Gln	Gly	Gln	Ser			
125						130						135						
ctc	cca	gga	tcc	tca	agg	gag	cac	atg	gca	cag	tgg	gaa	gtg	aga	agc	638		
Leu	Pro	Gly	Ser	Ser	Arg	Glu	His	Met	Ala	Gln	Trp	Glu	Val	Arg	Ser			
140						145						150						
cag	acc	cat	gtt	cca	aac	aga	gaa	cct	gtt	cag	gca	ctg	cct	tcc	tct	686		
Gln	Thr	His	Val	Pro	Asn	Arg	Glu	Pro	Val	Gln	Ala	Leu	Pro	Ser	Ser			
160						165						170						
gcc	agc	cgg	aaa	cgt	ctg	gac	aag	aaa	cgt	tca	gtg	cct	gta	gcc	act	734		
Ala	Ser	Arg	Lys	Arg	Leu	Asp	Lys	Lys	Arg	Ser	Val	Pro	Val	Ala	Thr			
175						180						185						
gta	gaa	ctg	gaa	gaa	aag	agg	ttc	aga	act	ctg	cct	tta	gtg	ccc	ccc	782		
Val	Glu	Leu	Glu	Glu	Lys	Arg	Phe	Arg	Thr	Leu	Pro	Leu	Val	Pro	Pro			
190						195						200						
cct	aca	agg	cct	gac	caa	tca	gga	ttt	aca	aga	ggg	aga	aga	ttg	gga	830		
Pro	Thr	Arg	Pro	Asp	Gln	Ser	Gly	Phe	Thr	Arg	Gly	Arg	Arg	Leu	Gly			
205						210						215						
gca	aga	aga	tgaggacatg	gacccccagat	tagaacacaa	ttcctcagtt										879		
Ala	Arg	Arg																
220																		
caagaagatt	ctgaatcccc	aagtccctgaa	gatataccag	actacctcct	gcaatacagg											939		
gccatccaca	gtgcagaaca	gcaacatgcc	tatgagcagg	actttgagac	agattatgct											999		
gaataccgca	tctctgatgc	cctgtgtggg	actgcaagcc	aaaggttcat	agagctggga											1059		
gcagagatta	aaagagttcg	gcgaggaact	ccagaataca	aggctcctgga	agacaagata											1119		
atccaggaat	ataaaaaagt	caggaagcag	tacccaagtt	acagagaaga	aaagcgtcgc											1179		
tgtgagtacc	ttcaccagaa	attgtcccac	attaaaggct	tcacctctgga	gtttgaggaa											1239		
aagaacaggg	gcagctgaag	ttatcaaggg	aatttttgag	cctctgctta	gtgaaacaca													

<220>  
 <221> CDS  
 <222> 64..903

<220>  
 <221> sig\_peptide  
 <222> 64..162  
 <223> Von Heijne matrix  
 score 10.6748773272319  
 seq LLLLPFLPLLLA/AP

<400> 73  
 agctcaaggg gcctcgagga ctctctgcgt ctctggagac aagggcacta cacgcacttc 60  
 aga atg aag agt tgc ggg agc atg ctg ggg ctc tgg ggg cag cgg ctc 108  
 Met Lys Ser Cys Gly Ser Met Leu Gly Leu Trp Gly Gln Arg Leu  
 -30 -25 -20  
 ccc gcg gcg tgg gtc ctg ctt ctg ttg cct ttc ctg ccg ctg ctg ctg 156  
 Pro Ala Ala Trp Val Leu Leu Leu Leu Pro Phe Leu Pro Leu Leu Leu  
 -15 -10 -5  
 ctt gca gcc ccc gcg ccc cac cgc gcg tcc tac aag ccg gtc atc gtg 204  
 Leu Ala Ala Pro Ala Pro His Arg Ala Ser Tyr Lys Pro Val Ile Val  
 1 5 10  
 gtg cat ggg ctc ttc gac agc tcg tac agc ttc cgc cac ctg ctg gaa 252  
 Val His Gly Leu Phe Asp Ser Ser Tyr Ser Phe Arg His Leu Leu Glu  
 15 20 25 30  
 tac atc aat gag aca cac ccc ggg act gtg gtg aca gtg ctc gat ctc 300  
 Tyr Ile Asn Glu Thr His Pro Gly Thr Val Val Thr Val Leu Asp Leu  
 35 40 45  
 ttc gat ggg aga gag agc ttg cga ccc ctg tgg gaa cag gtg caa ggg 348  
 Phe Asp Gly Arg Glu Ser Leu Arg Pro Leu Trp Glu Gln Val Gln Gly  
 50 55 60  
 ttc cga gag gct gtg gtc ccc atc atg gca aag gcc cct caa ggg gtg 396  
 Phe Arg Glu Ala Val Val Pro Ile Met Ala Lys Ala Pro Gln Gly Val  
 65 70 75  
 cat ctc atc tgc tac tcg cag ggg ggc ctt gtg tgc cgg gct ctg ctt 444  
 His Leu Ile Cys Tyr Ser Gln Gly Gly Leu Val Cys Arg Ala Leu Leu  
 80 85 90  
 tct gtc atg gat gat cac aac gtg gat tct ttc atc tcc ctc tcc tct 492  
 Ser Val Met Asp Asp His Asn Val Asp Ser Phe Ile Ser Leu Ser Ser  
 95 100 105 110  
 cca cag atg gga cag tat gga gac acg gac tac ttg aag tgg ctg ttc 540  
 Pro Gln Met Gly Gln Tyr Gly Asp Thr Asp Tyr Leu Lys Trp Leu Phe  
 115 120 125  
 ccc acc tcc atg cgg tct aac ctc tat cgg atc tgc tat agc ccc ctg 588  
 Pro Thr Ser Met Arg Ser Asn Leu Tyr Arg Ile Cys Tyr Ser Pro Leu  
 130 135 140  
 atc aat ggg gaa aga gac cat ccc aat gcc aca gta tgg cgg aag aac 636  
 Ile Asn Gly Glu Arg Asp His Pro Asn Ala Thr Val Trp Arg Lys Asn  
 145 150 155  
 ttt ctg cgt gtg ggc cac ctg gtg ctg att ggg ggc cct gat gat ggt 684  
 Phe Leu Arg Val Gly His Leu Val Leu Ile Gly Gly Pro Asp Asp Gly  
 160 165 170  
 gtt att act ccc tgg cag tcc agc ttc ttt ggt ttc tat gat gca aat 732  
 Val Ile Thr Pro Trp Gln Ser Ser Phe Phe Gly Phe Tyr Asp Ala Asn  
 175 180 185 190  
 gag acc gtc ctg gag atg gag gag caa ctg gtt tat ctg cgg gat tct 780  
 Glu Thr Val Leu Glu Met Glu Glu Gln Leu Val Tyr Leu Arg Asp Ser  
 195 200 205

```

ttt ggg ttg aag act cta ttg gcc cgg ggg gcc ata gtg agg tgt cca      828
Phe Gly Leu Lys Thr Leu Leu Ala Arg Gly Ala Ile Val Arg Cys Pro
      210      215      220
atg gcc ggt atc tcc cac aca gcc tgg cac tcc aac cgt acc ctt tat      876
Met Ala Gly Ile Ser His Thr Ala Trp His Ser Asn Arg Thr Leu Tyr
      225      230      235
gag acc tgc att gaa cct tgg ctc tcc tgaggatata ttcagggggtc      923
Glu Thr Cys Ile Glu Pro Trp Leu Ser
      240      245
cccaggaact cctcgggtcca gagaccaagt ggtggccttg gaaagcagat gtcaggcttt      983
ggtgtgcctg tgaccacctc attgctccca tattatcccc catttttagt agagacgggg      1043
ttttagtaga gacttggcct ccagaaccc ccttcctctg ctctcccatg aatgacaatt      1103
ccaggcctcc cctacctcat gtccctctcat ttgggggatt gctccgtgct gtccctttct      1163
ctcaaggccg aagttcggaa gtgagaaacc atgttttttaa cttgtggctg ctcttgctgc      1223
tgctgctcct ccgtatctgg ctgtatgggt ggagaaccca cccactgccc accacagggg      1283
tctccttcca ggccactcag gacattttta gcttctctcc tccccatggt cccttttttc      1343
tctaaagtcc cctgacatca gccctcccaa ctccctaagag ggactaccca tgagagtggg      1403
gttctgaggg tcccctatgg ggacagttcc gttcttgaag tgtcagtgtt ggggaatatc      1463
tgtggcctat gaggcccatc tcaggttttg ggatccccc gtccctatga tcagtgttgg      1523
agtaccccc tgggagagcc tagtttcttt gaggccccag gccctctttt aactaccttt      1583
gaataggtgt tatccctgta tttatggaaa taaagttcca tttcctcaaa aaaaaaaaaa      1643
aaaa

<210> 74
<211> 1646
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 64..585

<220>
<221> sig_peptide
<222> 64..162
<223> Von Heijne matrix
      score 10.6748773272319
      seq LLLLPFLPLLLLA/AP

<400> 74
agctcaaggg gcctcgagga ctctctgcgt ctctggagac aagggcacta cacgcacttc      60
aga atg aag agt tgc ggg agc atg ctg ggg ctc tgg ggg cag cgg ctc      108
  Met Lys Ser Cys Gly Ser Met Leu Gly Leu Trp Gly Gln Arg Leu
      -30      -25      -20
ccc gcg gcg tgg gtc ctg ctt ctg ttg cct ttc ctg ccg ctg ctg ctg      156
Pro Ala Ala Trp Val Leu Leu Leu Leu Pro Phe Leu Pro Leu Leu Leu
      -15      -10      -5
ctt gca gcc ccc gcg ccc cac cgc gcg tcc tac aag ccg gtc atc gtg      204
Leu Ala Ala Pro Ala Pro His Arg Ala Ser Tyr Lys Pro Val Ile Val
      1      5      10
gtg cat ggg ctc ttc gac agc tcg tac agc ttc cgc cac ctg ctg gaa      252
Val His Gly Leu Phe Asp Ser Ser Tyr Ser Phe Arg His Leu Leu Glu
      15      20      25      30
tac atc aat gag aca cac ccc ggg act gtg gtg aca gtg ctc gat ctc      300
Tyr Ile Asn Glu Thr His Pro Gly Thr Val Val Thr Val Leu Asp Leu
      35      40      45
ttc gat ggg aga gag agc ttg cga ccc ctg tgg gaa cag gtg caa ggg      348
Phe Asp Gly Arg Glu Ser Leu Arg Pro Leu Trp Glu Gln Val Gln Gly

```

50	55	60	
ttc cga gag gct gtg gtc ccc atc atg gca aag gcc cct caa ggg gtg			396
Phe Arg Glu Ala Val Val Pro Ile Met Ala Lys Ala Pro Gln Gly Val			
65	70	75	
cat ctc atc tgc tac tcg cag ggg ggc ctt gtg tgc cgg gct ctg ctt			444
His Leu Ile Cys Tyr Ser Gln Gly Gly Leu Val Cys Arg Ala Leu Leu			
80	85	90	
tct gtc atg gat gat cac aac gtg gat tct ttc atc tcc ctc tcc tct			492
Ser Val Met Asp Asp His Asn Val Asp Ser Phe Ile Ser Leu Ser Ser			
95	100	105	110
cca cag atg gga cag tat gga gac acg gac tac ttg aag tgg ctg ttc			540
Pro Gln Met Gly Gln Tyr Gly Asp Thr Asp Tyr Leu Lys Trp Leu Phe			
115	120	125	
ccc acc tcc atg cgg tct aac ctc tat cgg atc tgc tat agc ccc			585
Pro Thr Ser Met Arg Ser Asn Leu Tyr Arg Ile Cys Tyr Ser Pro			
130	135	140	
tgatcaatgg ggaaagagac catcccaatg ccacagtatg gcggaagaac tttctgcgtg			645
tgggccacct ggtgctgatt gggggccctg atgatggtgt tattactccc tggcagtcca			705
gcttcttttg tttctatgat gcaaatagaga ccgtcctgga gatggaggag caactggttt			765
atctgcggga ttctttttggg ttgaagactc tattggcccg gggggccata gtgaggtgtc			825
caatggcccg tatctcccac acagcctggc actccaaccg taccctttat gagacctgca			885
ttgaaccttg gctctcctga ggatatattc aggggtcccc aggaactcct cggtcacagag			945
accaagtggg ggccttgga agcagatgtc aggcctttggg gtgcctgtga ccacctcatt			1005
gctcccatat tatcccccat ttttagtaga gacgggggtt tagtagagac ttggcctccc			1065
agaacccct tctctgctc ctccatgaat gacaattcca ggcctcccct acctcatgtc			1125
ctctcatttg ggggattgct ccgtgctgtc cctttctctc aaggccgaag ttcggaagtg			1185
agaaaccatg tttttaactt gtggctgtc ttgctgtgtc tgctcctccg tatctggctg			1245
tatgggtgga gaaccacccc actgccacc acaggggtct ccttcaggc cactcaggac			1305
attttttagt tctctcctcc ccattgtccc tttttctct aaagtcccct gacatcagcc			1365
ctcccaactc ctaagaggga ctaccatga gagtggggt ctgaggctcc cctatgggga			1425
cagttccgtt cttgaagtgt cagtgttggg gaatatctgt ggcctatgag gcccatctca			1485
ggtttgggga tccccagtc cctatgatca gtgttgaggt acccccctgg gagagcctag			1545
tttctttgag gccccaggcc ctcttttaac tacctttgaa taggtgttat ccctgtattt			1605
atggaaataa agttccattt cctcaaaaaa aaaaaaaaaa a			1646

<210> 75  
 <211> 1963  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 274..753

<220>  
 <221> sig\_peptide  
 <222> 274..324  
 <223> Von Heijne matrix  
 score 4.4969823290892  
 seq FAAFCYMLSLVLC/AA

<400> 75			
cttcttcgat ttgcggacgg ttccctccag cgactctcga cacacgtttt cctgtcttcg			60
ccggagggcc ggggtctgggg tcgccggagc ctgcgggaat ccagcgctta ttcgctaacc			120
ctcgagtgc ttcgctagct gtgcgccctc ctgggcacta gcctggagag gagegtgcag			180
acgcggctcc ttggagggag tgcggtcctc tagggaggca tcgggctcct aggggcttct			240
tggcgtgtgt ggtgggattg ggggtccgccg gcc atg gcc ttc act ttc gct gcg			294
	Met Ala Phe Thr Phe Ala Ala		

-15

ttc tgc tac atg ctg tct ctg gtg ctg tgc gct	gcg ctc atc ttc ttc	342
Phe Cys Tyr Met Leu Ser Leu Val Leu Cys Ala	Ala Leu Ile Phe Phe	
-10	-5	1
gcc atc tgg cac ata att gcc ttt gat gag tta agg aca gat ttt aag	390	
Ala Ile Trp His Ile Ile Ala Phe Asp Glu Leu Arg Thr Asp Phe Lys		
10	15	20
agc ccc ata gac cag tgc aat cct gtt cat gcg agg gaa cgg ttg agg	438	
Ser Pro Ile Asp Gln Cys Asn Pro Val His Ala Arg Glu Arg Leu Arg		
25	30	35
aac atc gag cgc atc tgc ttc ctt ctg cga aag ctg gtg ctg cca gaa	486	
Asn Ile Glu Arg Ile Cys Phe Leu Leu Arg Lys Leu Val Leu Pro Glu		
40	45	50
tac tcc atc cat agc ctc ttc tgc att atg ttc ctg tgt gcg caa gag	534	
Tyr Ser Ile His Ser Leu Phe Cys Ile Met Phe Leu Cys Ala Gln Glu		
55	60	65
tgg ctc acg ctg ggg ctg aat gtc cct cta ctt ttc tat cac ttc tgg	582	
Trp Leu Thr Leu Gly Leu Asn Val Pro Leu Leu Phe Tyr His Phe Trp		
75	80	85
agg tat ttc cac tgt cca gca gat agc tca gaa cta gcc tac gac cca	630	
Arg Tyr Phe His Cys Pro Ala Asp Ser Ser Glu Leu Ala Tyr Asp Pro		
90	95	100
ccg gtg gtc atg aat ccc gac act ttg agt tac tgt cag aag gag gcc	678	
Pro Val Val Met Asn Pro Asp Thr Leu Ser Tyr Cys Gln Lys Glu Ala		
105	110	115
tgg tgt aag ctg gcc ttc tat ctc ctc tcc ttc ttc tac tac ctt tac	726	
Trp Cys Lys Leu Ala Phe Tyr Leu Leu Ser Phe Phe Tyr Tyr Leu Tyr		
120	125	130
tgc atg atc tac act tta gtg agc tct taacgcaaag accatgcaca	773	
Cys Met Ile Tyr Thr Leu Val Ser Ser		
135	140	
tcacacagaga ctgagatggg agaggcctga gacggagagg tgcattttctg ctggtgactg	833	
gaggaggggac cagaatgagg atacgtgaga aatagacccg gcaggcagtc agactgaatg	893	
ggagctggaa tcacgcagca gttgggagcc gagttaaccc tgcgtgtctg tgtcaccctg	953	
tttgtcaatc tttggcattc gaattccaca cacgggggtcc tagagccctt ctgagcatca	1013	
gtgggtgtggg ggagtaggtg acgaaacact agacctctcc tgagagagaa ttgctgcttc	1073	
ctgaatccac ttcattgaac agcaccttgc aagttcaaat gagttcctgg gageggaggc	1133	
tggaaggcca caaggtgctt gctaaggaaac agaagaccc agagtcaagg ccaagtctgc	1193	
aggacctgt tgaaagcctc gagaatgtct tggctgcccc agactcttgt tgcctttctt	1253	
ccaagccatg gccatgccct ttttctcaaa tgggaggggc tggagggtgt gtgggatttg	1313	
tcttcagctg caaccagcct tgagcctgct gggctatatt cagctgagga ggggtaatat	1373	
aggaaaaatg catttttgaa acgtttgcaa catgatcaag gtgttagttc tccaccacac	1433	
aagttgtatt cttcttttgc cacctcaaac catcacagag tctttaaatg caaatcaatt	1493	
ggtcaatgct agtcaaagct atgttcttac aaaaacccca gacagctcag agctcagaaa	1553	
atcctgtgga gtggctgctc tgtaccgtgg gcatccggca gccaggaagt gagacaacat	1613	
aattataact ttgttttatg atgctgcac atttgtactg tttaggtcga cgtgaggaca	1673	
tcaccttatt tagaattttc cgtttggcat tctcttttgg gtgggagtta tgctgggggt	1733	
tgtaataaat gacaaggctg agatttttat gatgtttaaa ttgggcacaa tgattttgac	1793	
cttattcccc aaacttcttt tcttttctac tgtttaacat acacaggcta tttatacacg	1853	
tccccagctc ccacttgaaa cctgtgactc aggtttatga atgggtgtttg tgtagcaaca	1913	
cattgtgtgc tatgtttatt aaaatgcagc gacaaaaaaa aaaaaaaaaa	1963	

<210> 76  
 <211> 1757  
 <212> DNA  
 <213> Homo sapiens  
 <220>

<221> CDS  
<222> 191..1468

<220>  
<221> sig\_peptide  
<222> 191..274  
<223> Von Heijne matrix  
score 4.02941490119842  
seq GXLLEPFVHQVGG/HS

<400> 76  
catttttggtg cgagagaaac aataggacgg aaacgccgag gaacccggct gaggcggcag 60  
cagagcatcc tggccagaac aagccaagga gccaagacga gagggacaca ctgacaaaca 120  
acagacagaa gacgtactgg ccgctggact ccgctgcctc ccccatctcc ccgccatctg 180  
cgcccgaggg atg agc cca gcc ttc agg gcc atg gat gtg gag ccc cgc 229  
Met Ser Pro Ala Phe Arg Ala Met Asp Val Glu Pro Arg  
-25 -20  
gcc aaa ggc gtc ctt ctg gag ccc ttt gtc cac cag gtc ggg ggg cac 277  
Ala Lys Gly Val Leu Glu Pro Phe Val His Gln Val Gly Gly His  
-15 -10 -5 1  
tca tgc gtg ctc cgc ttc aat gag aca acc ctg tgc aag ccc ctg gtc 325  
Ser Cys Val Leu Arg Phe Asn Glu Thr Thr Leu Cys Lys Pro Leu Val  
5 10 15  
cca agg gaa cat cag ttc tac gag acc ctc cct tct gag atg cgc aaa 373  
Pro Arg Glu His Gln Phe Tyr Glu Thr Leu Pro Ser Glu Met Arg Lys  
20 25 30  
ttc act ccc cag tac aaa ggt gtg gta tct gtg cgc ttt gaa gaa gat 421  
Phe Thr Pro Gln Tyr Lys Gly Val Val Ser Val Arg Phe Glu Glu Asp  
35 40 45  
gaa gac agg aac ttg tgt cta ata gca tat cca ttg aaa ggg gac cat 469  
Glu Asp Arg Asn Leu Cys Leu Ile Ala Tyr Pro Leu Lys Gly Asp His  
50 55 60 65  
gga att gtg gac att gta gat aat tca gac tgt gaa cca aaa agt aag 517  
Gly Ile Val Asp Ile Val Asp Asn Ser Asp Cys Glu Pro Lys Ser Lys  
70 75 80  
ctc cta agg tgg aca aca aac aaa aaa cat cat gtc tta gaa aca gaa 565  
Leu Leu Arg Trp Thr Thr Asn Lys Lys His His Val Leu Glu Thr Glu  
85 90 95  
aag acc cct aag gac tgg gtg cgt cag cac cgt aaa gag gag aaa atg 613  
Lys Thr Pro Lys Asp Trp Val Arg Gln His Arg Lys Glu Glu Lys Met  
100 105 110  
aag agc cat aag tta gaa gaa gaa ttt gag tgg cta aag aaa tct gaa 661  
Lys Ser His Lys Leu Glu Glu Glu Phe Glu Trp Leu Lys Lys Ser Glu  
115 120 125  
gtc ttg tac tac act gta gag aag aag ggg aat ata agt tcc cag ctt 709  
Val Leu Tyr Tyr Thr Val Glu Lys Lys Gly Asn Ile Ser Ser Gln Leu  
130 135 140 145  
aaa cac tat aac cct tgg agc atg aaa tgt cac cag caa cag tta cag 757  
Lys His Tyr Asn Pro Trp Ser Met Lys Cys His Gln Gln Gln Leu Gln  
150 155 160  
aga atg aag gag aat gca aag cat cgg aac cag tac aaa ttt atc tta 805  
Arg Met Lys Glu Asn Ala Lys His Arg Asn Gln Tyr Lys Phe Ile Leu  
165 170 175  
ctg gaa aac ctg act tcc cgc tat gag gtg cct tgt gtc ctt gac ctc 853  
Leu Glu Asn Leu Thr Ser Arg Tyr Glu Val Pro Cys Val Leu Asp Leu  
180 185 190  
aag atg ggc aca cga caa cat ggt gat gat gct tca gag gag aag gca 901  
Lys Met Gly Thr Arg Gln His Gly Asp Asp Ala Ser Glu Glu Lys Ala

195	200	205	
gcc aac cag atc cga aaa tgt cag cag agc aca tct gca gtc att ggt			949
Ala Asn Gln Ile Arg Lys Cys Gln Gln Ser Thr Ser Ala Val Ile Gly			
210	215	220	225
gtg cgt gtg tgt ggc atg cag gtg tac caa gca ggc agt ggg cag ctc			997
Val Arg Val Cys Gly Met Gln Val Tyr Gln Ala Gly Ser Gly Gln Leu			
230	235	240	
atg ttc atg aac aag tac cat gga cgg aag cta tct gtg cag ggc ttc			1045
Met Phe Met Asn Lys Tyr His Gly Arg Lys Leu Ser Val Gln Gly Phe			
245	250	255	
aag gag gca ctt ttc cag ttc ttc cac aat ggg cgg tac ctg cgc cgt			1093
Lys Glu Ala Leu Phe Gln Phe Phe His Asn Gly Arg Tyr Leu Arg Arg			
260	265	270	
gaa ctc ctg ggc cct gtg ctc aag aag ctg act gag ctc aag gca gtg			1141
Glu Leu Leu Gly Pro Val Leu Lys Lys Leu Thr Glu Leu Lys Ala Val			
275	280	285	
ttg gag cga cag gag tcc tac cgc ttc tac tca agc tcc ctg ctg gtc			1189
Leu Glu Arg Gln Glu Ser Tyr Arg Phe Tyr Ser Ser Ser Leu Leu Val			
290	295	300	305
att tat gat ggc aag gag cgg ccc gaa gtg gtc ctg gac tca gat gct			1237
Ile Tyr Asp Gly Lys Glu Arg Pro Glu Val Leu Asp Ser Asp Ala			
310	315	320	
gag gat ttg gag gac ctg tca gag gaa tca gct gat gag tct gct ggt			1285
Glu Asp Leu Glu Asp Leu Ser Glu Glu Ser Ala Asp Glu Ser Ala Gly			
325	330	335	
gcc tat gcc tac aaa ccc atc ggc gcc agc tct gta gat gtg cgc atg			1333
Ala Tyr Ala Tyr Lys Pro Ile Gly Ala Ser Ser Val Asp Val Arg Met			
340	345	350	
atc gac ttt gca cac acc acc tgc agg ctg tat ggc gag gac acc gtg			1381
Ile Asp Phe Ala His Thr Cys Arg Leu Tyr Gly Glu Asp Thr Val			
355	360	365	
gtg cat gag ggc cag gat gct ggc tat atc ttc ggg ctc cag agc ctg			1429
Val His Glu Gly Gln Asp Ala Gly Tyr Ile Phe Gly Leu Gln Ser Leu			
370	375	380	385
ata gac att gtc aca gag ata agt gag gag agt ggg gag tgagcttgct			1478
Ile Asp Ile Val Thr Glu Ile Ser Glu Glu Ser Gly Glu			
390	395		
agctgctcca gtacttgaga gcgactctgt gtcccaggca cagctgtgct gcgtcaggga			1538
ggaagccagt atggccagggt ggtggctcct gcagcctgga gctgatgtgc agtggcctct			1598
gtgagcccca gcttgagcca gtcccagctg tgcttgaggt ctttatttat tttaactatt			1658
tcttcaacat tccacatttg atgatgatac ctctttcttc cctgagtgtgta tatgttctaa			1718
tacaaatctt tttgtttatt gtaaaaaaaaa aaaaaaaaaa			1757

<210> 77  
 <211> 2027  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 48..950

<220>  
 <221> sig\_peptide  
 <222> 48..107  
 <223> Von Heijne matrix  
 score 6.64507667657896  
 seq LLPLLSLLVGAWL/KL

[illegible]

100



	260		265		270	
gca gac gca ggc cgg ccg cca ggg gag ctg taagcagccg ggtggtgaca						970
Ala Asp Ala Gly Arg Pro Pro Gly Glu Leu						
	275		280			
aggagaaaag ccttctaggg tcaactgtcat tccctggcca tgttgcaaac agcgcaattc						1030
caagctcgag agcttcagcc tcaggaaaga acttccccctt ccctgtctcc catccctctg						1090
tggcaggcgc ctctcaccag ggcaggagag gactcagcct cctgtgtttt ggagaagggg						1150
cccaatgtgt gttgacgat gctggggggcc aggtgtttct gttagaggcc aagtattatt						1210
gacacaggat tgcaaacaca caaacaattg gaacagagca ctctgaaagg ccatttttta						1270
agcattttaa aatctattct ctcccccttt ctccctggat gattcaggaa gctgacattg						1330
tttctcaag gcagaatttt cctgggttctg ttttctcagc cagttgctgt ggaaggagaa						1390
tgctttcttt ttggcctcat ctgtggtttc gtgtccctct gaaggaaact agtttccact						1450
gtgtaacagg cagacatgta actatttaaa gcacagttca gtcctaaaag ggtctggggag						1510
aaccagatga tgtactaggt gaagcattgc attgtgggaa tcacaaagca aatagtactc						1570
cagaaagaca aatatcagaa gcttcctatt cttttttttt tttttttttt tttggagaca						1630
gggtctttct ctgttgccca ggctagagt cactgggtgat cacggctcac tctagccttg						1690
aattcctggg cccaagcaat tctcccacct cagcctcctg agtagctggg actacaagtg						1750
tgcaccacca tgcctggcta attttttgaa tttttgtagt gatgggatct cgctctgttg						1810
cccagggtgg tctcgaactc ctggcctcaa gcgacccctc cacctcgacc tcccaaagtg						1870
ctgggattac aggtgtgagc cacctcgctt gggccccctt ctccatatgc ctccaaaaac						1930
atgtccctgg agagtgcct gctcccacac tgtcactgga tgtcatgggg ccaataaaat						1990
ctcctgcaat tgtgtatctc aaaaaaaaaa aaaaaaa						2027

<210> 78  
 <211> 1880  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 156..512

<220>  
 <221> sig\_peptide  
 <222> 156..206  
 <223> Von Heijne matrix  
 score 3.55618791452243  
 seq WLTAVASLLPSPG/NS

<400> 78	
atatacaggt ggcagctctc gtccccctgag agcgggcgaa ggccagggtc ccacactcgc	60
agcgtctcga cggcgctcgg gacctccctc gtccactgct tgagttccag aggtgggtgc	120
ttccctgtcc tgaacttcag agtgcgaggt cataa atg ggt tcc ggc tgg ctt	173
Met Gly Ser Gly Trp Leu	
-15	
act gca gta gcc tcg ctc ctc ccc agc ccc ggt aac tcc gag cta ccc	221
Thr Ala Val Ala Ser Leu Leu Pro Ser Pro Gly Asn Ser Glu Leu Pro	
-10 -5 1 5	
gtc cag gcc ctc ggg cgt cgc ggg ggc agg gac tgg gcg cgg aac gag	269
Val Gln Ala Leu Gly Arg Arg Gly Gly Arg Asp Trp Ala Arg Asn Glu	
10 15 20	
gca ggg agg gac ctg gaa aaa cca ccc aga ttg cat tgc agt ggg cga	317
Ala Gly Arg Asp Leu Glu Lys Pro Pro Arg Leu His Cys Ser Gly Arg	
25 30 35	
ggc cgc ctg gag gag ccg gtt ccc cct aac cac ctc ccc gtg ggg ctc	365
Gly Arg Leu Glu Glu Pro Val Pro Pro Asn His Leu Pro Val Gly Leu	
40 45 50	
tcg gtg cgc ggt tcc cag gtg ctc agc tct gct ggg ccc agg agg tgc	413

```

Ser Val Arg Gly Ser Gln Val Leu Ser Ser Ala Gly Pro Arg Arg Cys
 55                      60                      65
cgc ctc aca ggg acg cgg aac ccc gtg cgt ggc ccc cgc cgg gtg gaa      461
Arg Leu Thr Gly Thr Arg Asn Pro Val Arg Gly Pro Arg Arg Val Glu
 70                      75                      80                      85
cag ata gcg cgg ggc ggt ccg gag gct cgt cgc caa gca ggt gac tct      509
Gln Ile Ala Arg Gly Gly Pro Glu Ala Arg Arg Gln Ala Gly Asp Ser
                      90                      95                      100
tgc tgaaaaagtg gttggaacac ttaaggaaac ccggccccgc ctgttctttc      562
Cys
taggtctttg gagtttggat taatcatttg tgtagcccgt ttggataaac cgaagacttt      622
attaaatcag cgcgtttaac aggaattccg cagtagtata cacattagaa tcttgagtct      682
tggagttgaa catattcaca cagacttgcc ttcttcctgt ttagtttatg ccttggtgtc      742
cgttattgga acgctaagct tgtgggagtt gtttacatcc tactgctcaa ggtcatcgct      802
aagggtgat ttttcacaaa aagaatttgc aacctccggc atgaatgact taagggaagt      862
ctaatacccg tttctgattt tttttttttt ttaattttaa agttaatctt tctgggccgg      922
gcgcggtggc tcacgcctgt aatcccagca ctttgggagg ccgaggcgga tcacgaggtc      982
aggagttcga gaccagcctg accaacaatg tgaaaccccg tctctactaa aaacacaaaa      1042
attagccggg cggggtggcg cgcacctgta atcccagctg ctcgggaggc tgaggcagga      1102
gaatcgcttg aacctgggag gcggggggtt gcagtgagcc gagatctggc cattgcactc      1162
cagcgtgggc aacagagtga gactccatct caaaaaaaaaa ggtaatctt tccaactaga      1222
ttttcaagga tgaggatttt gttgttgttg ttgttgttgt tctcaaatgt attcccagg      1282
cttggaaacag agcctgacat atactaggca ctcaacaaat atttgttgaa tgattgtaat      1342
gagtaacacc catttttgca gatctttgtc ttctgagcct agggcatagg tcatcactgc      1402
aggggtgaga ttgtcaaaat gggagtctac aggttaattt agacttaaat gtttaaagag      1462
tatgtgctca ttcttcaaca aacttacttt tgttaaatta aaatggtaaa atgtggtgga      1522
ggggttgga tatatgtaat tcaagacagt tctgaataca aaaatgtttt actgtctatc      1582
accaccatct ataaatctaa ttcactaagg ataactctgt taaggtggct ggaaagaacc      1642
ttgaggagag aggccttatt aagtattggc tcaggaccac acctaaaatt ctcaaaacgt      1702
tgagattctg ttgttttgtt ttttaagcgc agagacccaa gttgaggaac agcctataaa      1762
ataactggcc tgtactctta catacatgaa agccatcaaa gacaaagact gaagaagaac      1822
ttttgcagat taaaggactt taagagacat gatcctgaac caaaaaaaaaa aaaaaaaaaa      1880

```

<210> 79  
 <211> 584  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 67..351

<220>  
 <221> sig\_peptide  
 <222> 67..183  
 <223> Von Heijne matrix  
 score 10.6473524146908  
 seq FLCALCSFCPISA/AS

```

<400> 79
ctgattcttc gaaatgatat aagtcctgag ggcttcagtc ccattcgccg actcatactt      60
gcaatc atg gac tac agc cgt gtc ttt cag ggt gtg ttc ttc acc ttc      108
      Met Asp Tyr Ser Arg Val Phe Gln Gly Val Phe Phe Thr Phe
                      -35                      -30
aag cat gct ttt gct gat ggt gct tgg gat ctt tca ttt ctc tgt gct      156
Lys His Ala Phe Ala Asp Gly Ala Trp Asp Leu Ser Phe Leu Cys Ala
-25                      -20                      -15                      -10
ctt tgc agt ttc tgc cca atc tca gct gcc tct ggc aga cct tac agg      204

```

[illegible]

```
<220>
<221> sig_peptide
<222> 259..375
<223> Von Heijne matrix
score 5.809301698725
seq FCVCVIAIGVVQA/LI
```

103

```

Pro Leu Ser Tyr Leu Leu Met Val Thr Val Ile Leu Leu Pro Tyr Val
55 60 65
agc aag gtc acc ggc tgg tgc aga gac agg ctc ctg ggc cac agg gag 627
Ser Lys Val Thr Gly Trp Cys Arg Asp Arg Leu Leu Gly His Arg Glu
70 75 80
ccc tgc gct cac cca gtg gaa gtc ttc tgc ttt gac ctc cac gag cca 675
Pro Ser Ala His Pro Val Glu Val Phe Ser Phe Asp Leu His Glu Pro
85 90 95 100
ctc agc aag gag cgc gtg gaa gcc ttc agc gac gga gtc tac gcc atc 723
Leu Ser Lys Glu Arg Val Glu Ala Phe Ser Asp Gly Val Tyr Ala Ile
105 110 115
gtg gcc acg ctt ctc atc ctg gac atc tgc ccc tcc tgc tcc ctt tgg 771
Val Ala Thr Leu Leu Ile Leu Asp Ile Cys Pro Ser Cys Ser Leu Trp
120 125 130
ctg gct gtt gct tcc ttc cag cgt ctg ctc ctc cgc ggc ctc atc tgc 819
Leu Ala Val Ala Ser Phe Gln Arg Leu Leu Leu Arg Gly Leu Ile Cys
135 140 145
ctc ttc gtc tgt tagagcgcgc gtctcgtctc agtcgtcacg tttttgggtt 871
Leu Phe Val Cys
150
ttgtgggggtt tttttttttt tttttttttg agacagtcct gctgtgtcgc ccaggctgga 931
gtatagtggc tcaagctcag ctactgcaa cctccgcctc ccaggttcaa gcaattctcc 991
tgcctcagcc tccaagtag ttgggattac aagcaccac caccatgcc agctaacttt 1051
ttgcattttt aatagagatg aggtttcacc aagttggcca ggctggtctt gaactcctga 1111
cctcaggtga tctgcccacc tcggcctccc aaagtgtctg gattacaggt gtaagccacc 1171
gtgcccggcc atcgtaatgt ttgaatttgc ttttttacat cttccatcct tttggagtgt 1231
cttgttccct cgtcatagtt cagcactgtg accaccttgg ggtagacac tatgggttta 1291
tatectgtac ttgatattct cgagtcgaag tctcctgatg ctctcaaaaa aaaaaaaaaa 1351

<210> 81
<211> 720
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 111..377

<220>
<221> sig_peptide
<222> 111..233
<223> Von Heijne matrix
score 5.26415334394122
seq LWFLAQIPSRVAG/SL

<400> 81
aaaccgaaac cagcgcctcca aacaattggg acccgggatc ttatgccagt gaggctgtgc 60
tgcggctgag cgggcctccc atccctctta aaagagttag gcatttagcc atg cct 116
Met Pro
-40
ccc acc cgg gac cct ttc cag cag cct aca tta gat aac gat gat tcc 164
Pro Thr Arg Asp Pro Phe Gln Gln Pro Thr Leu Asp Asn Asp Asp Ser
-35 -30 -25
tac tta gga gaa ctg cgg gct tcc aag gta ctg tgg ttt ctt gcg cag 212
Tyr Leu Gly Glu Leu Arg Ala Ser Lys Val Leu Trp Phe Leu Ala Gln
-20 -15 -10
att ccc agt agg gtc gcc ggt agt ctt tct gtc tgt gtg atg agc 260
Ile Pro Ser Arg Val Ala Gly Ser Leu Leu Ser Val Cys Val Met Ser

```

```

      -5              1              5
aga gat ggt aac ata aag gac tct ggt gaa gac act cag tcg ggt acc      308
Arg Asp Gly Asn Ile Lys Asp Ser Gly Glu Asp Thr Gln Ser Gly Thr
10              15              20              25
agg gaa gtc tgt ttt ctg cct gcc tcc cta tct cca tat tca agt cgg      356
Arg Glu Val Cys Phe Leu Pro Ala Ser Leu Ser Pro Tyr Ser Ser Arg
              30              35              40
cta acg ttt cag agg cgt ttt tgagcagagg aaagtagagt tctagtctag      407
Leu Thr Phe Gln Arg Arg Phe
              45
aggaacaagg ggctctggca gctcaaatca attaaccaag atccaattcc ctggagaatt      467
ttaaacccct cccactccac ccatcacttg cctggctaac atcagacact ggatcaaccc      527
taaaaaggag tccatccaca gcatccaagg atccatagtg tccccacaca ctgcagccac      587
caatggaggg tactcccgaa agaaagatgg tggctttctt tccacctagt gttgacagat      647
ccctgaacta attatagtga aacatactgc ggcccacttc cattaatatag atttgtgcaa      707
aaaaaaaaaa aaa      720

<210> 82
<211> 1029
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 223..432

<220>
<221> sig_peptide
<222> 223..336
<223> Von Heijne matrix
      score 4.17665217008018
      seq LVNVLFFFFTPLMT/LV

<400> 82
gtttttgtat tggaagcagt tgtttggcct tgctgagcaa acgtctatgc cttctccatt      60
acatccaaag gagaatagcc ccatgtgaag aatggaatca gtagatgttt ggtcgctgta      120
ccatatccac tcttaggata caacaagagc aagcccaatt ctcttggtgg tgtgggcagt      180
cggcttgcac cacgtaccta tctcagctct ttttggaaagc tt atg tcc tcc cca      234
                                Met Ser Ser Pro
                                -35
caa ctt cca gct ttc tta tgg gac aag ggt aca ctc acc act gcc ata      282
Gln Leu Pro Ala Phe Leu Trp Asp Lys Gly Thr Leu Thr Thr Ala Ile
              -30              -25              -20
tct aat cct gct tgc ctg gta aat gtt ctc ttc ttc ttt aca ccc ctg      330
Ser Asn Pro Ala Cys Leu Val Asn Val Leu Phe Phe Phe Thr Pro Leu
              -15              -10              -5
atg act ctg gtc act cta ctc atc ctg gtc tgg aaa gta acc aaa gac      378
Met Thr Leu Val Thr Leu Leu Ile Leu Val Trp Lys Val Thr Lys Asp
              1              5              10
aaa agc aac aag aac aga gag aca cac cca aga aag gag gca aca tgg      426
Lys Ser Asn Lys Asn Arg Glu Thr His Pro Arg Lys Glu Ala Thr Trp
              15              20              25              30
ctg cca taaagatctg gatctcttgg tggggactcc actgaggtga agacctgatt      482
Leu Pro
gtacaagaga ggcacggcca ctggagctgt ctcagagccc agagccaggg gagccagagc      542
tgcttttagcc accctgtttcc tccattgccat gatgtccccc caggcctcat ttccttctc      602
tgccaccatc cctcttataa tgcactcctc ctgcggttct ttggcttgtc ccagcttctg      662
agtttgaatg tctttttttt tttttttttt tttttgkgya tcttcaagac tgaaatagta      722

```



```

Val Ala Met Leu Ile Ala Pro Val Ala Gly Leu Ile Ala Ala Pro Ala
75      80      85      90
att gcc aca tct gtt cta ggt cct gtt gct gtt cct gcc act gcc atg      1161
Ile Ala Thr Ser Val Leu Gly Pro Val Ala Val Pro Ala Thr Ala Met
      95      100      105
cca cct gct gtc ctt gct gct cct cct tca gca gcc cct gga gtg ctc      1209
Pro Pro Ala Val Leu Ala Ala Pro Pro Ser Ala Ala Pro Gly Val Leu
      110      115      120
gtg gat gga gaa gcc gca cta gcc gtt ccg tgg gag gca tgt tgg att      1257
Val Asp Gly Glu Ala Ala Leu Ala Val Pro Trp Glu Ala Cys Trp Ile
      125      130      135
ccc tct ccc cca gca taagcagaag aggtggctgc agatacatca caaggcttgt      1312
Pro Ser Pro Pro Ala
      140
agagcccgagt ctcaactctga tcccccttctc tgtggagctc tgcagcctat accaagggga      1372
agagaaacag atgagattga gatgactgaa agggagatca gaactttcta ctccctctctt      1432
atcctggaggt taattcaagg gcttataatt agaagaacct gggtcgggtg tgggtggctca      1492
cgcttgtaat cccaacactt tgggaggcca aggagggcag atcgcttgag gccaggagtt      1552
caagaccagc cttgccaaca tagcaaaacc ccgactctac taaaaataca aaaaattagc      1612
tggacaggat ggcgcatgcc tgtaatccca gctactcagt aggctgaggt aggagtatcg      1672
cttgaactcg gatggcggag gctgcagtga gccaagactg cgccactcca ctgcactcca      1732
gcctgggcaa cagagtgaga cactgttttaa aaaaaaagaaa gaaaaaaaaa aaaaaa      1788

<210> 84
<211> 805
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 30..527

<220>
<221> sig_peptide
<222> 30..74
<223> Von Heijne matrix
      score 8.68924532952647
      seq PLLIIICLLPAIEG/KN

<400> 84
actggggcac agtaggagga acccagaag atg ctg cct ctc ctg atc atc tgt      53
      Met Leu Pro Leu Leu Ile Ile Cys
      -15      -10
ctc ctg cct gcc att gaa ggg aag aac tgc ctc cgc tgc tgg cca gaa      101
Leu Leu Pro Ala Ile Glu Gly Lys Asn Cys Leu Arg Cys Trp Pro Glu
      -5      1      5
ctg tct gcc ttg ata gac tat gac ctg cag atc ctc tgg gtg acc cca      149
Leu Ser Ala Leu Ile Asp Tyr Asp Leu Gln Ile Leu Trp Val Thr Pro
      10      15      20      25
ggg cca ccc aca gaa ctt tct caa aat cgt gac cat ttg gaa gaa gaa      197
Gly Pro Pro Thr Glu Leu Ser Gln Asn Arg Asp His Leu Glu Glu Glu
      30      35      40
aca gcc aaa ttc ttc act caa gta cac caa gcc att aaa acg tta cga      245
Thr Ala Lys Phe Phe Thr Gln Val His Gln Ala Ile Lys Thr Leu Arg
      45      50      55
gat gat aaa aca gta ctt ctg gaa gag atc tac acg cac aag aat ctc      293
Asp Asp Lys Thr Val Leu Leu Glu Glu Ile Tyr Thr His Lys Asn Leu
      60      65      70

```

[illegible]

```
<210> 85
<211> 814
<212> DNA
<213> Homo sapiens
```

```
<220>
<221> CDS
<222> 39..506
```

```
<220>
<221> sig_peptide
<222> 39..83
<223> Von Heijne matrix
score 5.91494342964539
seq ILMLTFIICGLLT/RV
```

<400> 85																	
attcctcagg acacagagct tcctctctcc caggagcc atg aat atc ctg atg ctg																	56
Met Asn Ile Leu Met Leu																	
-15 -10																	
acc ttc att atc tgt ggg ttg cta act cgg gtg acc aaa ggt agc ttt																	104
Thr	Phe	Ile	Ile	Cys	Gly	Leu	Leu	Thr	Arg	Val	Thr	Lys	Gly	Ser	Phe		
-5 1 5																	
gaa ccc caa aaa tgt tgg aag aat aat gta gga cat tgc aga aga cga																	152
Glu	Pro	Gln	Lys	Cys	Trp	Lys	Asn	Asn	Val	Gly	His	Cys	Arg	Arg	Arg		
10 15 20																	
tgt tta gat act gaa agg tac ata ctt ctt tgt agg aac aag cta tca																	200
Cys	Leu	Asp	Thr	Glu	Arg	Tyr	Ile	Leu	Leu	Cys	Arg	Asn	Lys	Leu	Ser		
25 30 35																	
tgc tgc att tct ata ata tca cat gaa tat act cga cga cca gca ttt																	248
Cys	Cys	Ile	Ser	Ile	Ile	Ser	His	Glu	Tyr	Thr	Arg	Arg	Pro	Ala	Phe		
40 45 50 55																	
cct gtg att cac cta gag gat ata aca ttg gat tat agt gat gtg gac																	296
Pro	Val	Ile	His	Leu	Glu	Asp	Ile	Thr	Leu	Asp	Tyr	Ser	Asp	Val	Asp		
60 65 70																	
tct ttt act ggt tcc cca gta tct atg ttg aat gat ctg ata aca ttt																	344
Ser	Phe	Thr	Gly	Ser	Pro	Val	Ser	Met	Leu	Asn	Asp	Leu	Ile	Thr	Phe		



```

      75      80      85
gac aca act aaa ttt gga gaa acc atg aca cct gag acc aat act cct 392
Asp Thr Thr Lys Phe Gly Glu Thr Met Thr Pro Glu Thr Asn Thr Pro
      90      95     100
gag act act atg cca cca tcc gag gcc act act ccc gag act act atg 440
Glu Thr Thr Met Pro Pro Ser Glu Ala Thr Thr Pro Glu Thr Thr Met
      105     110     115
cca cca tct gag act gct act tcc gag act atg cca cca cct tct cag 488
Pro Pro Ser Glu Thr Ala Thr Ser Glu Thr Met Pro Pro Pro Ser Gln
      120     125     130     135
aca gct ctt act cat aat taattaacat ttacttctgg tatggaacaa 536
Thr Ala Leu Thr His Asn
      140
ctagaaatac tgctggaaat aatatccaaa gagctgattc taccaatcca atttcaccag 596
gaaaattcca tcagggattg gatgaccatg gggatggaca taattgctac taccaacaca 656
acagccaaga gagttgcctt acaattagaa atgtgtagac agaaatgtat agaagataca 716
aggattctct taattggact taaattcttt atctgtcttc ctccgatgta ctcaaata 776
tgagctaatt tttgtcttaa gtgaaaaaaaa aaaaaaaa 814

<210> 86
<211> 598
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 115..429

<220>
<221> sig_peptide
<222> 115..210
<223> Von Heijne matrix
      score 8.2583062681354
      seq LVAAMVLLSVVFC/LY

<400> 86
attctaccag ctctggctga gcctgagctt ccaaaagtga gctgagctgt tcaaccttgg 60
atcttaatta ctcctagcag ggataattag gtccctcttt ctcagattac aggc atg 117
                                     Met
gca aag atg ttt gat ctc agg acg aag atc atg atc ggc atc gaa agc 165
Ala Lys Met Phe Asp Leu Arg Thr Lys Ile Met Ile Gly Ile Glu Ser
      -30      -25      -20
agc tta ctg gtt gcc gcg atg gtg ctc cta agt gtt gtg ttc tgt ctt 213
Ser Leu Leu Val Ala Ala Met Val Leu Leu Ser Val Val Phe Cys Leu
      -15      -10      -5      1
tac ttc aaa gta gct aag gca cta aaa gct gca aag gac cct gat gct 261
Tyr Phe Lys Val Ala Lys Ala Leu Lys Ala Ala Lys Asp Pro Asp Ala
      5      10      15
gtg gct gta aaa aat cac aac cca gac aag gtg tgt tgg gcc acg aac 309
Val Ala Val Lys Asn His Asn Pro Asp Lys Val Cys Trp Ala Thr Asn
      20      25      30
agc cag gcc aaa gcc acc acc atg gag tct tgt cca tct ctc cag tgc 357
Ser Gln Ala Lys Ala Thr Thr Met Glu Ser Cys Pro Ser Leu Gln Cys
      35      40      45
tgt gaa ggt tgt aga atg cat gcc agt tct gat tcc ctg cca cct tgc 405
Cys Glu Gly Cys Arg Met His Ala Ser Ser Asp Ser Leu Pro Pro Cys
      50      55      60      65
tgt tgt gac ata aat gag ggc ctc tgacttggga aagctgggca caaaaatctt 459

```

[illegible]

<220>  
 <221> sig\_peptide  
 <222> 133..213  
 <223> Von Heijne matrix  
 score 11.106948594338  
 seq LTSLILVTLISA/FV

<400> 88  
 atttccaggg agctgaggag ctgagggcag agctagcttt tggttatttg ggatgttatt 60  
 gccagtttcc tcccagggcc attgttacca cctgatcatt tgagtttttag tttctctagc 120  
 agatgctgac ta atg act gac cag gat cga atc atc aat tta gtt gtt ggc 171  
 Met Thr Asp Gln Asp Arg Ile Ile Asn Leu Val Val Gly  
 -25 -20 -15  
 agc tta aca tcc tta ttg att cta gta acg ctg ata agt gct ttt gtt 219  
 Ser Leu Thr Ser Leu Leu Ile Leu Val Thr Leu Ile Ser Ala Phe Val  
 -10 -5 1  
 ttc cct caa cta cct cca aaa ccg ttg aat ata ttc ttt gct gtc tgc 267  
 Phe Pro Gln Leu Pro Pro Lys Pro Leu Asn Ile Phe Phe Ala Val Cys  
 5 10 15  
 atc tct ttg agt agt att act gcc tgc ata atc tac tgg tat cga caa 315  
 Ile Ser Leu Ser Ser Ile Thr Ala Cys Ile Ile Tyr Trp Tyr Arg Gln  
 20 25 30  
 gga gac tta gaa ccg aaa ttt aga aag cta att tac tat atc ata ttt 363  
 Gly Asp Leu Glu Pro Lys Phe Arg Lys Leu Ile Tyr Tyr Ile Ile Phe  
 35 40 45 50  
 tct atc atc atg ttg tgt ata tgt gca aac ctg tac ttc cat gat gtg 411  
 Ser Ile Ile Met Leu Cys Ile Cys Ala Asn Leu Tyr Phe His Asp Val  
 55 60 65  
 gga agg tgaggctgcc aaggagaagt acttaccagg actcttcaaa atgatacatt 467  
 Gly Arg  
 aggacagtga gtaattttttg gataaggtat gctgaagaat ctccctgcaga agtctgatac 527  
 atgatttttca tgttaattgt aaatgttaat tccctcttgc aaggagagaca tatcctagat 587  
 cactttgctt tttctttaag gagctgatgt tgcacctaata cattccaacc cttaaagcta 647  
 aaacagcaca aaaaaatttc acttttgaaa tgaaattttt ataattgtat ggcaaaaggc 707  
 tatgtaaaaa caaatcttgc atcttaagac aaatattctt ttatttctgt taaactgaat 767  
 atacaattgt tccctaggca accaactttt gcttataact acaatttaaat ttcacgttga 827  
 caaaacacag tgaaaaagaca acttttgtgaa gatctaatta caataataaa taaaataatt 887  
 tacaaaaaaa aaaaaaaaa 905

<210> 89  
 <211> 514  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 113..364  
 <220>  
 <221> sig\_peptide  
 <222> 113..172  
 <223> Von Heijne matrix  
 score 4.37180298395146  
 seq SLLLSLPPHQGLT/FS

<400> 89  
 ttttttacat ggtgttccca cagctgggag gacaccaca tggtcggcgt gcaggatatt 60  
 tgcgtggacc ctagaaaagc caccacgacc tgtgggccat gatgctaccc ca atg gct 118

																Met Ala			
																-20			
gct	gct	gct	gtt	cct	tct	ctt	ctt	ctt	tct	ctt	cct	cct	cac	cag	ggg		166		
Ala	Ala	Ala	Val	Pro	Ser	Leu	Leu	Leu	Ser	Leu	Pro	Pro	His	Gln	Gly				
			-15					-10					-5						
ctc	act	ttc	tcc	aac	aaa	ata	caa	cct	ttt	gga	gct	caa	gga	gtc	ttg		214		
Leu	Thr	Phe	Ser	Asn	Lys	Ile	Gln	Pro	Phe	Gly	Ala	Gln	Gly	Val	Leu				
	1					5					10								
cat	ccg	gaa	cca	gga	ctg	cga	gac	tgg	ctg	ctg	cca	acg	tgc	tcc	aga		262		
His	Pro	Glu	Pro	Gly	Leu	Arg	Asp	Trp	Leu	Leu	Pro	Thr	Cys	Ser	Arg				
15					20					25					30				
caa	ttg	cga	gtc	gca	ctg	ccg	gag	aag	ggg	tcc	gag	ggc	agt	ctg	tgt		310		
Gln	Leu	Arg	Val	Ala	Leu	Pro	Glu	Lys	Gly	Ser	Glu	Gly	Ser	Leu	Cys				
			35					40					45						
caa	acg	cag	ctg	cca	gct	act	cca	tgc	ttc	ctg	cct	tcg	aat	acg	gtg		358		
Gln	Thr	Gln	Leu	Pro	Ala	Thr	Pro	Cys	Phe	Leu	Pro	Ser	Asn	Thr	Val				
		50					55					60							
aga	acg	tga	agtc	atg	agct	gct	gct	aagg	cat	gtg	gca	ac	ctt	ga	agaga	aggtc	414		
Arg	Thr																		
aag	ag	ct	tacc	agcc	ac	caaaa	aga	atg	ccag	cact	tc	ctgt	gt	cttt	gctt	tgg	att	catg	474
agaa	at	ata	c	gtt	c	tattt	g	ctt	caaaaa	aaaaaaaa									514
<210>	90																		
<211>	518																		
<212>	DNA																		
<213>	Homo sapiens																		
<220>																			
<221>	CDS																		
<222>	9..380																		
<220>																			
<221>	sig_peptide																		
<222>	9..104																		
<223>	Von Heijne matrix																		
	score 4.73369226787171																		
	seq AVFAVL FVFFLFA/ML																		
<400>	90																		
acat	ccta	atg	gtg	gtg	gtt	gaa	cca	gga	gcc	agt	tta	ttc	cca	aat	ggt		50		
		Met	Val	Val	Val	Glu	Pro	Gly	Ala	Ser	Leu	Phe	Pro	Asn	Gly				
				-30				-25					-20						



<221> CDS  
 <222> 185..634

<220>  
 <221> sig\_peptide  
 <222> 185..253  
 <223> Von Heijne matrix  
       score 9.49395175807817  
       seq SLLFICFFGESFC/IC

<400> 92  
 atattttgct gactggcaag gttatatgaa gtgcttttat tgaagcacca ttttaactaa 60  
 tagctcctgg tattttctgc ttcccttcgt aggggaattta gttattttat tttattattt 120  
 agctaattta gctattttta aatagctaaa ttttagctac ttttttttca attgacaaaag 180  
 aagg atg tct aat caa aga cta ccg ctg att ttt tct ctg ttg ttt atc 229  
       Met Ser Asn Gln Arg Leu Pro Leu Ile Phe Ser Leu Leu Phe Ile  
                   -20                  -15                  -10  
 tgc ttc ttc ggg gag agt ttc tgc att tgt gat gga act gtc tgg aca 277  
 Cys Phe Phe Gly Glu Ser Phe Cys Ile Cys Asp Gly Thr Val Trp Thr  
                   -5                  1                  5  
 aag gtt gga tgg gag att ctt cca gaa gaa gta cat tat tgg aaa ggt 325  
 Lys Val Gly Trp Glu Ile Leu Pro Glu Glu Val His Tyr Trp Lys Gly  
       10                  15                  20  
 tgt tta tat ctc att tat aat tta tta caa gct gtc ttc ttc gtc tta 373  
 Cys Leu Tyr Leu Ile Tyr Asn Leu Leu Gln Ala Val Phe Phe Val Leu  
       25                  30                  35                  40  
 ttt gtt ttg tct gtg cat tac ctg tgg aag aaa tgg aag aaa cac caa 421  
 Phe Val Leu Ser Val His Tyr Leu Trp Lys Lys Trp Lys Lys His Gln  
                   45                  50                  55  
 aaa aag ctg aaa aag caa gcc tcc tta gaa aaa cct ggt aat gat cta 469  
 Lys Lys Leu Lys Lys Gln Ala Ser Leu Glu Lys Pro Gly Asn Asp Leu  
                   60                  65                  70  
 gaa agc cca ttg atc aac aac att gac caa aca ctc cac aga gtg gca 517  
 Glu Ser Pro Leu Ile Asn Asn Ile Asp Gln Thr Leu His Arg Val Ala  
                   75                  80                  85  
 acc aca gca tca gtg ata tac aag atc tgg gag cac agg tct cac cat 565  
 Thr Thr Ala Ser Val Ile Tyr Lys Ile Trp Glu His Arg Ser His His  
                   90                  95                  100  
 cct tcc tct aag aaa att aag cac tgc aaa tta aag aag agt aaa 613  
 Pro Ser Ser Lys Lys Ile Lys His Cys Lys Leu Lys Lys Lys Ser Lys  
       105                  110                  115                  120  
 gaa gaa gga gcc aga aga tac taaataaatg catatgcaaa tgtagcttag 664  
 Glu Glu Gly Ala Arg Arg Tyr  
                   125  
 tcaattatag atatcacaaa agaaatctat catctaagga ttaaaaattg ttctttggaa 724  
 aaaaaaaaaa aaa 737

<210> 93  
 <211> 728  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 53..646

<220>  
 <221> sig\_peptide

<222> 53..91

<223> Von Heijne matrix

score 4.95353272042967

seq MLLGRLTSQLLRA/VP

<400> 93

aatttgagcc gcgtcgagct cccctgggac ctgtggccgc cgccacaga cc atg ctc 58  
Met Leu

ctg ggg cgc ctg act tcc cag ctg ttg agg gcc gtt cct tgg gca ggc 106  
Leu Gly Arg Leu Thr Ser Gln Leu Leu Arg Ala Val Pro Trp Ala Gly  
-10 -5 1 5

ggc cgc ccg cct tgg ccc gtc tct gga gtg ctg ggc agc cgg gtc tgc 154  
Gly Arg Pro Pro Trp Pro Val Ser Gly Val Leu Gly Ser Arg Val Cys  
10 15 20

ggg ccc ctt tac agc aca tcg ccg gcc ggc cca ggt agg gcg gcc tct 202  
Gly Pro Leu Tyr Ser Thr Ser Pro Ala Gly Pro Gly Arg Ala Ala Ser  
25 30 35

ctc cct cgc aag ggg gcc cag ctg gag ctg gag gag atg gtc ccc agg 250  
Leu Pro Arg Lys Gly Ala Gln Leu Glu Leu Glu Glu Met Val Pro Arg  
40 45 50

aag atg tcc gtc agc ccc ctg gag agc tgg ctc acg gcc cgc tgc ttc 298  
Lys Met Ser Val Ser Pro Leu Glu Ser Trp Leu Thr Ala Arg Cys Phe  
55 60 65

ctg ccc aga ctg gat acc ggg acc gca ggg act gtg gct cca ccg caa 346  
Leu Pro Arg Leu Asp Thr Gly Thr Ala Gly Thr Val Ala Pro Pro Gln  
70 75 80 85

tcc tac cag tgt ccg ccc agc cag ata ggg gaa ggg gcc gag cag ggg 394  
Ser Tyr Gln Cys Pro Pro Ser Gln Ile Gly Glu Gly Ala Glu Gln Gly  
90 95 100

gat gaa ggc gtc gcg gat gcg cct caa att cag tgc aaa aac gtg ctg 442  
Asp Glu Gly Val Ala Asp Ala Pro Gln Ile Gln Cys Lys Asn Val Leu  
105 110 115

aag atc cgc cgg cgg aag atg aac cac cac aag tac cgg aag ctg gtg 490  
Lys Ile Arg Arg Arg Lys Met Asn His His Lys Tyr Arg Lys Leu Val  
120 125 130

aag aag acg cgg ttc ctg cgg agg aag gtc cag gag gga cgc ctg aga 538  
Lys Lys Thr Arg Phe Leu Arg Arg Lys Val Gln Glu Gly Arg Leu Arg  
135 140 145

cgc aag cag atc aag ttc gag aaa gac ctg agg cgc atc tgg ctg aag 586  
Arg Lys Gln Ile Lys Phe Glu Lys Asp Leu Arg Arg Ile Trp Leu Lys  
150 155 160 165

gcg ggg cta aag gaa gcc ccc gaa ggc tgg cag acc ccc aag atc tac 634  
Ala Gly Leu Lys Glu Ala Pro Glu Gly Trp Gln Thr Pro Lys Ile Tyr  
170 175 180

ctg cgg ggc aaa tgagtctggc gccgcccttc ccgcccgttg ctgctgtgat 686  
Leu Arg Gly Lys  
185

ccgtagtaat aaattctcag aggacccaaa aaaaaaaaaa aa 728

<210> 94

<211> 582

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 247..510

Figure 1 consists of eight line graphs arranged in two rows of four. The top row shows the plasma concentration of diazepam (mg/ml) over time (hours) for four groups: (a) control, (b) diazepam, (c) diazepam + diazepam, and (d) diazepam + diazepam + diazepam. The bottom row shows the plasma concentration of diazepam (mg/ml) over time (hours) for four groups: (e) control, (f) diazepam, (g) diazepam + diazepam, and (h) diazepam + diazepam + diazepam. The graphs show that the plasma concentration of diazepam increases over time in all groups, with the highest concentration observed in the group receiving three doses of diazepam (d).

```
<210> 95
<211> 1913
<212> DNA
<213> Homo sapiens
```

```
<220>
<221> sig_peptide
<222> 143..277
<223> Von Heijne matrix
score 5.94057630118762
seq VLVDLAILGQAYA/FA
```

116



Val	Cys	Gly	Leu	Leu -15	Gln	Val	Leu	Val	Asp -10	Leu	Ala	Ile	Leu	Gly -5	Gln		
gcc	tac	gcc	ttc	gcc	cca	ccc	cca	gaa	gcc	ggc	gcc	cca	cgc	cgt	gca	316	
Ala	Tyr	Ala	Phe	Ala	Pro	Pro	Pro	Glu	Ala	Gly	Ala	Pro	Arg	Arg	Ala		
			1				5					10					
ccc	cac	tgg	cac	caa	ggc	cct	ctg	aca	gtg	ggg	agg	acg	agg	atg	tgg	364	
Pro	His	Trp	His	Gln	Gly	Pro	Leu	Thr	Val	Gly	Arg	Thr	Arg	Met	Trp		
	15					20					25						
gac	cgc	cag	ccg	cgg	gca	ctg	gtg	ggc	cct	gac	ctc	ccc	gcg	ggg	agg	412	
Asp	Arg	Gln	Pro	Arg	Ala	Leu	Val	Gly	Pro	Asp	Leu	Pro	Ala	Gly	Arg		
30					35					40					45		
gtg	ggt	gcc	gtg	gcc	cct	gca	ggt	gtg	gca	gag	atg	ggg	cac	ggg	cat	460	
Val	Gly	Ala	Val	Ala	Pro	Ala	Gly	Val	Ala	Glu	Met	Gly	His	Gly	His		
				50					55					60			
tgg	ggt	ctc	cat	cag	cct	ctg	tgg	ggt	gtc	tca	ggg	tgg	gca	gtg	ggg	508	
Trp	Gly	Leu	His	Gln	Pro	Leu	Trp	Gly	Val	Ser	Gly	Trp	Ala	Val	Gly		
			65					70					75				
gtg	ggg	ctg	gga	cgc	tgt	ttg	tgc	tca	gcg	ggg	aca	gcc	agg	gtt	gat	556	
Val	Gly	Leu	Gly	Arg	Cys	Leu	Cys	Ser	Ala	Gly	Thr	Ala	Arg	Val	Asp		
		80					85					90					
ctg	gcc	ccg	agg	gtt	ttg	gat	gtt	ttt	agg	atg	aca	taaaaagcaa				602	
Leu	Ala	Pro	Arg	Val	Leu	Asp	Val	Phe	Arg	Met	Thr						
	95					100					105						
gtgtttttccc			catttcctct			tatgaaacac			cgtctgagcc			caaggtacac			attgggcggc		662
ctgcaggaac			ctgctccagg			tggaacacac			ggccagcagc			cgcgaacctt			gaagctgggg		722
tgaccgcagg			agacctgtga			aggcctgtga			gcggagccct			cgacctcggt			acacctggc		782
cagacacctt			gcttggaact			gggtggcctc			tgctaccagg			gggtctggca			cgggggaggg		842
ctggggccttt			ctctgcctgg			tacacacgga			aaggcggctg			tgcggaacga			gggtcaccgt		902
gctccggggt			ttctgacagt			cggtgtttcc			tgggcctttg			gagtggctgc			gaggcctgaa		962
cgctttgtgg			atccgctgtg			tccagcccgg			ctgagcatcg			ccagggctag			ctcatgctgc		1022
tcttgtcagc			ctctggttct			cctcgagtc			ttggggacgt			ggcagatgcc			agcgaccatc		1082

```
<210> 96
<211> 670
<212> DNA
<213> Homo sapiens
```

```
<220>
<221> CDS
<222> 33..458

<220>
<221> sig_peptide
<222> 33..89
```

<223> Von Heijne matrix  
score 6.45239823575329  
seq SVFLLMVNGQVES/AQ

<400> 96  
agggtgggtcc ccccggcacc cccagacctg cc atg gcg acc gcg agt cct agc 53  
Met Ala Thr Ala Ser Pro Ser  
-15  
gtc ttt cta ctc atg gtc aac ggg cag gtg gag agc gcc cag ttt cca 101  
Val Phe Leu Leu Met Val Asn Gly Gln Val Glu Ser Ala Gln Phe Pro  
-10 -5 1  
gag tat gat gac ttc tac tgc aag tac tgc ttt gtg tac ggc cag gac 149  
Glu Tyr Asp Asp Phe Tyr Cys Lys Tyr Cys Phe Val Tyr Gly Gln Asp  
5 10 15 20  
tgg gcc ccc aca gcg ggt ctg gag gag ggg atc tca cag atc aca tcc 197  
Trp Ala Pro Thr Ala Gly Leu Glu Glu Gly Ile Ser Gln Ile Thr Ser  
25 30 35  
aag agc caa gat gtg cgg caa gca ctg gtg tgg aac ttc ccc att gat 245  
Lys Ser Gln Asp Val Arg Gln Ala Leu Val Trp Asn Phe Pro Ile Asp  
40 45 50  
gtc acc ttt aaa agc acc aac ccc tac ggc tgg cca cag atc gtg ctc 293  
Val Thr Phe Lys Ser Thr Asn Pro Tyr Gly Trp Pro Gln Ile Val Leu  
55 60 65  
agc gtg tat gga cca gat gtg ttc ggg aac gat gtg gtt cga ggc tat 341  
Ser Val Tyr Gly Pro Asp Val Phe Gly Asn Asp Val Val Arg Gly Tyr  
70 75 80  
ggg gcc gtg cac gtg ccc ttc tca cct ggc cgg cac aaa agg acc atc 389  
Gly Ala Val His Val Pro Phe Ser Pro Gly Arg His Lys Arg Thr Ile  
85 90 95 100  
ccc atg ttt gtc cca gaa tct acg tct aaa ctg cag aag ttt aca aga 437  
Pro Met Phe Val Pro Glu Ser Thr Ser Lys Leu Gln Lys Phe Thr Arg  
105 110 115  
tct gca agc tgc tcc acc cac tgaggacaaa tagaaacagg tcccctggga 488  
Ser Ala Ser Cys Ser Thr His  
120  
gtgctgagtc acgggggtcc cttcagccct gttccagcag cagaaggccg ggcgatttta 548  
ccctgtgccc tgtgaaaaat ctttgtgtct gagggggcag aggaaaaact cttgtcagat 608  
gggaaaaatg ctcatgacat aatgtgacat taaaaggtgg gaaacaaaaa aaaaaaaaaa 668  
aa 670

<210> 97  
<211> 939  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 1..336

<220>  
<221> sig\_peptide  
<222> 1..81  
<223> Von Heijne matrix  
score 3.68137078794859  
seq AHLCSDSLPEQQ/QD

<400> 97  
act tcc gaa gag aga acc gcc atg aag aga gaa ggg ggt gcc gcc cac 48

```

Thr Ser Glu Glu Arg Thr Ala Met Lys Arg Glu Gly Gly Ala Ala His
      -25      -20      -15
ctc tgc tcc gac agc ctc ccg gag tcc cag cag caa gac ggc aac cac      96
Leu Cys Ser Asp Ser Leu Pro Glu Ser Gln Gln Gln Asp Gly Asn His
      -10      -5      1      5
gca ccc aac ttc tcc agc cac ggc tca tgc cgc cgt cgc cag cgg scc      144
Ala Pro Asn Phe Ser Ser His Gly Ser Cys Arg Arg Arg Gln Arg Xaa
      10      15      20
gac atg aca agg cgc tgc atg ccc gct agg cca ggt ttc ccc tca tcc      192
Asp Met Thr Arg Arg Cys Met Pro Ala Arg Pro Gly Phe Pro Ser Ser
      25      30      35
cca gcc ccg ggg tgc tgc ccc ccg cgc tgc cat ctg aga ccc ggt agt      240
Pro Ala Pro Gly Ser Ser Pro Arg Cys His Leu Arg Pro Gly Ser
      40      45      50
acc gcc cat gct gca gcg gga aag aga aca gag agt cct ggg gac agg      288
Thr Ala His Ala Ala Ala Gly Lys Arg Thr Glu Ser Pro Gly Asp Arg
      55      60      65
tac cgt gca gag ggc ttg aga agg ggc cgg gtc gcg ggg gca agg gta      336
Tyr Arg Ala Glu Gly Leu Arg Arg Gly Arg Val Ala Gly Ala Arg Val
      70      75      80      85
tgagggggagg gctgcagacc gccgctcttc cagttcccg cctcctccgc gagctcaggc      396
gttggcattt cggggccttg caaatccccg ccccgccctc gcgcaggggc tactgggagt      456
tggagtttgc ttctctgtag ttgggcagct gctcttggtc tagtgaccac cagcctggac      516
agctacggag aaccgcctt aggtagaaag aaagtgattt tttcctttg caagagtttg      576
accggggacc ctaactgctt aatgcatatt tagatcgttt tctgtacgtt gtcagttcta      636
ctgatcctag tggtttagta atataaacct tttctatggt gtgggtgaaa ttatgtaacc      696
tgtgatgagg gaatcccttc cacgaattac tttgtagtcc agcgtgcacg ctagttcata      756
cttaaaagaa cttgcagatt tggaatgtga cgtgttttct ctttcagtaa cttcacgcct      816
ctccaagagg ctaatttttt tgtaaagatt ttgtgggagc tatgtaatga gatggggagt      876
ttcatctaata gacatcctct gacaataaaa aatgttttaa ttccccaaaa aaaaaaaaaa      936
aaa

<210> 98
<211> 661
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 174..443

<220>
<221> sig_peptide
<222> 174..269
<223> Von Heijne matrix
      score 4.13107367257584
      seq SSLAFCQVGFLTA/QP

<400> 98
aaaaaggaac tttcagtgat aatgaacaaa actcaggagc tatgtggatg acaggagcac      60
ctagatgacc gactttaccc acttcaaatg ctaccttgac cctagcactc tctccaccct      120
gcacccctcac ctcagaccat cagttgggta ggccaacagc tcaccatcaa ttc atg      176
                                   Met
ccc tgc cta gac caa cag ctc act gtt cat gcc cta ccc tgc cct gcc      224
Pro Cys Leu Asp Gln Gln Leu Thr Val His Ala Leu Pro Cys Pro Ala
      -30      -25      -20
cag ccc tcc tct ctg gcc ttc tgc caa gtg ggg ttc tta aca gca cag      272
Gln Pro Ser Ser Leu Ala Phe Cys Gln Val Gly Phe Leu Thr Ala Gln

```

```

-15          -10          -5          1
cct tca cct ccg aga agg cgc aat ggg aaa gac aga tac acg ttg gtt      320
Pro Ser Pro Pro Arg Arg Arg Asn Gly Lys Asp Arg Tyr Thr Leu Val
          5          10          15
ctg caa cac cag gaa tgc cag gat gat tta gcc acc tcc tca ctt gtc      368
Leu Gln His Gln Glu Cys Gln Asp Asp Leu Ala Thr Ser Ser Leu Val
          20          25          30
tac ctt tcc ctc ccc tgc ttc aaa gac ttg ggt cga tcg aag cac caa      416
Tyr Leu Ser Leu Pro Cys Phe Lys Asp Leu Gly Arg Ser Lys His Gln
          35          40          45
agc atc act gtt gct gac act aac aag tagtgccaag ggattgcctt      463
Ser Ile Thr Val Ala Asp Thr Asn Lys
50          55
taaggaagat caggagcggg acatctgggt gcaaagaaaa tctttctaata agccccattc      523
tagtgaccac cttcaacctc ctcatagcag gagagtttgg gagtagggga cttaggatgt      583
tttgttcttt taatcaattc agaaaatatg tatgtttgaa ataaaaataa aaataactga      643
gccaaaaaaa aaaaaaaa      661

<210> 99
<211> 647
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 282..521

<220>
<221> sig_peptide
<222> 282..386
<223> Von Heijne matrix
      score 3.64439944832387
      seq LEPGLSSSAACNG/KE

<400> 99
acttgctgtg caccggtacc gtagcgactg ggcttctgga ctgtatatcc tagctgcctt      60
gtcaacatct tcgagcatcg gcagctccgg aggccggggg aactggcagg taggaaacta      120
tgtgaaagaa tctcctgatg tcataatttc cgggtgtcac cggaacattt gatcatcatt      180
cctttggcaa ttccagcctt ctgtggaaag gccagtagaa agcattgatt tattcacctc      240
tacaggaatc agactcagcc tcttttggtt ttcagtgaag t atg cct ttt caa ttt      296
                                     Met Pro Phe Gln Phe
                                     -35
gga acc cag cca agg agg ttt cca gtg gaa gga gga gat tct tca att      344
Gly Thr Gln Pro Arg Arg Phe Pro Val Glu Gly Gly Asp Ser Ser Ile
-30          -25          -20          -15
gag ctg gaa cct ggg ctg agc tcc agt gct gcc tgt aat ggg aag gag      392
Glu Leu Glu Pro Gly Leu Ser Ser Ser Ala Ala Cys Asn Gly Lys Glu
          -10          -5          1
atg tca cca acc agg caa ctc cgg agg tgc cct gga agt cat tgc ctg      440
Met Ser Pro Thr Arg Gln Leu Arg Arg Cys Pro Gly Ser His Cys Leu
          5          10          15
aca ata act gat gtt ccc gtc act gtt tat gca aca acg aga aag cca      488
Thr Ile Thr Asp Val Pro Val Thr Val Tyr Ala Thr Thr Arg Lys Pro
          20          25          30
cct gca caa agc agc aag gaa atg cat cct aaa tagcaccatt aagtcttttg      541
Pro Ala Gln Ser Ser Lys Glu Met His Pro Lys
35          40          45
tcaaggtctg actaggtcaa gggtaatgga ccagtatcat ctggtgatct ggtaaacaaa      601

```

Figure 1. The effect of the number of iterations on the accuracy of the proposed algorithm. The accuracy of the proposed algorithm increases with the number of iterations. The accuracy of the proposed algorithm is 100% when the number of iterations is 1000.

```
<210> 100
<211> 1006
<212> DNA
<213> Homo sapiens
```

```
<220>  
<221> CDS  
<222> 251..643
```

```
<220>
<221> sig_peptide
<222> 251..295
<223> Von Heijne matrix
score 3.74215118492367
seq LLMFTQLLLCGFL/YV
```

<400> 100																
aggaagccag	agggctggaa	atacagcagc	ctttgaagta	ccctctgtta	atttggatgg		60									
atctcagtg	gccccgttcg	agacctctcc	accaacacct	tctgatcttg	cgatttgctc		120									
ttcttgactt	taattagtat	ctaggaaagt	ctaaactttg	gacctacctc	tttttttgat		180									
actcattttt	gtactttttgc	tctctgggat	tggttttctta	aagaatctgg	atccttttta		240									
atatgtcaaa	atg agt ctg ctg atg ttt aca caa cta ctg ctc tgt gga						289									
	Met Ser Leu Leu Met Phe Thr Gln Leu Leu Cys Gly															
	-15		-10		-5											
ttt tta tat gtt cgg gtt gat gga tcg cgt ctt cgc cag gag gac ttt							337									
Phe Leu Tyr Val Arg Val Asp Gly Ser Arg Leu Arg Gln Glu Asp Phe																
	1		5		10											
ccc ccg cgg att gtg gag cat cct tcc gat gtc atc gtc tct aag ggc							385									
Pro Pro Arg Ile Val Glu His Pro Ser Asp Val Ile Val Ser Lys Gly																
15		20		25		30										
gag ccc acg act ctg aac tgc aag gcg gag ggc cgg cca acg ccc acc							433									
Glu Pro Thr Thr Leu Asn Cys Lys Ala Glu Gly Arg Pro Thr Pro Thr																
	35		40		45											
att gag tgg tac aaa gat ggg gag cga gtg gag act gac aag gac gat							481									
Ile Glu Trp Tyr Lys Asp Gly Glu Arg Val Glu Thr Asp Lys Asp Asp																
	50		55		60											
ccc ccg tcc cac agg atg ctt ctg ccc agc gga tcc tta ttc ttc ttg							529									
Pro Arg Ser His Arg Met Leu Leu Pro Ser Gly Ser Leu Phe Phe Leu																
	65		70		75											
cgc atc gtg cac ggg cgc agg agt aaa cct gat gaa gga agc tac gtt							577									
Arg Ile Val His Gly Arg Arg Ser Lys Pro Asp Glu Gly Ser Tyr Val																
	80		85		90											
tgt gtt gcg agg aac tat ctt ggt gaa gca gtg agt cga aat gcg tct							625									
Cys Val Ala Arg Asn Tyr Leu Gly Glu Ala Val Ser Arg Asn Ala Ser																
	95		100		105		110									
ctg gaa gtg gca tgt aag tgaacataat gaacctcatg tgcacattta							673									
Leu Glu Val Ala Cys Lys																
	115															
cttttatttta tttcaagtaa gttttgatgt gttcccatag acgctgaaac ctaaagaatc							733									
aatcaacaca ctgcataatt ttacttggtc ttcttcagag aagtctggtc aagatagtat							793									
caagccaggg tgttgtagta agtttgttta tatgaaatca agatgaccaa tatgttatta							853									
taagaaagca ggcggggcgc ggtgggtcac gctctgtaatc ccagcacttt gggaggcgga							913									
ggcggggcgga tcacgaggtc aggagatcga gaccatcctg ggtagcacgg tggggccccc							973									
ttcttacaaa aaatacaaaa aaaaaaaaaa aaa							1000									

121

<211> 1059  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 179..475

<220>  
<221> sig\_peptide  
<222> 179..295  
<223> Von Heijne matrix  
score 4.14109371250204  
seq PSLIAGL FVGCLA/GY

<400> 101  
gtttttccag gagggagcgg cctttgctca gcgcgagacg gctgggcgcc gagtgggaca 60  
gcgctgggtgc ggagactgct tccggactcc aggtaccgcg cttggcgcca gctggcccca 120  
gacttctgtc ttttcagctg cagtgaaggc tcggggctgc agaattgcaa ccttgcca 178  
atg gac ctg atc ggt ttt ggt tat gca gcc ctc gtg aca ttt gga agc 226  
Met Asp Leu Ile Gly Phe Gly Tyr Ala Ala Leu Val Thr Phe Gly Ser  
-35 -30 -25  
att ttt gga tat aag cgg aga ggt ggt gtt ccg tct ttg att gct ggt 274  
Ile Phe Gly Tyr Lys Arg Arg Gly Gly Val Pro Ser Leu Ile Ala Gly  
-20 -15 -10  
ctt ttt gtt gga tgt ttg gcc ggc tat gga gct tac cgt gtc tcc aat 322  
Leu Phe Val Gly Cys Leu Ala Gly Tyr Gly Ala Tyr Arg Val Ser Asn  
-5 1 5  
gac aaa cga gat gta aaa gtg tca ctg ttt aca gct ttc ttc ctg gct 370  
Asp Lys Arg Asp Val Lys Val Ser Leu Phe Thr Ala Phe Phe Leu Ala  
10 15 20 25  
acc ata atg ggt gtg aga ttt aag agg tcc aag aaa ata atg cct gct 418  
Thr Ile Met Gly Val Arg Phe Lys Arg Ser Lys Lys Ile Met Pro Ala  
30 35 40  
ggt ttg gtt gca ggt tta agc ctc atg atg atc ctg aga ctt gtc ttg 466  
Gly Leu Val Ala Gly Leu Ser Leu Met Met Ile Leu Arg Leu Val Leu  
45 50 55  
ttg ctg ctc tgagcatctg gaggaacaga aaactaagtt catgtcatcc 515  
Leu Leu Leu  
60  
tgctgtaatg ggcagagcat attttttttg tattttaaag ataaacttca atatggaatg 575  
ctagaaacac aaatagcact gtcacctcta atatgaacat tagtttgagg tagttttttt 635  
ctaaagcaaa aatttttaact gtttttcta tgtcaagcac tatttttcatt aaaagtgtct 695  
aatgaatcat gatatactct tccatttggt gtgtctatatt tttatatatt tgggtattttt 755  
tgaaaattcc aaatactcat gtctcaagta agcttaaaact acaacttgct acataaagga 815  
agtcttaagt ggagttcaca gaatgataat gtatctatatt gtcatttggt ttatatattga 875  
aattattaga aattatgctt tttccatttt aattgtattg ctgccagtgc tatttttttc 935  
tttaaaaaat tttattotta gcacactgtt atgtcccta tgaatgtatt cagtattcaa 995  
ataaaagaca ttttgggtcca aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1055  
aaaa' 1059

<210> 102  
<211> 514  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS

<222> 34..327

<220>

<221> sig\_peptide

<222> 34..162

<223> Von Heijne matrix

score 5.69273078757386

seq LGDALLFLRPAGS/CA

<400> 102

```

agagacctat ggggttcgcc tgaagccccc gga atg tgt gag aca ctt ctt act      54
                               Met Cys Glu Thr Leu Leu Thr
                               -40
agt aaa tgg gct tca gta tcc ccc atc cct gca ctc ctg cag gaa ggt      102
Ser Lys Trp Ala Ser Val Ser Pro Ile Pro Ala Leu Leu Gln Glu Gly
-35                               -30                               -25
gag aat cgg gac agt cgc agg ctg gga gac gct ctg ctt ttc ctg cgt      150
Glu Asn Arg Asp Ser Arg Arg Leu Gly Asp Ala Leu Leu Phe Leu Arg
-20                               -15                               -10                               -5
cct gct ggg agc tgc gcg ctc cag gta tcc tgg cct gcc gcc cta gcc      198
Pro Ala Gly Ser Cys Ala Leu Gln Val Ser Trp Pro Ala Ala Leu Ala
1                               5                               10
ggc cca agg agc cac aca gga cag ttg acc caa cac ttc tgc cac ctg      246
Gly Pro Arg Ser His Thr Gly Gln Leu Thr Gln His Phe Cys His Leu
15                               20                               25
aag aac gac acc tgc att cct cca tct ctg gga cca cca agg aac tca      294
Lys Asn Asp Thr Cys Ile Pro Pro Ser Leu Gly Pro Pro Arg Asn Ser
30                               35                               40
ggg agc ttg gaa tct ctc aga tca aaa aga tac tgactcatcg gatagccatg      347
Gly Ser Leu Glu Ser Leu Arg Ser Lys Arg Tyr
45                               50                               55
gcactctgaa aacggccttc cttgtgtgta cattatttgc aacaagcaac aagtttataa      407
gcacttttgtt aaaattgcat gtgaggggta aaatattaaa gtcagtgcgt caacttgaaa      467
taaattgatga gttattgatt actgctaaag aaaaaaaaaa aaaaaaa      514

```

<210> 103

<211> 1158

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 303..953

<220>

<221> sig\_peptide

<222> 303..359

<223> Von Heijne matrix

score 5.47911600153114

seq LCCSGCVPSLCCS/SY

<400> 103

```

aaaaacttcc gccgccgcgt ccgccgcctc cggaactaaa cgggggtgagg tcacattcgg      60
ttatctctaa cgttggaaaaa cgatggagct aacacccatt atggagatta accacttttc      120
atcagggtttt taacttaagt cgtgaggaat acaacgggtga acacaagatt cattttatct      180
tcattcaccat gggacgtatc ctgttggtga gttctctggg tcagacctct gaagacttct      240
cagatggatc ctagtctctg ggcttgccct gaaattactc gctgctcagg gagagagttg      300
aa atg gtt ggc atc ctc cca ctc tgt tgc tcc ggc tgt gtc ccc tcg      347

```

Met	Val	Gly	Ile	Leu	Pro	Leu	Cys	Cys	Ser	Gly	Cys	Val	Pro	Ser		
				-15					-10					-5		
ctc	tgt	tgt	tcc	agc	tat	gtc	ccc	tct	gtt	gct	cca	act	gca	gct	cat	395
Leu	Cys	Cys	Ser	Ser	Tyr	Val	Pro	Ser	Val	Ala	Pro	Thr	Ala	Ala	His	
			1					5					10			
tct	gtt	aga	gtt	cct	cat	tca	gct	ggg	cac	tgt	ggc	cag	agg	gtg	ttg	443
Ser	Val	Arg	Val	Pro	His	Ser	Ala	Gly	His	Cys	Gly	Gln	Arg	Val	Leu	
		15					20					25				
gcc	tgc	tcc	ctt	cct	caa	gta	ttc	tta	aag	cca	tgg	att	ttt	gtg	gag	491
Ala	Cys	Ser	Leu	Pro	Gln	Val	Phe	Leu	Lys	Pro	Trp	Ile	Phe	Val	Glu	
	30					35					40					
cat	ttt	tct	tcc	tgg	ctc	tcc	ctt	gag	tta	ttt	tcc	ttt	ctt	cgc	tat	539
His	Phe	Ser	Ser	Trp	Leu	Ser	Leu	Glu	Leu	Phe	Ser	Phe	Leu	Arg	Tyr	
45				50						55				60		
ctt	ggg	act	ctt	ctt	tgt	gct	tgc	gga	cat	cgg	ttg	aga	gaa	gga	cga	587
Leu	Gly	Thr	Leu	Leu	Cys	Ala	Cys	Gly	His	Arg	Leu	Arg	Glu	Gly	Arg	
			65						70				75			
ctt	ctt	cct	tgt	ctc	ctt	ggg	gtt	ggc	tcg	tgg	ttg	ctc	ttc	aac	aac	635
Leu	Leu	Pro	Cys	Leu	Leu	Gly	Val	Gly	Ser	Trp	Leu	Leu	Phe	Asn	Asn	
			80					85					90			
tgg	act	gga	ggc	tct	tgg	ttt	tct	ctt	cat	ctt	caa	caa	gtc	agt	ctc	683
Trp	Thr	Gly	Gly	Ser	Trp	Phe	Ser	Leu	His	Leu	Gln	Gln	Val	Ser	Leu	
		95				100						105				
tct	caa	ggg	tct	cac	gtt	gca	gca	ttc	tta	cca	gag	gcc	att	ggg	cct	731
Ser	Gln	Gly	Ser	His	Val	Ala	Ala	Phe	Leu	Pro	Glu	Ala	Ile	Gly	Pro	
	110					115					120					
gga	gtt	cca	gtt	cca	gtg	tct	gga	gag	tcc	acc	tca	gct	cag	caa	tct	779
Gly	Val	Pro	Val	Pro	Val	Ser	Gly	Glu	Ser	Thr	Ser	Ala	Gln	Gln	Ser	
125					130				135						140	
cat	gcc	ggg	tgg	caa	ttg	tca	gca	gaa	gcc	gat	gcc	tgc	cca	tca	gtt	827
His	Ala	Gly	Trp	Gln	Leu	Ser	Ala	Glu	Ala	Asp	Ala	Cys	Pro	Ser	Val	
			145						150					155		
ctt	tac	tct	gag	gtg	tta	gag	tgg	aat	aaa	aat	ata	aat	act	tat	act	875
Leu	Tyr	Ser	Glu	Val	Leu	Glu	Trp	Asn	Lys	Asn	Ile	Asn	Thr	Tyr	Thr	
			160					165					170			
agt	ttt	cat	gac	ttc	tgc	tta	ata	ttg	ggg	att	ttt	ktt	gtt	ttg	ttt	923
Ser	Phe	His	Asp	Phe	Cys	Leu	Ile	Leu	Gly	Ile	Phe	Xaa	Val	Leu	Phe	
		175					180					185				
tgt	ttt	ggc	ggg	gat	agg	ctt	acc	tta	cat	taaaccaggc	cttagccttt					973
Cys	Phe	Gly	Gly	Asp	Arg	Leu										

```
<210> 104
<211> 1563
<212> DNA
<213> Homo sapiens
```

```
<220>  
<221> CDS  
<222> 97..645
```

```
<220>
<221> sig_peptide
<222> 97..156
```



<223> Von Heijne matrix  
score 8.42885652997473  
seq AVVGCLLVPPAEA/NK

<220>

<221> misc\_feature

<222> 972

<223> n=a, g, c or t

<400> 104

```

aatagaagct aggagagggc ggggacaact gggctcttttg cggctgcagc gggcttgtag      60
gtgtccggct ttgctggccc agcaagcctg ataagc atg aag ctc tta tct ttg      114
                                     Met Lys Leu Leu Ser Leu
                                     -20                               -15
gtg gct gtg gtc ggg tgt ttg ctg gtg ccc cca gct gaa gcc aac aag      162
Val Ala Val Val Gly Cys Leu Leu Val Pro Pro Ala Glu Ala Asn Lys
                                     -10                               -5                               1
agt tct gaa gat atc cgg tgc aaa tgc atc tgt cca cct tat aga aac      210
Ser Ser Glu Asp Ile Arg Cys Lys Cys Ile Cys Pro Pro Tyr Arg Asn
                                     5                               10                               15
atc agt ggg cac att tac aac cag aat gta tcc cag aag gac tgc aac      258
Ile Ser Gly His Ile Tyr Asn Gln Asn Val Ser Gln Lys Asp Cys Asn
                                     20                               25                               30
tgc ctg cac gtg gtg gag ccc atg cca gtg cct ggc cat gac gtg gag      306
Cys Leu His Val Val Glu Pro Met Pro Val Pro Gly His Asp Val Glu
35                               40                               45                               50
gcc tac tgc ctg ctg tgc gag tgc agg tac gag gag cgc agc acc acc      354
Ala Tyr Cys Leu Leu Cys Glu Cys Arg Tyr Glu Glu Arg Ser Thr Thr
                                     55                               60                               65
acc atc aag gtc atc att gtc atc tac ctg tcc gtg gtg ggt gcc ctg      402
Thr Ile Lys Val Ile Ile Val Ile Tyr Leu Ser Val Val Gly Ala Leu
                                     70                               75                               80
ttg ctc tac atg gcc ttc ctg atg ctg gtg gac cct ctg atc cga aag      450
Leu Leu Tyr Met Ala Phe Leu Met Leu Val Asp Pro Leu Ile Arg Lys
85                               90                               95
ccg gat gca tac act gag caa ctg cac aat gag gag gag aat gag gat      498
Pro Asp Ala Tyr Thr Glu Gln Leu His Asn Glu Glu Glu Asn Glu Asp
100                               105                               110
gct cgc tct atg gca gca gct gct gca tcc ctc ggg gga ccc cga gca      546
Ala Arg Ser Met Ala Ala Ala Ala Ser Leu Gly Gly Pro Arg Ala
115                               120                               125                               130
aac aca gtc ctg gag cgt gtg gaa ggt gcc cag cag cgg tgg aag ctg      594
Asn Thr Val Leu Glu Arg Val Glu Gly Ala Gln Gln Arg Trp Lys Leu
135                               140                               145
cag gtg cag gag cag cgg aag aca gtc ttc gat cgg cac aag atg ctc      642
Gln Val Gln Glu Gln Arg Lys Thr Val Phe Asp Arg His Lys Met Leu
150                               155                               160
agc tagatgggct ggtgtgggtg ggtcaaggcc ccaacaccat ggctgccagc      695
Ser
ttccaggctg gacaaagcag ggggctactt ctcccttccc tcggttccag tcttcccttt      755
aaaagcctgt ggcatttttc ctcccttctcc ctaacttttag aaatgttgta cttggctatt      815
ttgattaggg aagaggggatg tggctctctga tctctgttgt cttcttgggt ctttgggggt      875
gaagggaggg ggaaggcagg cc casaaggg aatggagaca ttcgaggcgg cctcaggagt      935
ggatgcgata ttgtctctcc tkggcctccc actcttngcc gccttccagc tctgagtctt      995
gggaatgttg ttacccttgg aagataaagy ctgggtcttc aggaactcag tgtctgggag      1055
gaaagcatgg ccagcattc agcatgtgtt cctttctgca gtggttctta tcaccacctc      1115
cctcccagcc ccagcgctc agccccagcc ccagctccag ccctgaggac agctctgatg      1175
ggagagctgg gccccctgag cccactgggt cttcagggtg cactggaagc tgggtgttcgc      1235

```

```

tgccccctgt gcacttctcg cactggggca tggagtggcc atgcatactc tgctgccggt 1295
ccccccacct gcacttgagg ggtctgggca gtcctctctc tccccagtgt ccacagtcac 1355
tgagccagac ggtcgggttg aacatgagac tcgaggctga gcgtggatct gaacaccaca 1415
gccccgttac ttgggttgcc tcttgtccct gaacttcgtt gtaccagtgc atggagagaa 1475
aattttgtcc tcttgtctta gagttgtgtg taaatcaagg aagccatcat taaattgttt 1535
tatttctctc taaaaaaaaa aaaaaaaaaa 1563

```

<210> 105  
 <211> 1621  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 80..820

<220>  
 <221> sig\_peptide  
 <222> 80..118  
 <223> Von Heijne matrix  
 score 5.76690322882439  
 seq MLVLRSA LTRALA/SR

```

<400> 105
acctttccac tcgggaaacc ttcagaggag tctcagaaag gacacggctg gctgcttttc 60
tcagcgccga agccgcgcc atg ctc gtc ctc aga agc gcc ctg act cgg gcg 112
          Met Leu Val Leu Arg Ser Ala Leu Thr Arg Ala
                    -10                    -5
ctg gcc tca cgg acg ctg gcg cct cag atg tgc tca tct ttt gct acg 160
Leu Ala Ser Arg Thr Leu Ala Pro Gln Met Cys Ser Ser Phe Ala Thr
          1          5          10
gga ccc aga caa tac gat gga ata ttc tat gaa ttt cgt tct tat tac 208
Gly Pro Arg Gln Tyr Asp Gly Ile Phe Tyr Glu Phe Arg Ser Tyr Tyr
15          20          25          30
ctt aag ccc tca aag atg aat gag ttc ctg gaa aat ttt gag aaa aac 256
Leu Lys Pro Ser Lys Met Asn Glu Phe Leu Glu Asn Phe Glu Lys Asn
          35          40          45
gct cat ctt cgg aca gct cac tct gaa ttg gtt gga tac tgg agt gta 304
Ala His Leu Arg Thr Ala His Ser Glu Leu Val Gly Tyr Trp Ser Val
          50          55          60
gaa ttt gga ggc aga atg aat aca gtg ttt cat att tgg aag tat gat 352
Glu Phe Gly Gly Arg Met Asn Thr Val Phe His Ile Trp Lys Tyr Asp
          65          70          75
aat ttt gct cat cga act gaa gtt cag aaa gcc ttg gcc aaa gat aag 400
Asn Phe Ala His Arg Thr Glu Val Gln Lys Ala Leu Ala Lys Asp Lys
          80          85          90
gaa tgg caa gaa caa ttc ctc att cca aat ttg gct ctc att gat aaa 448
Glu Trp Gln Glu Gln Phe Leu Ile Pro Asn Leu Ala Leu Ile Asp Lys
95          100          105          110
caa gag agt gag att act tat ctg gta cca tgg tgc aaa tta gaa aaa 496
Gln Glu Ser Glu Ile Thr Tyr Leu Val Pro Trp Cys Lys Leu Glu Lys
          115          120          125
cct cca aaa gaa gga gtc tat gaa ctg gcc act ttt cag atg aaa cct 544
Pro Pro Lys Glu Gly Val Tyr Glu Leu Ala Thr Phe Gln Met Lys Pro
          130          135          140
ggg ggg cca gct ctg tgg ggt gat gca ttt aaa agg gca gtt cat gct 592
Gly Gly Pro Ala Leu Trp Gly Asp Ala Phe Lys Arg Ala Val His Ala
145          150          155

```

```

cat gtc aat cta ggc tac aca aaa cta gtt gga gtg ttc cac aca gag      640
His Val Asn Leu Gly Tyr Thr Lys Leu Val Gly Val Phe His Thr Glu
      160                      165                      170
tac gga gca ctc aac aga gtt cat gtt ctt tgg tgg aat gag agt gca      688
Tyr Gly Ala Leu Asn Arg Val His Val Leu Trp Trp Asn Glu Ser Ala
      175                      180                      185                      190
gat agt cgt gca gct ggg aga cat aag tcc cat gag gat ccc aga gtt      736
Asp Ser Arg Ala Ala Gly Arg His Lys Ser His Glu Asp Pro Arg Val
                        195                      200                      205
gtg gca gct gtt cgg gaa agt gtc aac tac cta gta tct cag cag aat      784
Val Ala Ala Val Arg Glu Ser Val Asn Tyr Leu Val Ser Gln Gln Asn
                        210                      215                      220
atg ctt ctg att cct aca tcg ttt tca cca ctg aaa tagttttcta      830
Met Leu Leu Ile Pro Thr Ser Phe Ser Pro Leu Lys
      225                      230
ctgaaataca aaacatttca ttaactgcta taggatctct ctgctaattgg tgcttaaatt      890
ctcccaagag gttctcactt ttatttgaag gaggtggtaa gttaatttgc tatgtttctt      950
gcattatgaa ggctacatct gtgctttgta agtaccactt caaaaaatag ttctgtttac     1010
tttctgcatg gtatttccagt gtctgtcata cattaaaaat acttgtcact gttttaagat     1070
cttgactctt catttgtttc agaatagctc ttctactgta ttctgacaac tctttgcttt     1130
atagcatttt gttgtattca aatgataatg gtagcatttc catgcttgtg acagcatttt     1190
taagttatta atatatttta tcaacctttc catcatgtct gttttcctgg ttttttttgg     1250
ttgttttttg accagtaaaa tttattttgt aataccaaat aggatttaag aaaattaacg     1310
tatttcttta ctatggaaaa ccacattgtc atttgtgaca tcatctatat taaatatggt     1370
tttcacatta gttatttgtc acttacttgg aaaatgatgc tgttaggtcc tggattataa     1430
aatctagaaa agacttgttg gtttatgtgc tgaaatgtct ttatttataa ttaattttaa     1490
ctactatttta ctttatttctg gatcctgttt aacaaagata cttgagacat ccatttgttt     1550
taatgaaatc tgtatggata tggaaatgct tgccttaata aaagcctaca tatacaaaaa     1610
aaaaaaaaaa a                                                         1621

```

<210> 106  
 <211> 557  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 77..388

<220>  
 <221> sig\_peptide  
 <222> 77..217  
 <223> Von Heijne matrix  
       score 4.57105404339594  
       seq FLYLTLNQSCIFA/NY

```

<400> 106
aacacccctcc ctggaccctc tgcctggagg acggggaatc acagcagctg gtttgggggtg      60
cctcccaaac caaaag atg ttc tct ccg cgc caa gct ttg acg ccc gac ccc      112
      Met Phe Ser Pro Arg Gln Ala Leu Thr Pro Asp Pro
                        -45                      -40
ctg cac tct ccc gcc tac tca ccg gtc cta ggg ggt tgg tcc cgc ttt      160
Leu His Ser Pro Ala Tyr Ser Pro Val Leu Gly Gly Trp Ser Arg Phe
      -35                      -30                      -25                      -20
cgt agt gtg gat ttt cgt ttc ctc tac ttg act cta aat caa tcc tgt      208
Arg Ser Val Asp Phe Arg Phe Leu Tyr Leu Thr Leu Asn Gln Ser Cys
                        -15                      -10                      -5
ata ttc gca aac tac aaa gag gcg cat gca aat aga tac tgt act gag      256

```

```

Ile Phe Ala Asn Tyr Lys Glu Ala His Ala Asn Arg Tyr Cys Thr Glu
      1           5           10
ggc aga tac acg cgc gag atc cag agg ctt aca tcc cca gcc gct tgg      304
Gly Arg Tyr Thr Arg Glu Ile Gln Arg Leu Thr Ser Pro Ala Ala Trp
      15           20           25
ccc acc aga gac aag aac agg atg ata agc aat gga atg gca ttg aac      352
Pro Thr Arg Asp Lys Asn Arg Met Ile Ser Asn Gly Met Ala Leu Asn
      30           35           40           45
tct cct gct gaa gga ctt gca ttt caa tgt aga ttc tgaggctggg      398
Ser Pro Ala Glu Gly Leu Ala Phe Gln Cys Arg Phe
      50           55
tgaaaacttc tctgtcacct ttactacagc attctcaccc atttatattt ctttcccctt      458
ctacatctct attactgttg cactatgtta tgcattacac catggcaaaa ttaatcaatt      518
aatacaataa aagcttaatt ttaaaaaaaaa aaaaaaaaaa      557

```

```

<210> 107
<211> 600
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 139..513

```

```

<220>
<221> sig_peptide
<222> 139..201
<223> Von Heijne matrix
      score 5.86857787719223
      seq  IVMGVQVVGRAFA/RA

```

```

<400> 107
gaggcaatgc gcatgcccag cgccgtatcg cgcacgctct ctgcggcttt ccttgacctc      60
tgacccgccc accacgcttg atccccggcc gcggggccag gaagtcggag tttgagcccc      120
ggaggcagag cggctgcc atg gcc aag tac ctg gcc cag atc att gtg atg      171
      Met Ala Lys Tyr Leu Ala Gln Ile Ile Val Met
      -20           -15
ggc gtg cag gtg gtg ggc agg gcc ttt gca cgg gcc ttg cgg cag gag      219
Gly Val Gln Val Val Gly Arg Ala Phe Ala Arg Ala Leu Arg Gln Glu
-10           -5           1           5
ttt gca gcc agc cgg gcc gca gct gat gcc cga gga cgc gct gga cac      267
Phe Ala Ala Ser Arg Ala Ala Ala Asp Ala Arg Gly Arg Ala Gly His
      10           15           20
cgg tct gca gcc gct tcc aac ctc tcc ggc ctc agc ctc cag gag gca      315
Arg Ser Ala Ala Ala Ser Asn Leu Ser Gly Leu Ser Leu Gln Glu Ala
      25           30           35
cag cag att ctc aac gtg tcc aag ctg agc cct gag gag gtc cag aag      363
Gln Gln Ile Leu Asn Val Ser Lys Leu Ser Pro Glu Glu Val Gln Lys
      40           45           50
aac tat gaa cac tta ttt aag gtg aat gat aaa tcc gtg ggt ggc tcc      411
Asn Tyr Glu His Leu Phe Lys Val Asn Asp Lys Ser Val Gly Gly Ser
      55           60           65           70
ttc tac ctg cag tca aag gtg gtc cgc gca aag gag cgc ctg gat gag      459
Phe Tyr Leu Gln Ser Lys Val Val Arg Ala Lys Glu Arg Leu Asp Glu
      75           80           85
gaa ctc aaa atc cag gcc cag gag gac aga gaa aaa ggg cag atg ccc      507
Glu Leu Lys Ile Gln Ala Gln Glu Asp Arg Glu Lys Gly Gln Met Pro
      90           95           100

```

cat acg tgactgctcg gctccccccg cccaccccg cgcttctaatt ttatagcttg 563  
 His Thr  
 gtaataaatt tcttttctac aaaaaaaaaa aaaaaaa 600

<210> 108  
 <211> 1129  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 81..986

<220>  
 <221> sig\_peptide  
 <222> 81..134  
 <223> Von Heijne matrix  
 score 5.03543461931947  
 seq ITLLGLAVNVVTT/LV

<400> 108  
 acagcgcggc gggcgctctcg ctgctcgagc cgccgctgca gctctactgg acctggctgc 60  
 tccagtggat cccgctctgg atg gcc ccc aac tcc atc acc ctg ctg ggg ctc 113  
 Met Ala Pro Asn Ser Ile Thr Leu Leu Gly Leu  
 -15 -10  
 gcc gtc aac gtg gtc acc acg ctc gtg ctc atc tcc tac tgt ccc acg 161  
 Ala Val Asn Val Val Thr Thr Leu Val Leu Ile Ser Tyr Cys Pro Thr  
 -5 1 5  
 gcc acc gaa gag gca cca tac tgg aca tac ctt tta tgt gca ctg gga 209  
 Ala Thr Glu Glu Ala Pro Tyr Trp Thr Tyr Leu Cys Ala Leu Gly  
 10 15 20 25  
 ctt ttt att tac cag tca ctg gat gct att gat ggg aaa caa gcc aga 257  
 Leu Phe Ile Tyr Gln Ser Leu Asp Ala Ile Asp Gly Lys Gln Ala Arg  
 30 35 40  
 aga aca aac tct tgt tcc cct tta ggg gag ctc ttt gac cat ggc tgt 305  
 Arg Thr Asn Ser Cys Ser Pro Leu Gly Glu Leu Phe Asp His Gly Cys  
 45 50 55  
 gac tct ctt tcc aca gta ttt atg gca gtg gga gct tca att gcc gct 353  
 Asp Ser Leu Ser Thr Val Phe Met Ala Val Gly Ala Ser Ile Ala Ala  
 60 65 70  
 cgc tta gga act tat cct gac tgg ttt ttt ttc tgc tct ttt att ggg 401  
 Arg Leu Gly Thr Tyr Pro Asp Trp Phe Phe Phe Cys Ser Phe Ile Gly  
 75 80 85  
 atg ttt gtg ttt tat tgc gct cat tgg cag act tat gtt tca ggc atg 449  
 Met Phe Val Phe Tyr Cys Ala His Trp Gln Thr Tyr Val Ser Gly Met  
 90 95 100 105  
 ttg aga ttt gga aaa gtg gat gta act gaa att cag ata gct tta gtg 497  
 Leu Arg Phe Gly Lys Val Asp Val Thr Glu Ile Gln Ile Ala Leu Val  
 110 115 120  
 att gtc ttt gtg ttg tct gca ttt gga gga gca aca atg tgg gac tat 545  
 Ile Val Phe Val Leu Ser Ala Phe Gly Gly Ala Thr Met Trp Asp Tyr  
 125 130 135  
 acg ggc acc agt gtc ttg tca cct gga ctc cac ata gga cta att att 593  
 Thr Gly Thr Ser Val Leu Ser Pro Gly Leu His Ile Gly Leu Ile Ile  
 140 145 150  
 ata ctg gca ata atg atc tat aaa aag tca gca act gat gtg ttt gaa 641  
 Ile Leu Ala Ile Met Ile Tyr Lys Lys Ser Ala Thr Asp Val Phe Glu  
 155 160 165

```

aag cat cct tgt ctt tat atc cta atg ttt gga tgt gtc ttt gct aaa      689
Lys His Pro Cys Leu Tyr Ile Leu Met Phe Gly Cys Val Phe Ala Lys
170                               175                               180                               185
gtc tca caa aaa tta gtg gta gct cac atg acc aaa agt gaa cta tat      737
Val Ser Gln Lys Leu Val Val Ala His Met Thr Lys Ser Glu Leu Tyr
190                               195                               200
ctt caa gac act gtc ttt ttg ggg cca ggt ctt ttg ttt tta gac cag      785
Leu Gln Asp Thr Val Phe Leu Gly Pro Gly Leu Leu Phe Leu Asp Gln
205                               210                               215
tac ttt aat aac ttt ata gac gaa tat gtt gtt cta tgg atg gca atg      833
Tyr Phe Asn Asn Phe Ile Asp Glu Tyr Val Val Leu Trp Met Ala Met
220                               225                               230
gtg att tct tca ttt gat atg gtg ata tac ttt agt gct ttg tgc ctg      881
Val Ile Ser Ser Phe Asp Met Val Ile Tyr Phe Ser Ala Leu Cys Leu
235                               240                               245
caa att tca aga cac ctt cat cta aat ata ttc aag act gca tgt cat      929
Gln Ile Ser Arg His Leu His Leu Asn Ile Phe Lys Thr Ala Cys His
250                               255                               260                               265
caa gca cct gaa cag gtt caa gtt ctt tct tca aag agt cat cag aat      977
Gln Ala Pro Glu Gln Val Gln Val Leu Ser Ser Lys Ser His Gln Asn
270                               275                               280
aac atg gat tgaagagact tccgaacact tgctatctct tgctgctgct      1026
Asn Met Asp
gtttcatgga aggagatatt aaacatttgt ttaattttta tttaagtgtt atacctat    1086
cagcaaataa aatattttcat tgcttgaaaa aaaaaaaaaa aaa      1129

```

<210> 109  
 <211> 778  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 266..586

<220>  
 <221> sig\_peptide  
 <222> 266..307  
 <223> Von Heijne matrix  
 score 4.534746808071  
 seq ILVTVPGVCPAQC/CW

```

<400> 109
tagatgtag aattggatt tggtcttgct ttttggttgc gatggagtta tataactaagt      60
tacttatact aaggcattag tagtctcata tctgaggagc aattgtatatt ttagttcagc      120
taaattaatg cctcttttta aatactaact tgtactactt ttgtggctgt gaatggatc      180
ttttattgaa ctgaggcagc ttttaaaaga cttgcctgat catttagagc actcccatg      240
aggttaaatt agacttgaat ctgta atg att ctc gta act gtt cct ggt gtg      292
                               Met Ile Leu Val Thr Val Pro Gly Val
                               -10
tgt cca gca caa tgt tgc tgg gca gag cag agg ggc aga ggc tca ggt      340
Cys Pro Ala Gln Cys Cys Trp Ala Glu Gln Arg Gly Arg Gly Ser Gly
-5                               1                               5                               10
atg tac ttc att gac aag tgg gca agg cca tcc tgg gta cca cat tgg      388
Met Tyr Phe Ile Asp Lys Trp Ala Arg Pro Ser Trp Val Pro His Trp
15                               20                               25
ctt aat gat ctc ttc att gtg aag tcc ggc tac ctc gtt tgc ata aga      436
Leu Asn Asp Leu Phe Ile Val Lys Ser Gly Tyr Leu Val Cys Ile Arg

```

```

      30      35      40
act aca gta atc agg caa ggc att gtc aga att ggg agg aat aaa atc      484
Thr Thr Val Ile Arg Gln Gly Ile Val Arg Ile Gly Arg Asn Lys Ile
      45      50      55
agt gag tct gga agg agt gct ctg tat aca att gca aag aac aaa atg      532
Ser Glu Ser Gly Arg Ser Ala Leu Tyr Thr Ile Ala Lys Asn Lys Met
      60      65      70      75
gtc atc ttt aag gta cct gat tgc atg cac tta aat gca gat tat ttt      580
Val Ile Phe Lys Val Pro Asp Cys Met His Leu Asn Ala Asp Tyr Phe
      80      85      90
gga gtt tgaaaaggga ctattaatga aatctttctt ttccctcctt tctctttttc      636
Gly Val
ccttccccgc cactgattca gtgagctgga gattggatca cagccgaagg agtaaagggtg      696
ctgcaatgat gttagctgtg gccactgtgg atttttcgca agaacattaa taaactaaaa      756
acttcaaaaa aaaaaaaaaa aa      778

<210> 110
<211> 1301
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 59..745

<220>
<221> sig_peptide
<222> 59..160
<223> Von Heijne matrix
      score 5.94384548075359
      seq LGAAALALLLANT/DV

<400> 110
attcaaaacc aggctgaaga ttggaaggaa gttggccagc ctcggctgca ggacagaa      58
atg tct ttc ctc cag gac cca agt ttc ttc acc atg ggg atg tgg tcc      106
Met Ser Phe Leu Gln Asp Pro Ser Phe Phe Thr Met Gly Met Trp Ser
      -30      -25      -20
att ggt gca gga gcc ctg ggg gct gct gcc ttg gca ttg ctg ctt gcc      154
Ile Gly Ala Gly Ala Leu Gly Ala Ala Leu Ala Leu Leu Leu Ala
      -15      -10      -5
aac aca gac gtg ttt ctg tcc aag ccc cag aaa gcg gcc ctg gag tac      202
Asn Thr Asp Val Phe Leu Ser Lys Pro Gln Lys Ala Ala Leu Glu Tyr
      1      5      10
ctg gag gat ata gac ctg aaa aca ctg gag aag gaa cca agg act ttc      250
Leu Glu Asp Ile Asp Leu Lys Thr Leu Glu Lys Glu Pro Arg Thr Phe
      15      20      25      30
aaa gca aag gag cta tgg gaa aaa aat gga gct gtg att atg gcc gtg      298
Lys Ala Lys Glu Leu Trp Glu Lys Asn Gly Ala Val Ile Met Ala Val
      35      40      45
cgg agg cca ggc tgt ttc ctc tgt cga gag gaa gct gcg gat ctg tcc      346
Arg Arg Pro Gly Cys Phe Leu Cys Arg Glu Glu Ala Ala Asp Leu Ser
      50      55      60
tcc ctg aaa agc atg ttg gac cag ctg ggc gtc ccc ctc tat gca gtg      394
Ser Leu Lys Ser Met Leu Asp Gln Leu Gly Val Pro Leu Tyr Ala Val
      65      70      75
gta aag gag cac atc agg act gaa gtg aag gat ttc cag cct tat ttc      442
Val Lys Glu His Ile Arg Thr Glu Val Lys Asp Phe Gln Pro Tyr Phe
      80      85      90

```

aaa	gga	gaa	atc	ttc	ctg	gat	gaa	aag	aaa	aag	ttc	tat	ggt	cca	caa	490
Lys	Gly	Glu	Ile	Phe	Leu	Asp	Glu	Lys	Lys	Lys	Phe	Tyr	Gly	Pro	Gln	
95					100					105					110	
agg	cgg	aag	atg	atg	ttt	atg	gga	ttt	atc	cgt	ctg	gga	gtg	tgg	tac	538
Arg	Arg	Lys	Met	Met	Phe	Met	Gly	Phe	Ile	Arg	Leu	Gly	Val	Trp	Tyr	
			115						120					125		
aac	ttc	ttc	cga	gcc	tgg	aac	gga	ggc	ttc	tct	gga	aac	ctg	gaa	gga	586
Asn	Phe	Phe	Arg	Ala	Trp	Asn	Gly	Gly	Phe	Ser	Gly	Asn	Leu	Glu	Gly	
			130					135					140			
gaa	ggc	ttc	atc	ctt	ggg	gga	gtt	ttc	gtg	gtg	gga	tca	gga	aag	cag	634
Glu	Gly	Phe	Ile	Leu	Gly	Gly	Val	Phe	Val	Val	Gly	Ser	Gly	Lys	Gln	
		145					150					155				
ggc	att	ctt	ctt	gag	cac	cga	gaa	aaa	gaa	ttt	gga	gac	aaa	gta	aac	682
Gly	Ile	Leu	Leu	Glu	His	Arg	Glu	Lys	Glu	Phe	Gly	Asp	Lys	Val	Asn	
	160					165					170					
cta	ctt	tct	gtt	ctg	gaa	gct	gct	aag	atg	atc	aaa	cca	cag	act	ttg	730
Leu	Leu	Ser	Val	Leu	Glu	Ala	Ala	Lys	Met	Ile	Lys	Pro	Gln	Thr	Leu	
175				180						185					190	
gcc	tca	gag	aaa	aaa	tgatt	gtgtg	aaact	gcccc	gctcaggg	gat	aaccaggg	ac				785
Ala	Ser	Glu	Lys	Lys												
			195													
attcacctgt	gttcattgga				tgtattgttt		ccactcgtgt		ccctaaggag		tgagaaaccc					845
atttatactc	tactctcagt				atggattatt		aatgtatttt		aatattctgt		ttaggcccac					905
taaggcaaaa	tagcccaaaa				acaagactga		caaaaatctg		aaaaactaat		gaggattatt					965
aagctaaaac	ctgggaaata				ggagggttaa		aattgactgc		caggctgggt		gcagtggctc					1025
acacctgtaa	tcccagcact				ttgggaggcc		aagggtgagca		agtcacttga		ggtcggggagt					1085
tcgagaccag	cctgagcaac				atggcgaaac		cccgtctcta		ctaaaaatac		aaaaatcacc					1145
cgggtgtggt	ggcaggcacc				tgtagttccc		gctacccggt		aggctgaggc		aggagaatca					1205
cttgaacctg	ggaggtgag				gttgcggtga		gctgagatca		caccactgta		ttccagcctg					1265
qqtqactqaq	actctaacta				aaaaaaaaaa		aaaaaaaa									1301

```
<210> 111
<211> 1300
<212> DNA
<213> Homo sapiens
```

```
<220>  
<221> CDS  
<222> 59..676
```

```
<220>
<221> sig_peptide
<222> 59..160
<223> Von Heijne matrix
score 5.94384548075359
seq LGAAALALLLANT/DV
```

<400> 111																							
attcaaaacc aggctgaaga ttggaaggaa gttggccagc ctcggctgca ggacagaa																58							
atg tct ttc ctc cag gac cca agt ttc ttc acc atg ggg atg tgg tcc																106							
Met	Ser	Phe	Leu	Gln	Asp	Pro	Ser	Phe	Phe	Thr	Met	Gly	Met	Trp	Ser								
				-30								-25								-20			
att ggt gca gga gcc ctg ggg gct gct gcc ttg gca ttg ctg ctt gcc																154							
Ile	Gly	Ala	Gly	Ala	Leu	Gly	Ala	Ala	Ala	Leu	Ala	Leu	Leu	Leu	Ala								
				-15								-10								-5			
aac aca gac gtg ttt ctg tcc aag ccc cag aaa gcg gcc ctg gag tac																202							
Asn	Thr	Asp	Val	Phe	Leu	Ser	Lys	Pro	Gln	Lys	Ala	Ala	Leu	Glu	Tyr								
		1				5						10											



```

ctg gag gat ata gac ctg aaa aca ctg gag aag gaa cca agg act ttc      250
Leu Glu Asp Ile Asp Leu Lys Thr Leu Glu Lys Glu Pro Arg Thr Phe
15          20          25          30
aaa gca aag gag cta tgg gaa aaa aat gga gct gtg att atg gcc gtg      298
Lys Ala Lys Glu Leu Trp Glu Lys Asn Gly Ala Val Ile Met Ala Val
          35          40          45
cgg agg cca ggc tgt ttc ctc tgt cga gag gaa gct gcg gat ctg tcc      346
Arg Arg Pro Gly Cys Phe Leu Cys Arg Glu Glu Ala Ala Asp Leu Ser
          50          55          60
tcc ctg aaa agc atg ttg gac cag ctg ggc gtc ccc ctc tat gca gtg      394
Ser Leu Lys Ser Met Leu Asp Gln Leu Gly Val Pro Leu Tyr Ala Val
          65          70          75
gta aag gag cac atc agg act gaa gtg aag gat ttc cag cct tat ttc      442
Val Lys Glu His Ile Arg Thr Glu Val Lys Asp Phe Gln Pro Tyr Phe
          80          85          90
aaa gga gaa atc ttc ctg gat gaa aag aaa aag ttc tat ggt cca caa      490
Lys Gly Glu Ile Phe Leu Asp Glu Lys Lys Lys Phe Tyr Gly Pro Gln
          95          100          105          110
agg cgg aag atg atg ttt atg gga ttt atc cgt ctg gga gtg tgg tac      538
Arg Arg Lys Met Met Phe Met Gly Phe Ile Arg Leu Gly Val Trp Tyr
          115          120          125
aac ttc ttc cga gcc tgg aac gga ggc ttc tct gga aac ctg gaa gga      586
Asn Phe Phe Arg Ala Trp Asn Gly Gly Phe Ser Gly Asn Leu Glu Gly
          130          135          140
gaa ggc ttc atc ctt ggg gga gtt ttc gtg gtg gga tca gga agc agg      634
Glu Gly Phe Ile Leu Gly Gly Val Phe Val Val Gly Ser Gly Ser Arg
          145          150          155
gca ttc ttc ttg agc acc gag aaa aag aat ttg gag aca aag      676
Ala Phe Phe Leu Ser Thr Glu Lys Lys Asn Leu Glu Thr Lys
          160          165          170
taaacctact ttctgttctg gaagctgcta agatgatcaa accacagact ttggcctcag      736
agaaaaaatg attgtgtgaa actgcccagc tcagggataa ccagggacat tcacctgtgt      796
tcatgggatg tattgtttcc actcgtgtcc ctaaggagtg agaaacccat ttatactcta      856
ctctcagtat ggattattaa tgtattttta tattctgttt aggccacta aggcaaaata      916
gccccaaaac aagactgaca aaaatctgaa aaactaatga ggattattaa gctaaaacct      976
gggaaatagg aggtttaaaa ttgactgccca ggctgggtgc agtggctcac acctgtaatc      1036
ccagcacttt gggaggccaa ggtgagcaag tcacttgagg tcgggagttc gagaccagcc      1096
tgagcaacat ggcgaaaccc cgtctctact aaaaatacaa aaatcacccg ggtgtggtgg      1156
caggcacctg tagtcccagc taccggggag gctgaggcag gagaatcact tgaacctggg      1216
aggtggaggt tgcggtgagc tgagatcaca ccactgtatt ccagcctggg tgactgagac      1276
tctaactaaa aaaaaaaaaa aaaa      1300

```

<210> 112

<211> 1617

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 15..278

<220>

<221> sig\_peptide

<222> 15..146

<223> Von Heijne matrix

score 12.2610572403264

seq PLFLLLLLLGSVTA/DI

```

<400> 112
gagaggagag gaga atg gcg gcg gaa ggc tgg att tgg cgt tgg ggc tgg      50
                Met Ala Ala Glu Gly Trp Ile Trp Arg Trp Gly Trp
                                -40                                -35

ggc cgg cgg tgc ctg gga agg cct ggg ctt ctc ggc ccc ggc cct ggc      98
Gly Arg Arg Cys Leu Gly Arg Pro Gly Leu Leu Gly Pro Gly Pro Gly
                -30                -25                -20

ccc act aca cct ctc ttt ctt ctt ttg ttg ttg ggg tct gtg act gcg      146
Pro Thr Thr Pro Leu Phe Leu Leu Leu Leu Leu Gly Ser Val Thr Ala
                -15                -10                -5

gat ata act gac ggc aac att gaa cat ctc aag cgg gag cat tcg ctc      194
Asp Ile Thr Asp Gly Asn Ile Glu His Leu Lys Arg Glu His Ser Leu
1                5                10                15

att aag ccc tac caa ggg gtc ggt tcc agc tcc ccc tct ggg act tcc      242
Ile Lys Pro Tyr Gln Gly Val Gly Ser Ser Ser Pro Ser Gly Thr Ser
                20                25                30

agg gca gca cta tgc tca cga gcc agt acg tac gtc tgaccctga      288
Arg Ala Ala Leu Cys Ser Arg Ala Ser Thr Tyr Val
                35                40

cgagcgcagc aaagaggggt ctatctggaa ccaccagccg tgcttcctca aagactggga      348
aatgcacgtc cacttcaaag tccacggcac aggggaagaag aacctccatg gagacggcat      408
cgccttgttg tacaccgggg accgcctcgt gccagggcct gtgtttggaa gcaaagataa      468
cttccacggc ttagcctatc tcctggacac ctaccccaat gatgagacca ctgagcgcgt      528
gttcccgtac atctcggtga tgggtgaacaa tggctccctg tcctacgacc acagcaagga      588
tgggcgctgg accgagctgg cgggctgcac ggctgacttc cgcaaccgcg atcacgacac      648
cttcctggct gtgcgtact cccggggccg tctgacggtg atgaccgacc tggaggacaa      708
gaacgagtgg aagaactgca ttgacatcac gggagtgcgc ctgcccaccg gctactactt      768
cggggcctcc gccggcaccg gcgacctgtc tgacaatcat gacatcatct ccatgaagct      828
gttccagctg atggtggagc acacgcccga cgaggagagc atcgactgga ccaagatcga      888
gcccagcgtc aacttcctca agtcgcccga agacaacgtg gacgaccca cggggaactt      948
ccgcagcggg cccctgacgg ggtggcgggt gtctctgctg ctgctgtgcg ctctcctggg      1008
catcgttgtc tgcgccgtgg tggggggccgt ggtgttccag aagcggcagg agcggaaacaa      1068
gcgctttctac tgagtggcgc ctccggcggg gcctgtccct gggcccagga gccaatgtga      1128
actttttttt taccgggatt ataaaagaac aacaagatga ccttatttct taactgtttc      1188
aaataaatga ttaaagtatt ttcatacatt ttgcttcttg cccagcaggg acaggtggca      1248
gagccgaggg ttaggggtctg gcacccccca cagctggaga cggaggctct cctggggctg      1308
gtgtctcagg agcaggggtc tgtgtctaca gatgggctgt ggcccctgca ggcagctgtt      1368
gaacactgga ggggtcccccg gaccacactg ggggtgggctc ctgaggacgt ggggaagtga      1428
ttttgttttg tgggtgtgtg cacgtgtggc gacggataag gcctgaactg gaaaccagg      1488
ccttctgtgt caccctgagc tgcttctga gacagatgct caagtgaggc tgcaggcgcg      1548
gtgtggtggg gccgagtgtg accgtttgct aaataaagtg aaatacccaa caaaaaaaaa      1608
aaaaaaaaa
1617

<210> 113
<211> 1634
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 167..619

<220>
<221> sig_peptide
<222> 167..262
<223> Von Heijne matrix
score 6.8501239662158
seq LLSSCGLPPSTAS/AV

```



<220>  
<221> CDS  
<222> 223..417

<220>  
<221> sig\_peptide  
<222> 223..270  
<223> Von Heijne matrix  
score 4.19788230215007  
seq LACVRESTSVAWA/CK

<400> 114  
ttagggggcc tgtcaccag cacgtgcac gggggctgtc ccgggggtca ggggagggag 60  
gccagcgggc mgtgtcgggg tccgccccga ccccatccac gaccccgact cctatccgat 120  
cctatccccg gccccgctcg ggctttccc cttgcgcctt ggctcggctg gctcgacgag 180  
cagtaagtgc gtagccgccc tccgaagccg ggcgtgcacg gg atg gca gag ttg 234  
Met Ala Glu Leu  
-15  
gcg tgc gtg cgt gag tcc acc agt gtg gca tgg gca tgt aag gtg cgc 282  
Ala Cys Val Arg Glu Ser Thr Ser Val Ala Trp Ala Cys Lys Val Arg  
-10 -5 1  
gga ggg act gca cct tct cca tca ggt gca gaa ggc cac gtc atg ctg 330  
Gly Gly Thr Ala Pro Ser Pro Ser Gly Ala Glu Gly His Val Met Leu  
5 10 15 20  
aac aag agc cga gaa gta gaa tcg cca gtg tca agc cgt cca cgt tgt 378  
Asn Lys Ser Arg Glu Val Glu Ser Pro Val Ser Ser Arg Pro Arg Cys  
25 30 35  
ggg atg ccc act gtt ccc cca gga tca ctc aag acc ctg tgacttgagg 427  
Gly Met Pro Thr Val Pro Pro Gly Ser Leu Lys Thr Leu  
40 45  
tcactgatga gtggaccaag tgaagtccac aagatggctg ctgtgggtcc aggcacacg 487  
tccacatgca aatccatcca gaggcaggaa ctgggaatag gcttggagggt ggccaggaca 547  
gcaagtgggc tgtctgtata aacctcccct ccacttgagg aggaaaatca ccccccaagt 607  
cgattttctg tccatcttat tgatcagaga gcgttataaa ttcacccatt aaataatctg 667  
gacaagggga aaaaaaaaaa aaaaaa 693

<210> 115  
<211> 784  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 166..732

<220>  
<221> sig\_peptide  
<222> 166..237  
<223> Von Heijne matrix  
score 6.60662787180923  
seq KMVHLLVLSGAWG/MQ

<400> 115  
attattgggt gggggaaacc cacgagggga cgcggccgag gagggctcgt gtccacccgg 60  
gggcgtggga gtgaggtacc agattcagcc catttgggcc cgacgcctct gttctcggaa 120  
tccgggtgct gcggattgag gtcccgggtc ctaacggact gcaag atg gag gaa ggc 177  
Met Glu Glu Gly

```

ggg aac cta gga ggc ctg att aag atg gtc cat cta ctg gtc ttg tca      225
Gly Asn Leu Gly Gly Leu Ile Lys Met Val His Leu Leu Val Leu Ser
-20                               -15                               -10                               -5
ggg gcc tgg ggc atg caa atg tgg gtg acc ttc gtc tca ggc ttc ctg      273
Gly Ala Trp Gly Met Gln Met Trp Val Thr Phe Val Ser Gly Phe Leu
                               1                               5                               10
ctt ttc cga agc ctt ccc cga cat acc ttc gga cta gtg cag agc aaa      321
Leu Phe Arg Ser Leu Pro Arg His Thr Phe Gly Leu Val Gln Ser Lys
                               15                               20                               25
ctc ttc ccc ttc tac ttc cac atc tcc atg ggc tgt gsc ttc atc aac      369
Leu Phe Pro Phe Tyr Phe His Ile Ser Met Gly Cys Xaa Phe Ile Asn
                               30                               35                               40
ctc tgc atc ttg gct tca cag cat gct tgg gct cag ctc aca ttc tgg      417
Leu Cys Ile Leu Ala Ser Gln His Ala Trp Ala Gln Leu Thr Phe Trp
45                               50                               55                               60
gag gcc agc cag ctt tac ctg ctg ttc ctg agc ctt acg ctg gcc act      465
Glu Ala Ser Gln Leu Tyr Leu Leu Phe Leu Ser Leu Thr Leu Ala Thr
                               65                               70                               75
gtc aac gcc cgc tgg ctg gaa ccc cgc acc aca gct gcc atg tgg gcc      513
Val Asn Ala Arg Trp Leu Glu Pro Arg Thr Thr Ala Ala Met Trp Ala
                               80                               85                               90
ctg caa acc gtg gag aag gag cga ggc ctg ggt ggg gag gta cca ggc      561
Leu Gln Thr Val Glu Lys Glu Arg Gly Leu Gly Gly Glu Val Pro Gly
                               95                               100                               105
agc cac cag ggt ccc gat ccc tac cgc cag ctg cga gag aag gac ccc      609
Ser His Gln Gly Pro Asp Pro Tyr Arg Gln Leu Arg Glu Lys Asp Pro
110                               115                               120
aag tac agt gct ctc cgc cag aat ttc ttc cgc tac cat ggg ctg tcc      657
Lys Tyr Ser Ala Leu Arg Gln Asn Phe Phe Arg Tyr His Gly Leu Ser
125                               130                               135                               140
tct ctt tgc aat ctg ggc tgc gtc ctg agc aat ggg ctc tgt ctc gct      705
Ser Leu Cys Asn Leu Gly Cys Val Leu Ser Asn Gly Leu Cys Leu Ala
                               145                               150                               155
ggc ctt gcc ctg gaa ata agg agc ctc tagcatgggc cctgcatgct      752
Gly Leu Ala Leu Glu Ile Arg Ser Leu
                               160                               165
aataaatgct tctccaaaaa aaaaaaaaaa aa      784

```

<210> 116  
 <211> 804  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 75..623

<220>  
 <221> sig\_peptide  
 <222> 75..215  
 <223> Von Heijne matrix  
 score 8.34104221735598  
 seq RLLLPCLVRMALC/AP

```

<400> 116
agtacggtgg ccgacgggag tcagacgctg gggatgaatg aagggtgctgg gtgcaggatc      60
aacaaacagt aata atg act gaa tgt aca agt ctt cag ttt gtc agc cct      110
Met Thr Glu Cys Thr Ser Leu Gln Phe Val Ser Pro

```

```

-45      -40
ttt gct ttt gag gca atg cag aag gtg gat gtt gtt tgc ctg gca tct 158
Phe Ala Phe Glu Ala Met Gln Lys Val Asp Val Val Cys Leu Ala Ser
-35      -30      -25      -20
tta agt gat cca gaa tta aga ctt ctt ctg ccc tgt ttg gta cgg atg 206
Leu Ser Asp Pro Glu Leu Arg Leu Leu Leu Pro Cys Leu Val Arg Met
-15      -10      -5
gca ctt tgt gca cct gct gac cag agc caa agc tgg gct cag gat aag 254
Ala Leu Cys Ala Pro Ala Asp Gln Ser Gln Ser Trp Ala Gln Asp Lys
1      5      10
aaa ctc atc ctt cgc ctt ctt tct gga gtg gaa gct gtc aac tcc att 302
Lys Leu Ile Leu Arg Leu Ser Gly Val Glu Ala Val Asn Ser Ile
15      20      25
gtt gca ttg ttg tcc gtg gac ttt cat gct tta gaa caa gat gcc agc 350
Val Ala Leu Leu Ser Val Asp Phe His Ala Leu Glu Gln Asp Ala Ser
30      35      40      45
aaa gaa cag cag ctt aga ccg agt ctt gcc ctg ttg ccc agg ctg gag 398
Lys Glu Gln Gln Leu Arg Pro Ser Leu Ala Leu Leu Pro Arg Leu Glu
50      55      60
tgc ggt ggc gtg atc tcg gct cac tgc aac ctc cac ctc ctg ggt tca 446
Cys Gly Gly Val Ile Ser Ala His Cys Asn Leu His Leu Leu Gly Ser
65      70      75
agt gat tct tct gcc tca gtc tcc cga gta gat ggg act aca ggc acg 494
Ser Asp Ser Ser Ala Ser Val Ser Arg Val Asp Gly Thr Thr Gly Thr
80      85      90
cgc cac cat gcc cgg ctt ttt tgt att att agt aga gac gag gtt tca 542
Arg His His Ala Arg Leu Phe Cys Ile Ile Ser Arg Asp Glu Val Ser
95      100      105
cca tat tgg cca ggc tgg tct cga act ccc aac ctt gtg atc cac ctg 590
Pro Tyr Trp Pro Gly Trp Ser Arg Thr Pro Asn Leu Val Ile His Leu
110      115      120      125
cct cag cct ccc aaa gta ctg gga tta ccg gcg tgagccactg tgccctggcct 643
Pro Gln Pro Pro Lys Val Leu Gly Leu Pro Ala
130      135
atgtggtgga gtatttatta tacgtaggat gtgaatccct gaaatacaca ggcaaactaa 703
atagcatttc agaagtaaca gaacatttta gaacacttta tacatccttt tatagcttat 763
ttcaataaaaa gataattttt atacaaaaaa aaaaaaaaaa a 804

```

<210> 117  
 <211> 484  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 30..335

<220>  
 <221> sig\_peptide  
 <222> 30..71  
 <223> Von Heijne matrix  
 score 4.49063834776683  
 seq FLTALLWRGRIPG/RQ

```

<400> 117
gcagagtctt gagcagcgcg gcaggcacc atg ttc ctg act gcg ctc ctc tgg 53
Met Phe Leu Thr Ala Leu Leu Trp
-10

```

```

cgc ggc cgc att ccc ggc cgt cag tgg atc ggg aag cac cgg cgg ccg      101
Arg Gly Arg Ile Pro Gly Arg Gln Trp Ile Gly Lys His Arg Arg Pro
-5                               1                               5                               10
cgg ttc gtg tgc ttg cgc gcc aag cag aac atg atc cgc cgc ctg gag      149
Arg Phe Val Ser Leu Arg Ala Lys Gln Asn Met Ile Arg Arg Leu Glu
15                               20                               25
atc gag gcg gag aac cat tac tgg ctg agc atg ccc tac atg acc cgg      197
Ile Glu Ala Glu Asn His Tyr Trp Leu Ser Met Pro Tyr Met Thr Arg
30                               35                               40
gag cag gag cgc ggc cac gcc gcg gtg cgc agg agg gag gcc ttc gag      245
Glu Gln Glu Arg Gly His Ala Ala Val Arg Arg Arg Glu Ala Phe Glu
45                               50                               55
gcc ata aag gcg gcc gcc act tcc aag ttc ccc ccg cat aga ttc att      293
Ala Ile Lys Ala Ala Ala Thr Ser Lys Phe Pro Pro His Arg Phe Ile
60                               65                               70
gcg gac cag ctc gac cat ctc aat gtc acc aag aaa tgg tcc      335
Ala Asp Gln Leu Asp His Leu Asn Val Thr Lys Lys Trp Ser
75                               80                               85
taatcctgag tcgtcaccct tggattttat ggatcacgga gctgaccatc tttacctggg      395
cctggaactg aaaaactgta gcttgtgtga aaatgagcct ttggaccagt ctttattaaa      455
acaaacaaac acaaaaaaaaa aaaaaaaaaa      484

```

```

<210> 118
<211> 985
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 21..752

```

```

<220>
<221> sig_peptide
<222> 21..107
<223> Von Heijne matrix
      score 3.61056351168286
      seq FPLYLLNFLGLWS/WI

```

```

<400> 118
gtttttttcc cttctgagca atg gag ctt acc atc ttt atc ctg aga ctg gcc      53
Met Glu Leu Thr Ile Phe Ile Leu Arg Leu Ala
-25                               -20
att tac atc ctg aca ttt ccc ttg tac ctg ctg aac ttt ctg ggc ttg      101
Ile Tyr Ile Leu Thr Phe Pro Leu Tyr Leu Leu Asn Phe Leu Gly Leu
-15                               -10                               -5
tgg agc tgg ata tgc aaa aaa tgg ttc ccc tac ttc ttg gtg agg ttc      149
Trp Ser Trp Ile Cys Lys Lys Trp Phe Pro Tyr Phe Leu Val Arg Phe
1                               5                               10
act gtg ata tac aac gaa cag atg gca agc aag aag cgg gag ctc ttc      197
Thr Val Ile Tyr Asn Glu Gln Met Ala Ser Lys Lys Arg Glu Leu Phe
15                               20                               25                               30
agt aac ctg cag gag ttt gcg gcc ccc tcc ggg aaa ctc tcc ctg ctg      245
Ser Asn Leu Gln Glu Phe Ala Gly Pro Ser Gly Lys Leu Ser Leu Leu
35                               40                               45
gaa gtg gcc tgt gcc acg ggg gcc aac ttc aag ttc tac cca cct ggg      293
Glu Val Gly Cys Gly Thr Gly Ala Asn Phe Lys Phe Tyr Pro Pro Gly
50                               55                               60
tgc agg gtg acc tgt att gac ccc aac ccc aac ttt gag aag ttt ttg      341

```

Cys	Arg	Val	Thr	Cys	Ile	Asp	Pro	Asn	Pro	Asn	Phe	Glu	Lys	Phe	Leu	
		65					70					75				
atc	aag	agc	att	gca	gag	aac	cga	cac	ctg	cag	ttt	gag	cgc	ttt	gtg	389
Ile	Lys	Ser	Ile	Ala	Glu	Asn	Arg	His	Leu	Gln	Phe	Glu	Arg	Phe	Val	
	80					85					90					
gta	gct	gcc	ggg	gag	aac	atg	cac	cag	gtg	gct	gat	ggc	tct	gtg	gat	437
Val	Ala	Ala	Gly	Glu	Asn	Met	His	Gln	Val	Ala	Asp	Gly	Ser	Val	Asp	
95					100					105					110	
gtg	gtg	gtc	tgc	acc	ctg	gtg	ctg	tgc	tct	gtg	aag	aac	cag	gag	cgg	485
Val	Val	Val	Cys	Thr	Leu	Val	Leu	Cys	Ser	Val	Lys	Asn	Gln	Glu	Arg	
				115					120					125		
att	ctc	cgc	gag	gtg	tgc	aga	gtg	ctg	aga	ccg	gga	ggg	gct	ttc	tat	533
Ile	Leu	Arg	Glu	Val	Cys	Arg	Val	Leu	Arg	Pro	Gly	Gly	Ala	Phe	Tyr	
				130				135					140			
ttc	atg	gag	cat	gtg	gca	gct	gag	tgt	tcg	act	tgg	aat	tac	ttc	tgg	581
Phe	Met	Glu	His	Val	Ala	Ala	Glu	Cys	Ser	Thr	Trp	Asn	Tyr	Phe	Trp	
	145					150					155					
caa	caa	gtc	ctg	gat	cct	gcc	tgg	cac	ctt	ctg	ttt	gat	ggg	tgc	aac	629
Gln	Gln	Val	Leu	Asp	Pro	Ala	Trp	His	Leu	Leu	Phe	Asp	Gly	Cys	Asn	
	160					165					170					
ctg	acc	aga	gag	agc	tgg	aag	gcc	ctg	gag	cgg	gcc	agc	ttc	tct	aag	677
Leu	Thr	Arg	Glu	Ser	Trp	Lys	Ala	Leu	Glu	Arg	Ala	Ser	Phe	Ser	Lys	
	175				180					185					190	
ctg	aag	ctg	cag	cac	atc	cag	gcc	cca	ctg	tcc	tgg	gag	ttg	gtg	cgc	725
Leu	Lys	Leu	Gln	His	Ile	Gln	Ala	Pro	Leu	Ser	Trp	Glu	Leu	Val	Arg	
				195				200						205		
cct	cat	atc	tat	gga	tat	gct	gtg	aaa	tagt	gtgagc	tggcag	ttaa				772
Pro	His	Ile	Tyr	Gly	Tyr	Ala	Val	Lys								
				210				215								
gagctgaatg	gctcaaagaa	tttaaagctt	cagttttaca	tttaaaatgc	taggtgggtg											832
cctgtaatcc	caggtacttg	gaaggctgag	gcaggagaat	ctcttgaacc	cagaaggcga											892
agggtgcagt	gaaccgagat	catgccattg	tactctagcc	tgggtgacaa	gagcaagact											952
ccgtctcaaa	aaaaaataaa	aaaaaaaaaa	aaa													985

<210> 119  
 <211> 839  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 185..715

<220>  
 <221> sig\_peptide  
 <222> 185..253  
 <223> Von Heijne matrix  
 score 9.49395175807817  
 seq SLLFICFFGESFC/IC

<400> 119  
 atatttttgct gactggcaag gttatatgaa gtgcttttat tgaagcacca ttttaactaa 60  
 cagctcctgg tattttctgc ttcccttcgt aggggaattta gttattttat tttattattt 120  
 agctaattta gctattttta aatagctaaa ttttagctac ttttttttca attgacaaag 180  
 aagg atg tct aat caa aga cta ccg ctg att ttt tct ctg ttg ttt atc 229  
 Met Ser Asn Gln Arg Leu Pro Leu Ile Phe Ser Leu Leu Phe Ile  
 -20 -15 -10  
 tgc ttc ttc ggg gag agt ttc tgc att tgt gat gga act gtc tgg aca 277



Cys	Phe	Phe	Gly	Glu	Ser	Phe	Cys	Ile	Cys	Asp	Gly	Thr	Val	Trp	Thr		
			-5					1				5					
aag	ggt	gga	tgg	gag	att	ctt	cca	gaa	gaa	gta	cat	tat	tgg	aaa	ggt	325	
Lys	Val	Gly	Trp	Glu	Ile	Leu	Pro	Glu	Glu	Val	His	Tyr	Trp	Lys	Val		
	10					15					20						
aag	ggt	tct	cca	tct	cac	tgc	ctg	cct	tat	ctt	ctg	gat	aaa	cta	tgc	373	
Lys	Gly	Ser	Pro	Ser	His	Cys	Leu	Pro	Tyr	Leu	Leu	Asp	Lys	Leu	Cys		
25					30					35				40			
tgc	gac	ttt	gct	aac	atg	gat	ata	ttt	cag	ggg	tgt	tta	tat	ctc	att	421	
Cys	Asp	Phe	Ala	Asn	Met	Asp	Ile	Phe	Gln	Gly	Cys	Leu	Tyr	Leu	Ile		
				45					50					55			
tat	aat	tta	tta	caa	gct	gtc	ttc	ttc	gtc	tta	ttt	ggt	ttg	tct	gtg	469	
Tyr	Asn	Leu	Leu	Gln	Ala	Val	Phe	Phe	Val	Leu	Phe	Val	Leu	Ser	Val		
			60					65					70				
cat	tac	ctg	tgg	aag	aaa	tgg	aag	aaa	cac	caa	aaa	aag	ctg	aaa	aag	517	
His	Tyr	Leu	Trp	Lys	Lys	Trp	Lys	Lys	His	Gln	Lys	Lys	Leu	Lys	Lys		
	75					80						85					
caa	gcc	tcc	tta	gaa	aaa	cct	ggg	aat	gat	cta	gaa	agc	cca	ttg	atc	565	
Gln	Ala	Ser	Leu	Glu	Lys	Pro	Gly	Asn	Asp	Leu	Glu	Ser	Pro	Leu	Ile		
	90					95					100						
aac	aac	att	gac	caa	aca	ctc	cac	aga	gtg	gca	acc	aca	gca	tca	gtg	613	
Asn	Asn	Ile	Asp	Gln	Thr	Leu	His	Arg	Val	Ala	Thr	Thr	Ala	Ser	Val		
	105				110					115					120		
ata	tac	aag	atc	tgg	gag	cac	agg	tct	cac	cat	cct	tcc	tct	aag	aaa	661	
Ile	Tyr	Lys	Ile	Trp	Glu	His	Arg	Ser	His	His	Pro	Ser	Ser	Lys	Lys		
				125				130						135			
att	aag	cac	tgc	aaa	tta	aag	aag	aag	agt	aaa	gaa	gaa	gga	gcc	aga	709	
Ile	Lys	His	Cys	Lys	Leu	Lys	Lys	Lys	Ser	Lys	Glu	Glu	Gly	Ala	Arg		
			140					145					150				
aga	tac	taaataaatg	catatgcaaa	tgtagcttac	tcaattatag	atatcacaaa										765	
Arg	Tyr																
agaaatctat	catctaagga	ttaaaaattg	ttcttttgaa	acctttataa	aaaaaaaaaga											825	
aaaaaaaaaaaa	aaaa															839	

<210> 120  
 <211> 583  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 54..527

<220>  
 <221> sig\_peptide  
 <222> 54..116  
 <223> Von Heijne matrix  
 score 6.80928714315144  
 seq ALXSLNLAPPTVA/AP

<400> 120  
 aacgtcatct aggagcaccg agcagcttgg ctaaaagtaa ggggtgctgtg ctg atg  
 Met  
 gcc ctg tgc gca ctg acc cgc gct ctg ccs tct ctg aac ctg gcg ccc  
 Ala Leu Cys Ala Leu Thr Arg Ala Leu Pro Ser Leu Asn Leu Ala Pro  
 -20 -15 -10 -5  
 ccg acc gtc gcc gcc cct gcc ccg agt ctg ttc ccc gcc gcc cag atg  
 Pro Thr Val Ala Ala Pro Ala Pro Ser Leu Phe Pro Ala Ala Gln Met

```

      1           5           10
atg aac aat ggc ctc ctc caa cag ccc tct gcc ttg atg ttg ctc ccc      200
Met Asn Asn Gly Leu Leu Gln Pro Ser Ala Leu Met Leu Leu Pro
      15           20           25
tgc cgc cca gtt ctt act tct gtg gcc ctt aat gcc aac ttt gtg tcc      248
Cys Arg Pro Val Leu Thr Ser Val Ala Leu Asn Ala Asn Phe Val Ser
      30           35           40
tgg aag agt cgt acc aag tac acc att aca cca gtg aag atg agg aag      296
Trp Lys Ser Arg Thr Lys Tyr Thr Ile Thr Pro Val Lys Met Arg Lys
      45           50           55           60
tct ggg ggc cga gac cac aca ggt gct gga aac gtg cgt aga aca gta      344
Ser Gly Gly Arg Asp His Thr Gly Ala Gly Asn Val Arg Arg Thr Val
      65           70           75
ggc cga gta tcc aac gtt gat cat aac aaa cgg gtc att ggc aag gca      392
Gly Arg Val Ser Asn Val Asp His Asn Lys Arg Val Ile Gly Lys Ala
      80           85           90
ggg cgc aac cgc tgg ctg ggc aag agg cct aac agt ggg cgg tgg cac      440
Gly Arg Asn Arg Trp Leu Gly Lys Arg Pro Asn Ser Gly Arg Trp His
      95           100           105
cgc aag ggg ggc tgg gct ggc cga aag att cgg cca cta ccc ccc atg      488
Arg Lys Gly Gly Trp Ala Gly Arg Lys Ile Arg Pro Leu Pro Pro Met
      110           115           120
aag agt tac gtg aag ctg cct tct gct tct gcc caa agc tgatatccct      537
Lys Ser Tyr Val Lys Leu Pro Ser Ala Ser Ala Gln Ser
      125           130           135
gtactctaataaaaatgccccccccccctcaaaaaaaaaaaaaa      583

```

<210> 121  
 <211> 1024  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 129..686

<220>  
 <221> sig\_peptide  
 <222> 129..185  
 <223> Von Heijne matrix  
 score 6.45239823575329  
 seq SVFLLMVNGQVES/AQ

```

<400> 121
cttcgcgaag gtgtcgctgc caagaaacgt gtcctgcgcg ctacgccgtc tgtttctagg      60
gcaacgccgg cgtctcttag caaccgcgcg cggcctagggt ggggtcccccc ggcacccccca      120
gacctgcc atg gcg acc gcg agt cct agc gtc ttt cta ctc atg gtc aac      170
      Met Ala Thr Ala Ser Pro Ser Val Phe Leu Leu Met Val Asn
      -15           -10
ggg cag gtg gag agc gcc cag ttt cca gag tat gat gac ctc tac tgc      218
Gly Gln Val Glu Ser Ala Gln Phe Pro Glu Tyr Asp Asp Leu Tyr Cys
      -5           1           5           10
aag tac tgc ttt gtg tac ggc cag gac tgg gcc ccc aca gcg ggt ctg      266
Lys Tyr Cys Phe Val Tyr Gly Gln Asp Trp Ala Pro Thr Ala Gly Leu
      15           20           25
gag gag ggg atc tca cag atc aca tcc aag agc caa gat gtg cgg caa      314
Glu Glu Gly Ile Ser Gln Ile Thr Ser Lys Ser Gln Asp Val Arg Gln
      30           35           40

```

```

gca ctg gtg tgg aac ttc ccc att gat gtc acc ttt aaa agc acc aac      362
Ala Leu Val Trp Asn Phe Pro Ile Asp Val Thr Phe Lys Ser Thr Asn
   45                               50                               55
ccc tac ggc tgg cca cag atc gtg ctc agc gtg tat gga cca gat gtg      410
Pro Tyr Gly Trp Pro Gln Ile Val Leu Ser Val Tyr Gly Pro Asp Val
   60                               65                               70                               75
ttc ggg aac gat gtg gtt cga ggc tat ggg gcc gtg cac gtg ccc ttc      458
Phe Gly Asn Asp Val Val Arg Gly Tyr Gly Ala Val His Val Pro Phe
                               80                               85                               90
tca cct ggc cgg cac aaa agg acc atc ccc atg ttt gtc cca gaa tct      506
Ser Pro Gly Arg His Lys Arg Thr Ile Pro Met Phe Val Pro Glu Ser
   95                               100                               105
acg tct aaa ctg cag aag ttt aca agc tgg ttc atg ggg cgg cgg ccc      554
Thr Ser Lys Leu Gln Lys Phe Thr Ser Trp Phe Met Gly Arg Arg Pro
   110                               115                               120
gag tac aca gac ccc aag gtg gtg gct cag ggt gaa ggc cgg gaa gct      602
Glu Tyr Thr Asp Pro Lys Val Val Ala Gln Gly Glu Gly Arg Glu Ala
   125                               130                               135
atc aca gct ccc cgg aaa gct gtc ttc tct gtc cat ggc ctc acc tca      650
Ile Thr Ala Pro Arg Lys Ala Val Phe Ser Val His Gly Leu Thr Ser
   140                               145                               150                               155
ccc agg gca ctg gcc ttg gtc cac atc aag ggg acc tgaagcttcc      696
Pro Arg Ala Leu Ala Leu Val His Ile Lys Gly Thr
                               160                               165
ctgaagcctc tagcctgtgg tgtgcacgta caagcctcag gccccatttg tccagcctgt      756
cagcagctgg gaaatactaa gtcaccctct tctgggtatg ttttaattttc caatttttct      816
caacattact gaaatgtcta aatgtggaaa agttgacatc attttacagt gaacaccaca      876
taccacaccac ctagatttta ccattaccaa tttcctgttc cgtacttgta tattcacata      936
tatccaacta ttcacccctg cttcaatcca tcctattttt attgcatttc aaaataaact      996
gtgaaatcag gaaaaaaaaa aaaaaaaaaa      1024

<210> 122
<211> 760
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 165..614

<220>
<221> sig_peptide
<222> 165..305
<223> Von Heijne matrix
      score 5.10820788278539
      seq ALGLALCSTKALS/VG

<400> 122
aatttccgat gccaggcacc ctcaaggcac agaggctggg gctcatgttg ggggcacttg      60
gcctctccag gcctcgaagg cttctcctgg gctgatgcga gctggggaac gggaggggacg      120
gacgtgggag cgagaacgtc acactggagg cagctgggtg cacg atg ggg gac aga      176
                               Met Gly Asp Arg
                               -45
gtg aaa ggt agc aag tca aga gcc ttc gtg tca cca tgg cca cac acc      224
Val Lys Gly Ser Lys Ser Arg Ala Phe Val Ser Pro Trp Pro His Thr
      -40                               -35                               -30
ccg atg gct tcc ggc ttg agg gac ccc tgg ctg cag ccc aca gcc ctg      272
Pro Met Ala Ser Gly Leu Arg Asp Pro Trp Leu Gln Pro Thr Ala Leu

```



```

1           5           10           15
tct ctg atc act gta gca ctt ggt tct tta ata tct tta tct tgc tct 422
Ser Leu Ile Thr Val Ala Leu Gly Ser Leu Ile Ser Leu Ser Cys Ser
          20          25          30
acc ttg tta tat ttt tct tgt gaa ctt aaa att ccc tgt gag gac gta 470
Thr Leu Leu Tyr Phe Ser Cys Glu Leu Lys Ile Pro Cys Glu Asp Val
          35          40          45
aac ctt tgaaggtatg tctcatatct ctgaacctct ttaaaatgcc tagcatccct 526
Asn Leu
          50
gtgtgggtgc caattgcttg tgtattgaat taaattgtga ttgttaactt gaaaaaaaaa 586
aaaaaaaaa 594

<210> 124
<211> 559
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 16..297

<220>
<221> sig_peptide
<222> 16..93
<223> Von Heijne matrix
      score 6.65836819891491
      seq FCGSACLLAVIRA/FF

<400> 124
ttacacaggg gataa atg gca gca atc gag att gaa gtc aag cct aac cag 51
          Met Ala Ala Ile Glu Ile Glu Val Lys Pro Asn Gln
          -25          -20          -15
ggc ttt tgc ggg agc gca tgc ctt ttg gct gta att cgt gca ttt ttt 99
Gly Phe Cys Gly Ser Ala Cys Leu Leu Ala Val Ile Arg Ala Phe Phe
          -10          -5          1
ttt aag aaa aac gcc tgc ctt ctg cgt gag att ctc cag agc aaa ctg 147
Phe Lys Lys Asn Ala Cys Leu Leu Arg Glu Ile Leu Gln Ser Lys Leu
          5          10          15
ggc ggc atg ggc cct gtg gtc ttt tgc tac aga ggg ctt cct ctt tgg 195
Gly Gly Met Gly Pro Val Val Phe Ser Tyr Arg Gly Leu Pro Leu Trp
          20          25          30
ctc ttt gcc tgg ttg ttt cca aga tgt act gtg cct ctt act ttc ggt 243
Leu Phe Ala Trp Leu Phe Pro Arg Cys Thr Val Pro Leu Thr Phe Gly
          35          40          45          50
ttt gaa aac atg agg ggg ttg ggc gtg gta gct tac gcc tgt aat ccc 291
Phe Glu Asn Met Arg Gly Leu Gly Val Val Ala Tyr Ala Cys Asn Pro
          55          60          65
agc act tagggaggcc gaggcgggag gatggcttga ggtccgtagt tgagaccagc 347
Ser Thr
ctggccaaca tgggtgaagcc tgggtctctac aaaaaaataa taacaaaaat tagccgggtg 407
tgggtggctcg tgcctgtggt cccagctgct ccggtggctg aggcgggagg atctcttgag 467
cttaggcttt tgagctatca tggcgccagt gcactccagc gtgggcaaca gagcgagacc 527
ctgtctctca aaaacaaaaa aaaaaaaaaa aa 559

<210> 125
<211> 744
<212> DNA

```

<213> Homo sapiens

<220>

<221> CDS

<222> 216..635

<220>

<221> sig\_peptide

<222> 216..335

<223> Von Heijne matrix

score 4.38054120608596

seq ITLVSAAPGKVIC/EM

<400> 125

```

gcttcgtcac aaggggtgca tgaaagtcag tgagcaaata gcggaccacc ggggctgcca      60
gctcgctga ctcccgccct cttgcgctcc taggggcgga gaaggggtgcg ggctcttcgc      120
cctttgtgtc ctccctcttt cactaacttc tggactttcc agctcttccg aagttcgttc      180
ttgcgcaaag cccaaaggct ggaaaaccgt ccacg atg acc agc atg act cag      233
                               Met Thr Ser Met Thr Gln
                               -40                               -35
tct ctg cgg gag gtg ata aag gcc atg acc aag gct cgc aat ttt gag      281
Ser Leu Arg Glu Val Ile Lys Ala Met Thr Lys Ala Arg Asn Phe Glu
                               -30                               -25                               -20
aga gtt ttg gga aag att act ctt gtc tct gct gct cct ggg aaa gtg      329
Arg Val Leu Gly Lys Ile Thr Leu Val Ser Ala Ala Pro Gly Lys Val
                               -15                               -10                               -5
att tgt gaa atg aaa gta gaa gaa gag cat acc aat gca ata ggc act      377
Ile Cys Glu Met Lys Val Glu Glu Glu His Thr Asn Ala Ile Gly Thr
                               1                               5                               10
ctc cac ggc ggt ttg aca gcc acg tta gta gat aac ata tca aca atg      425
Leu His Gly Gly Leu Thr Ala Thr Leu Val Asp Asn Ile Ser Thr Met
15                               20                               25                               30
gct ctg cta tgc acg gaa agg gga gca ccc gga gtc agt gtc gat atg      473
Ala Leu Leu Cys Thr Glu Arg Gly Ala Pro Gly Val Ser Val Asp Met
                               35                               40                               45
aac ata acg tac atg tca cct gca aaa tta gga gaa gat ata gtg att      521
Asn Ile Thr Tyr Met Ser Pro Ala Lys Leu Gly Glu Asp Ile Val Ile
                               50                               55                               60
aca gca cat gtt ctg aag caa gga aaa aca ctt gca ttt acc tct gtg      569
Thr Ala His Val Leu Lys Gln Gly Lys Thr Leu Ala Phe Thr Ser Val
                               65                               70                               75
gat ctg acc aac aag gcc aca gga aaa tta ata gca caa gga aga cac      617
Asp Leu Thr Asn Lys Ala Thr Gly Lys Leu Ile Ala Gln Gly Arg His
80                               85                               90
aca aaa cac ctg gga aac tgagagaaca gcagaatgac ctaaagaaac      665
Thr Lys His Leu Gly Asn
95                               100
ccaacaatga atatcaagta tagatttgac tcaaacaatt gtaatttttg aaataaacta      725
gcaaaaaaaaa aaaaaaaaaa
744

```

<210> 126

<211> 824

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 164..280

<220>  
 <221> sig\_peptide  
 <222> 164..268  
 <223> Von Heijne matrix  
 score 5.73290676305402  
 seq TLPLCPVTSPVWG/WS

<400> 126  
 tgtgttcaat cgtgtgaatg gccggcgggc cccctccacg tccccatcct tcgaggggac 60  
 ccaggagacc tacacagtgg cccacgagga gaatgtccgc tttgtgtccg aaggtagcga 120  
 gcggggccag aggggtgcggc ataggctgct gggtcgcaaa acc atg gac ccg gga 175  
 Met Asp Pro Gly  
 -35  
 tgg ccc cac ttc aag ctg acc cac agc cgc tgc atg gct gtg ctt ttc 223  
 Trp Pro His Phe Lys Leu Thr His Ser Arg Cys Met Ala Val Leu Phe  
 -30 -25 -20  
 ctt ggc act ctg ccc ttg tgt cct gtg acc agc cct gtg tgg ggc tgg 271  
 Leu Gly Thr Leu Pro Leu Cys Pro Val Thr Ser Pro Val Trp Gly Trp  
 -15 -10 -5 1  
 agt cca ggg tgaccatcag gccttgggtg ggcgatgggg tgccctgggac 320  
 Ser Pro Gly  
 ctggctcagc ccgactgccc tcctcccaca gcctggcagc aggtgcaaca gcagctggat 380  
 ggtggcccag ccggtgaggg cgggccaagg cctgtgcagt acgtggagag gacccccaat 440  
 ccccggtgc agaactttgt gcccatattac ctagacgagt ggtgggcgca gcagttcctg 500  
 gcgagaatca ccagctgttc ctagtggctg ctgggagggg gcgctgctac acggccgacc 560  
 tgtcgccagg agagaagcat ggcgcctgc ccaccactg cgcctggctg ggtgccggcc 620  
 acacctgaag tgccagcatt tggacttttg cacctttttt tcccttggcc cggtgtccc 680  
 aaccaagctg ccatggccaa gggccgaacc cgtctgacct cagccctgct cactgtgccc 740  
 agggaccagc gaccagcccc tggggctggc agggaggagc tccaggctaa taaagtggag 800  
 aaactgtcaa aaaaaaaaaa aaaa 824

<210> 127  
 <211> 526  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 68..301

<220>  
 <221> sig\_peptide  
 <222> 68..190  
 <223> Von Heijne matrix  
 score 4.68908216483476  
 seq AYLLYILLTGALQ/FG

<400> 127  
 acatccggtg tggctgacgg gtccctccaag agtttggggc gcggaccgga gtaccttgcg 60  
 tgcagtt atg tcg gcg tcg gta gtg tct gtc att tcg cgg ttc tta gaa 109  
 Met Ser Ala Ser Val Val Ser Val Ile Ser Arg Phe Leu Glu  
 -40 -35 -30  
 gag tac ttg agc tcc act ccg cag cgt ctg aag ttg ctg gac gcg tac 157  
 Glu Tyr Leu Ser Ser Thr Pro Gln Arg Leu Lys Leu Leu Asp Ala Tyr  
 -25 -20 -15  
 ctg ctg tat ata ctg ctg acc ggg gcg ctg cag ttc ggt tac tgt ctc 205  
 Leu Leu Tyr Ile Leu Leu Thr Gly Ala Leu Gln Phe Gly Tyr Cys Leu

```

-10          -5          1          5
ctc gtg ggg acc ttc ccc ttc aac tct ttt ctc tcg ggc ttc atc tct      253
Leu Val Gly Thr Phe Pro Phe Asn Ser Phe Leu Ser Gly Phe Ile Ser

          10          15          20
tgt gtg ggg agt ttc atc cta gcg ggt tca ctc ttt gaa ttt cct gga      301
Cys Val Gly Ser Phe Ile Leu Ala Gly Ser Leu Phe Glu Phe Pro Gly

          25          30          35
taagagttct ggagatggca gcttattgga cacatggatt ttcttcagat ttgcacttac      361
tgctagctct gctttttatg caggagaaaa gccagagatt cactgtgtgt cagaacaact      421
ttctaacaaa catttattaa tccagcctct gcctttcatt aaatgtaacc ttttgccttc      481
caaattaaag aactccatgc cactcctcaa aaaaaaaaaa aaaaa      526

<210> 128
<211> 618
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 179..427

<220>
<221> sig_peptide
<222> 179..298
<223> Von Heijne matrix
      score 7.72883276007822
      seq CLVVVTMATLSLA/RP

<400> 128
aagcgaagag atgggtctgc actttggagg agccggacac tgttgacttt cctgatgtga      60
aatctaccca ggaacaaaac accagtgact gcagcagcag cggcagcgcc tcggttcctg      120
agcccaccgc aggctgaagg cattgcgcgt agtccatgcc cgtagaggaa gtgtgcag      178
atg gga tta acg tcc aca tgg aga tat gga aga gga ccg ggg att ggt      226
Met Gly Leu Thr Ser Thr Trp Arg Tyr Gly Arg Gly Pro Gly Ile Gly
-40          -35          -30          -25
acc gta acc atg gtc agc tgg ggt cgt ttc atc tgc ctg gtc gtg gtc      274
Thr Val Thr Met Val Ser Trp Gly Arg Phe Ile Cys Leu Val Val Val
          -20          -15          -10
acc atg gca acc ttg tcc ctg gcc cgg ccc tcc ttc agt tta gtt gag      322
Thr Met Ala Thr Leu Ser Leu Ala Arg Pro Ser Phe Ser Leu Val Glu
          -5          1          5
gat acc aca tta gag cca gaa gat gcc atc tca tcc gga gat gat gag      370
Asp Thr Thr Leu Glu Pro Glu Asp Ala Ile Ser Ser Gly Asp Asp Glu
10          15          20
gat gac acc gat ggt gcg gaa gat ttt gtc agt gag aac agt aac aac      418
Asp Asp Thr Asp Gly Ala Glu Asp Phe Val Ser Glu Asn Ser Asn Asn
25          30          35          40
aag agt aag taactgccc gctccgatgg tccccgagag aggagcatgg      467
Lys Ser Lys
agggaagttc tgccgtgtcac ctgtcttctt gtgcactctt ctgcgccatg ctgtgtcccc      527
cggcccttgc ctttccccgc tgtgtctact ttcttgactt tcaaacctga gaataaacca      587
gtgttgctgc acataaaaaa aaaaaaaaaa a      618

<210> 129
<211> 776
<212> DNA
<213> Homo sapiens

```



<220>  
<221> CDS  
<222> 22..297

<220>  
<221> sig\_peptide  
<222> 22..66  
<223> Von Heijne matrix  
score 4.68058603039206  
seq VLAGSLLGPTSRS/AA

<400> 129  
actgcggggac ccactgcgga t atg gct gtc ttg gct gga tcc ctg ttg ggc 51  
Met Ala Val Leu Ala Gly Ser Leu Leu Gly  
-15 -10  
ccc acg agt agg tcg gca gcg ttg ctg ggt ggc agg tgg ctc cag ccc 99  
Pro Thr Ser Arg Ser Ala Ala Leu Leu Gly Gly Arg Trp Leu Gln Pro  
-5 1 5 10  
cgg gcc tgg ctg ggg ttc cca gac gcc tgg ggc ctc ccc acc ccg cag 147  
Arg Ala Trp Leu Gly Phe Pro Asp Ala Trp Gly Leu Pro Thr Pro Gln  
15 20 25  
cag gcc cgg ggc aag gct cgc ggg aat gag tat cag ccg agc aat atc 195  
Gln Ala Arg Gly Lys Ala Arg Gly Asn Glu Tyr Gln Pro Ser Asn Ile  
30 35 40  
aaa cgc aag aac aag cac ggc tgg gtc cgg cgc ctg agc acg ccg gcc 243  
Lys Arg Lys Asn Lys His Gly Trp Val Arg Arg Leu Ser Thr Pro Ala  
45 50 55  
ggc gtg cag gtc atc ctt cgc cga atg ctc aag ggc cgc aag tcg ctg 291  
Gly Val Gln Val Ile Leu Arg Arg Met Leu Lys Gly Arg Lys Ser Leu  
60 65 70 75  
agc cat tgaggatcgc gacgcagtcg gcggggaccc tcatggaagc atcgccctcg 347  
Ser His  
cctcggacct tgccctggcgc tattttttgca gggagctggg gagcaggaac gcctcggacc 407  
tgagtgtctt ccatattgtg ggtttgaagt ctggatggga gccttgccaa gtcccttttt 467  
aggcttttta attaggaagc atttcgaacc tgcgcaacag accaaagaac agtacaaaga 527  
acatccgtgt acccagtacc ctgactaccg actacctaca acccgtccct gccccatcct 587  
gagttctttt gaagctgata tcaggcatcg gattattttt tctgtaaata tttcagaatg 647  
tatctctcca agatgagagc tcattaaaag ataattacaa agcttatcac atccaaaaaga 707  
attatcaata attttgaaat attattaaac gtgtaataaa tgttcaaagt tcaaaaaaaaa 767  
aaaaaaaaa 776

<210> 130  
<211> 998  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 9..845

<220>  
<221> sig\_peptide  
<222> 9..134  
<223> Von Heijne matrix  
score 6.13963522287438  
seq RSLALAAPSSNG/SP

<400> 130

aacgaaaag atg gcg gcg ccc gta agg cgg acg ctg tta ggg gtg gcg ggg	50
Met Ala Ala Pro Val Arg Arg Thr Leu Leu Gly Val Ala Gly	
-40 -35 -30	
ggt tgg cgg cgg ttc gag agg ctc tgg gcc ggc agt cta agc tct cgc	98
Gly Trp Arg Arg Phe Glu Arg Leu Trp Ala Gly Ser Leu Ser Ser Arg	
-25 -20 -15	
agc ctg gct ctt gca gcc gca ccc tca agc aac gga tcc cca tgg cgc	146
Ser Leu Ala Leu Ala Ala Ala Pro Ser Ser Asn Gly Ser Pro Trp Arg	
-10 -5 1	
ttg ttg ggc gcg ttg tgc ctg cag cgg cca cct gta gtc tcc aag ccg	194
Leu Leu Gly Ala Leu Cys Leu Gln Arg Pro Pro Val Val Ser Lys Pro	
5 10 15 20	
ttg acc cca ttg cag gaa gag atg gcg tct cta ctg cag cag att gag	242
Leu Thr Pro Leu Gln Glu Glu Met Ala Ser Leu Leu Gln Gln Ile Glu	
25 30 35	
ata gag aga agc ctg tat tca gac cac gag ctt cgt gct ctg gat gaa	290
Ile Glu Arg Ser Leu Tyr Ser Asp His Glu Leu Arg Ala Leu Asp Glu	
40 45 50	
aac cag cga ctg gca aag aag aaa gct gac ctt cat gat gaa gaa gat	338
Asn Gln Arg Leu Ala Lys Lys Lys Ala Asp Leu His Asp Glu Glu Asp	
55 60 65	
gaa cag gat ata ttg ctg gcg caa gat ttg gaa gat atg tgg gag cag	386
Glu Gln Asp Ile Leu Leu Ala Gln Asp Leu Glu Asp Met Trp Glu Gln	
70 75 80	
aaa ttt cta cag ttc aaa ctt gga gct cgc ata aca gaa gct gat gaa	434
Lys Phe Leu Gln Phe Lys Leu Gly Ala Arg Ile Thr Glu Ala Asp Glu	
85 90 95 100	
aag aat gac cga aca tcc ctg aac agg aac cta gac agg aac ctt gtc	482
Lys Asn Asp Arg Thr Ser Leu Asn Arg Asn Leu Asp Arg Asn Leu Val	
105 110 115	
ctg tta gtc aga gag aag ttt gga gac cag gat gtt tgg ata ctg ccc	530
Leu Leu Val Arg Glu Lys Phe Gly Asp Gln Asp Val Trp Ile Leu Pro	
120 125 130	
cag gca gag tgg cag cct ggg gag acc ctt cga gga aca gct gaa cga	578
Gln Ala Glu Trp Gln Pro Gly Glu Thr Leu Arg Gly Thr Ala Glu Arg	
135 140 145	
acc ctg gcc aca ctc tca gaa aac aac atg gaa gcc aag ttc cta gga	626
Thr Leu Ala Thr Leu Ser Glu Asn Asn Met Glu Ala Lys Phe Leu Gly	
150 155 160	
aat gca ccc tgt ggg cac tac aca ttc aag ttc ccc cag gca atg cgg	674
Asn Ala Pro Cys Gly His Tyr Thr Phe Lys Phe Pro Gln Ala Met Arg	
165 170 175 180	
aca gag agt aac ctc gga gcc aag gtg ttc ttc ttc aaa gca ctg cta	722
Thr Glu Ser Asn Leu Gly Ala Lys Val Phe Phe Phe Lys Ala Leu Leu	
185 190 195	
tta act gga gac ttt tcc cag gct ggg aat aag ggc cat cat gtg tgg	770
Leu Thr Gly Asp Phe Ser Gln Ala Gly Asn Lys Gly His His Val Trp	
200 205 210	
gtc att aag gat gag ctg ggt gac tat ttg aaa cca aaa tac ctg gcc	818
Val Ile Lys Asp Glu Leu Gly Asp Tyr Leu Lys Pro Lys Tyr Leu Ala	
215 220 225	
caa gtt agg agg ttt gtt tca gac ctc tgatggggccg agctgcctgt	865
Gln Val Arg Arg Phe Val Ser Asp Leu	
230 235	
ggacgggtgct cagacaagtc tgggattaga gcctcaagga cattgtgtga ttgcctcaca	925
tttgcaggta atatcaagca gcaaactaaa ttctgagaaa taaacgagtc tattaccaaa	985
aaaaaaaaaa aaa	998

<210> 131  
<211> 779  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 27..578

<220>  
<221> sig\_peptide  
<222> 27..119  
<223> Von Heijne matrix  
score 4.50637135496675  
seq TALMVGAASLLEG/RP

```

<400> 131
atcttttctgg actggccctg cagagg atg gca tgc acc act act gcc ccc gcc      53
                               Met Ala Cys Thr Thr Thr Ala Pro Ala
                               -30                               -25
cag gaa cac atg ctt ctc acc cct ctc act gct ctg atg gtg ggg gct      101
Gln Glu His Met Leu Leu Thr Pro Leu Thr Ala Leu Met Val Gly Ala
          -20          -15          -10
gct tct ctg ctt gag ggc cgg cca cag atc tca gct cca tac tcc cga      149
Ala Ser Leu Leu Glu Gly Arg Pro Gln Ile Ser Ala Pro Tyr Ser Arg
          -5          1          5          10
gct gca tgt tgc agc cct ggg gca ctg gga tgt cct gca gct cgg gtt      197
Ala Ala Cys Cys Ser Pro Gly Ala Leu Gly Cys Pro Ala Ala Arg Val
          15          20          25
ggg att ctg gat ctg atg tat tcc tgg gtt gcc agg aaa gtg ctc agg      245
Gly Ile Leu Asp Leu Met Tyr Ser Trp Val Ala Arg Lys Val Leu Arg
          30          35          40
tgc agc aat act ggg ctg cag ggg ctg cac tgt gca cca gct tat gca      293
Cys Ser Asn Thr Gly Leu Gln Gly Leu His Cys Ala Pro Ala Tyr Ala
          45          50          55
gca cag ctt ggt atg gac cct ggg agg ggc caa cga gca gga ggg cct      341
Ala Gln Leu Gly Met Asp Pro Gly Arg Gly Gln Arg Ala Gly Gly Pro
          60          65          70
gta gag cag aca tac ttc agt ccc atg ggg aag ctg ccc act ctt tcg      389
Val Glu Gln Thr Tyr Phe Ser Pro Met Gly Lys Leu Pro Thr Leu Ser
          75          80          85          90
tgg ctg gaa ggc tgt aca gca gtc atg acg ctg gca tct gct tgg ctt      437
Trp Leu Glu Gly Cys Thr Ala Val Met Thr Leu Ala Ser Ala Trp Leu
          95          100          105
ctg ggg agc cct cgg gaa act tac aat cat gag aag gtg aag gag aag      485
Leu Gly Ser Pro Arg Glu Thr Tyr Asn His Glu Lys Val Lys Glu Lys
          110          115          120
cag tgt cca ttc tcc agt atg gtt ttg ggg gag tat ggc ttc cta cct      533
Gln Cys Pro Phe Ser Ser Met Val Leu Gly Glu Tyr Gly Phe Leu Pro
          125          130          135
act gtg gac cac ctg tca act ctg ggc tgt aac atg aga gaa ttg      578
Thr Val Asp His Leu Ser Thr Leu Gly Cys Asn Met Arg Glu Leu
          140          145          150
tgaacttctg tcttgtttga gccatgggtt cattctcttt ttcagccatg tagcctgtgc      638
tgtaactcag taccacatta gcaactagt aaagtcaatg tgggttaaatt tgtcattctt      698
caggtagaa catttcttcc ttttattctt gtgtttttgg ctaaataaac tgggaaatta      758
tagtaaaaaa aaaaaaaaaa a

```

<210> 132  
 <211> 1025  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 408..710

<220>  
 <221> sig\_peptide  
 <222> 408..533  
 <223> Von Heijne matrix  
 score 5.66440183652506  
 seq QLCFHLSWLYSWA/SQ

```

<400> 132
atggtttgtt gtgagttcca tgtcctcttg gatcagtcac tgtggccatg catgtttggc      60
cacatgatta atccagtcctg ggcatgacc ttttcttcat ccaaaacaag gtgatgggaa      120
gacaaaaaca atagctacta caaacaatag gagtttataa ttatgtgctg atgtattcga      180
agatgtgttg acagtcgtga gtgtgtatcc taggaaaggc gagctggact ctgtctccat      240
ggtggctctc accccagggg cctaggaaca gcctgtcacc acacaattac ttttataacc      300
ctggagatga aaatctcctt gtcctcaaaa tacttccaga agaacaacca gatgggaagg      360
accttggttg ggactctttc cagttcactt ggggcagagg gaattta atg gct cac      416
                               Met Ala His
                               -40
gta gct gaa aag gat ggg cta gat tgg gct tca ggc tgc atc cca gga      464
Val Ala Glu Lys Asp Gly Leu Asp Trp Ala Ser Gly Cys Ile Pro Gly
                               -35                               -30                               -25
ctc caa aca ggg atc tgt ctc ttt ggc tct cag ctc tgc ttt cat ttg      512
Leu Gln Thr Gly Ile Cys Leu Phe Gly Ser Gln Leu Cys Phe His Leu
                               -20                               -15                               -10
agt tgg ctt tat tct tgg gct tca cag tgt ggc ccc aca gca cca gtt      560
Ser Trp Leu Tyr Ser Trp Ala Ser Gln Cys Gly Pro Thr Ala Pro Val
                               -5                               1                               5
att gat aaa aag agc tcc cct ttg ctg aca gaa ctg ctg gat ttg gtt      608
Ile Asp Lys Lys Ser Ser Pro Leu Leu Thr Glu Leu Leu Asp Leu Val
10                               15                               20                               25
ctc att ggt cca gac gag gaa ggt atc cag cct caa gtc atc att gtg      656
Leu Ile Gly Pro Asp Glu Glu Gly Ile Gln Pro Gln Val Ile Ile Val
                               30                               35                               40
gcc agg aag atg gaa tac acc aaa tgg aca ggc ctg gca tgt acc cac      704
Ala Arg Lys Met Glu Tyr Thr Lys Trp Thr Gly Leu Ala Cys Thr His
                               45                               50                               55
aga gac tgagagttgg tgctggtggt tgtggtggca gatgatatta cctgaagaag      760
Arg Asp
ggacgaatgg gtgctgggca ggacaaagca tcagctgtcc agttcaggcc tctcctcttt      820
ccctggtgtc ttcattttcc tccgtctccc tgctgtccct taccctctgc ccaatctcat      880
tactcctggt cttgggagtt gccttctgag gatactccac tgggggtacc tgagcctgga      940
ttagaggggca gggggaggat attgcctagc caaagtgggt gttcaataaa gaaccatttg      1000
gagatggcaa aaaaaaaaaa aaaaaa
                               1025

```

<210> 133  
 <211> 607  
 <212> DNA  
 <213> Homo sapiens

<220>

<221> CDS  
<222> 247..501

<220>  
<221> sig\_peptide  
<222> 247..306  
<223> Von Heijne matrix  
score 6.43040298500966  
seq LLLVTLVASTVPG/NS

<400> 133  
tgttacaaat attccctatg atctctcctt taaatattct tatcaggata ttggaaattc 60  
ttgattttca caactctgct tcagtggcat atgttttagct ttttgtcttc tgaattaatt 120  
gggcttctga tggctccctag aggtatcagc tactcagtca gaaaacatac atggggaaga 180  
aactgaagtt catgccacaa actgtagcag ctttggaca gaagggacca gacaacctca 240  
aggaga atg ggc cca aat acc aaa aat tta ctc ttg gtg acc ctt gtt 288  
Met Gly Pro Asn Thr Lys Asn Leu Leu Leu Val Thr Leu Val  
-20 -15 -10  
gct tct act gta cca ggc aac tct ctt ggg cag gat ttt act ttt gca 336  
Ala Ser Thr Val Pro Gly Asn Ser Leu Gly Gln Asp Phe Thr Phe Ala  
-5 1 5 10  
cac tta gaa aga tcc tgc acc agg gaa aat cgg tct cct ggg gag gta 384  
His Leu Glu Arg Ser Cys Thr Arg Glu Asn Arg Ser Pro Gly Glu Val  
15 20 25  
ttc cag caa cca tgc aag tct gga ggc ggg ggg gtt gga gaa cca aat 432  
Phe Gln Gln Pro Cys Lys Ser Gly Gly Gly Gly Val Gly Glu Pro Asn  
30 35 40  
gcc caa ggg cag cta ctt agc cag cac cca cta cct gcc ttc att aat 480  
Ala Gln Gly Gln Leu Leu Ser Gln His Pro Leu Pro Ala Phe Ile Asn  
45 50 55  
tgt tct cac ggg cag gcc ttt tgaaccaccc tggtacagaa caccaaccct 531  
Cys Ser His Gly Gln Ala Phe  
60 65  
ggtgcttttag gctgtctgtg ccatttctag gcaatgaacg agtagttact gtaccaaccc 591  
aaaaaaaaaa aaaaaa 607

<210> 134  
<211> 774  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 333..602  
  
<220>  
<221> sig\_peptide  
<222> 333..416  
<223> Von Heijne matrix  
score 4.79986448293481  
seq VPALPLLSSLCA/MV

<400> 134  
ctcttcagtc cggggcttgg ttgaacggac tcaccaggaa acgtgacttt cgtgtccgac 60  
ctctgctgta tcaggattcg attcttggtg ttaaacaaga caacgctgaa ggctcgggtg 120  
agcagccctg caaagggttt tccagcgtc ttgggagggt ggctgtgccc tgcttgcccc 180  
acctggccca cctggcccac cattacctga aggggaagcat gaacagcctt tgacgtggga 240  
gtggcgactg ctgagagggg actgtctgta cacaagcaat gtagccttat gggacctgag 300

[illegible]

```
<210> 135
<211> 611
<212> DNA
<213> Homo sapiens
```

```
<220>
<221> CDS
<222> 110..376
```

```
<220>
<221> sig_peptide
<222> 110..208
<223> Von Heijne matrix
      score 3.64796206065748
      seq LVPHSPLPGALSS/AP
```

```
<220>  
<221> misc_feature  
<222> 347  
<223> n=a, g, c or t
```

<400> 135																					
tctt	gtca	aac	actg	ccca	ct	cagc	gagg	aa	gcag	ccgc	ga	cgcc	ca	act	tctgtt	gga	60				
gcct	gcgc	ag	ccag	aggc	ctcaga	aagcc	acagga	acat	ggccta	ggc	atg	gct	cag				118				
															Met	Ala	Gln				
cca	gca	gcc	ccc	tcc	ctg	acg	cgg	ccc	ttc	ctg	gca	gag	gcc	ccg	aca		166				
Pro	Ala	Ala	Pro	Ser	Leu	Thr	Arg	Pro	Phe	Leu	Ala	Glu	Ala	Pro	Thr						
					-30						-25						-20				-15
gca	ctg	gtc	cca	cac	agc	ccc	ctg	cct	ggg	gcc	ctg	tca	agc	gcc	cct		214				
Ala	Leu	Val	Pro	His	Ser	Pro	Leu	Pro	Gly	Ala	Leu	Ser	Ser	Ala	Pro						
					-10						-5						1				
ggc	ccg	aag	cag	ccc	ccg	acg	gca	agc	aca	ggc	ccg	gag	ctg	ctg	ctg		262				
Gly	Pro	Lys	Gln	Pro	Pro	Thr	Ala	Ser	Thr	Gly	Pro	Glu	Leu	Leu	Leu						

```

      5          10          15
ctg cct ctt tcc tcc ttc atg ccc tgc ggg gcg gct gca cca gcc agg 310
Leu Pro Leu Ser Ser Phe Met Pro Cys Gly Ala Ala Pro Ala Arg
      20          25          30
gtg tca tca cag cgg gct act cct agg gat aag ccc ncc ggt ccc ctc 358
Val Ser Ser Gln Arg Ala Thr Pro Arg Asp Lys Pro Xaa Gly Pro Leu
      35          40          45          50
atc cct ggc cag tgt ccc tgacccccat ctactccttc ctgggggactt 406
Ile Pro Gly Gln Cys Pro
      55
ctcagcgcca gccattggc gcctgcgttg cccgcatecca ggccctgcgg caggccctgt 466
gctagcgtgt tcgcaccagg aacgcaggtg ctgggctgtc ggggaggcct caggccacct 526
ccaggaacag aacacagttt taagtttgat tttttttatt tcaaaatgct ttgcaattaa 586
atgaattact gttcaaaaaa aaaaa 611

<210> 136
<211> 925
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 22..417

<220>
<221> sig_peptide
<222> 22..66
<223> Von Heijne matrix
      score 5.47092708754574
      seq RVLCAPAAGAVRA/LR

<400> 136
agtcgaggag tcaaggcagc a atg aat cgt gtc ttg tgt gcc ccg gcg gcc 51
                        Met Asn Arg Val Leu Cys Ala Pro Ala Ala
                        -15          -10
ggg gcc gtc cgg gcg ctg agg ctc ata ggc tgg gct tcc cga agc ctt 99
Gly Ala Val Arg Ala Leu Arg Leu Ile Gly Trp Ala Ser Arg Ser Leu
-5          1          5          10
cat ccg ttg ccc ggt tcc cgg gat cgg gcc cac cct gcc gcc gag gaa 147
His Pro Leu Pro Gly Ser Arg Asp Arg Ala His Pro Ala Ala Glu Glu
      15          20          25
gag gac gac cct gac cgc ccc att gag ttt tcc tcc agc aaa gcc aac 195
Glu Asp Asp Pro Asp Arg Pro Ile Glu Phe Ser Ser Ser Lys Ala Asn
      30          35          40
cct cac cgc tgg tgc gtg ggc cat acc atg gga aag gga cat cag cgg 243
Pro His Arg Trp Ser Val Gly His Thr Met Gly Lys Gly His Gln Arg
      45          50          55
ccc tgg tgg aag gtg ctg ccc ctc agc tgc ttc ctc gtg gcg ctg atc 291
Pro Trp Trp Lys Val Leu Pro Leu Ser Cys Phe Leu Val Ala Leu Ile
      60          65          70          75
atc tgg tgc tac ctg agg gag gag agc gag gcg gac cag tgg ttg aga 339
Ile Trp Cys Tyr Leu Arg Glu Glu Ser Glu Ala Asp Gln Trp Leu Arg
      80          85          90
cag gtg tgg gga gag gtg cca gag ccc agt gat cgt tct gag gag cct 387
Gln Val Trp Gly Glu Val Pro Glu Pro Ser Asp Arg Ser Glu Glu Pro
      95          100          105
gag act cca gct gcc tac aga gcg aga act tgacgggggtg cccgctgggg 437
Glu Thr Pro Ala Ala Tyr Arg Ala Arg Thr

```

```

110      115
ctggcaggaa gggagccgac agccgccctt cggatttgat gtcacgtttg cccgtgactg 497
tcctggctat gcgtgcgtcc tcagcactga aggacttggc tggatggatgg ggcacttggc 557
tatgctgatt cgcgtgaagg cggagcagaa tctcagcaga tcggaaactg ctcctcgcct 617
ggctcttgat gtccaaggat tccatcggca agacttctca gatccttggg gaagggttca 677
gttgcaactgt atgctgttgg atttgccaa gctttgtata acataatcat gtttccaaag 737
cacttctggt gacacttgtc atccagtgtt agtttgcagg taatttgctt tctgagatag 797
aatatctggc agaagtgtga aactgtattg catgctgcgg cctgtgcaag gaacacttcc 857
acatgtgagt ttacacaac aacaaatgaa aataaatttt aattttataa taaaaaaaaa 917
aaaaaaaaa 925

<210> 137
<211> 674
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 62..367

<220>
<221> sig_peptide
<222> 62..103
<223> Von Heijne matrix
      score 4.49063834776683
      seq FLTALLWRGRIPG/RQ

<400> 137
acgccacggc gtctgctggc ggccgcggag acgcagagtc ttgagcagcg cggcaggcac 60
c atg ttc ctg act gcg ctc ctc tgg cgc ggc cgc att ccc ggc cgt cag 109
  Met Phe Leu Thr Ala Leu Leu Trp Arg Gly Arg Ile Pro Gly Arg Gln
      -10      -5      1
tgg atc ggg aag cac cgg cgg ccg cgg ttc gtg tgg ttg cgc gcc aag 157
Trp Ile Gly Lys His Arg Arg Pro Arg Phe Val Ser Leu Arg Ala Lys
      5      10      15
cag aac atg atc cgc cgc ctg gag atc gat gcg gag aac cat tac tgg 205
Gln Asn Met Ile Arg Arg Leu Glu Ile Asp Ala Glu Asn His Tyr Trp
      20      25      30
ctg agc atg ccc tac atg acc cgg gag cag gag cgc ggc cac gcc gsg 253
Leu Ser Met Pro Tyr Met Thr Arg Glu Gln Glu Arg Gly His Ala Xaa
      35      40      45      50
dtg cgc agg agg gag gcc ttc gag gcc ata aag gcg gcc gcc act tcc 301
Xaa Arg Arg Arg Glu Ala Phe Glu Ala Ile Lys Ala Ala Ala Thr Ser
      55      60      65
aag ttc ccc ccg cat aga ttc att gcg gac cag ctc gac cat ctc aat 349
Lys Phe Pro Pro His Arg Phe Ile Ala Asp Gln Leu Asp His Leu Asn
      70      75      80
gtc acc aag aaa tgg tcc taatcctgag tagtcaccct tggattttat 397
Val Thr Lys Lys Trp Ser
      85
ggatcacgga gctgaccatc tttaacctgt cctggaactg aaaaactgta gcttgtgtga 457
aaatgagcct ttggaccagt ctttattaaa acaaacaaac atgagtagtc tgcatatcga 517
atatctagag ctctaaaccc cccaatactt aaaagtctaa ttgctgtcct gtggtttcat 577
tagtctgata ggaagatagg gatttctctca gtcacagatg atatttttgaa ggaaagctgc 637
aataaagcca caatgattcg aaaaaaaaaa aaaaaaaa 674

<210> 138
<211> 1725

```



<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 107..1618

<220>  
<221> sig\_peptide  
<222> 107..178  
<223> Von Heijne matrix  
score 6.19650168602189  
seq LGLYSLVLSGALA/YA

<400> 138  
agagctcagc cggtcgcacg gacggacagt tggaagccgg accccagagc ctgaggtggg 60  
cagtgtgccca ggggtcccttg cggcctcctc aagccctgtc caggct atg ggc atc 115  
Met Gly Ile  
aag aca gca ttg ccg gcg gct gag ctg ggc ctc tac tct ctg gtg ctg 163  
Lys Thr Ala Leu Pro Ala Ala Glu Leu Gly Leu Tyr Ser Leu Val Leu  
-20 -15 -10  
agt ggg gcc ctg gcc tat gct ggc cgg ggc ctc ctt gag gct tca caa 211  
Ser Gly Ala Leu Ala Tyr Ala Gly Arg Gly Leu Leu Glu Ala Ser Gln  
-5 1 5 10  
gat ggg gcc cac agg aag gcc ttc cgg gag tct gtg cga cct ggc tgg 259  
Asp Gly Ala His Arg Lys Ala Phe Arg Glu Ser Val Arg Pro Gly Trp  
15 20 25  
gag tac att ggc cgg aag atg gat gtg gct gac ttc gag tgg gtg atg 307  
Glu Tyr Ile Gly Arg Lys Met Asp Val Ala Asp Phe Glu Trp Val Met  
30 35 40  
tgg ttc acc tcc ttt cgc aac gtc atc atc ttt gcc ctc tcc gga cat 355  
Trp Phe Thr Ser Phe Arg Asn Val Ile Ile Phe Ala Leu Ser Gly His  
45 50 55  
gtg ctg ttt gct aaa ctc tgc acg atg gtt gcc cca aag ctc cgc tcc 403  
Val Leu Phe Ala Lys Leu Cys Thr Met Val Ala Pro Lys Leu Arg Ser  
60 65 70 75  
tgg atg tat gct gtg tac ggg gcc ttg gct gtg atg ggc aca atg ggc 451  
Trp Met Tyr Ala Val Tyr Gly Ala Leu Ala Val Met Gly Thr Met Gly  
80 85 90  
cct tgg tac ctg ctg ctg ctg ctt ggt cac tgt gtg ggc ctc tat gtg 499  
Pro Trp Tyr Leu Leu Leu Leu Leu Gly His Cys Val Gly Leu Tyr Val  
95 100 105  
gcc tcg ctt ttg ggc cag ccc tgg ctc tgt ctt ggc ctt ggc ttg gcc 547  
Ala Ser Leu Leu Gly Gln Pro Trp Leu Cys Leu Gly Leu Gly Leu Ala  
110 115 120  
agc ctg gcc tcc ttc aag atg gac ccc cta atc tct tgg cag agc ggg 595  
Ser Leu Ala Ser Phe Lys Met Asp Pro Leu Ile Ser Trp Gln Ser Gly  
125 130 135  
ttt gta aca ggc act ttt gat ctt caa gag gtg ctg ttt cat ggg ggc 643  
Phe Val Thr Gly Thr Phe Asp Leu Gln Glu Val Leu Phe His Gly Gly  
140 145 150 155  
agc agc ttc aca gtg ctg cgt tgc acc agc ttt gca ctg gag agc tgt 691  
Ser Ser Phe Thr Val Leu Arg Cys Thr Ser Phe Ala Leu Glu Ser Cys  
160 165 170  
gcc cac cct gac cgc cac tac tcc tta gct gac ctg ctc aag tac agc 739  
Ala His Pro Asp Arg His Tyr Ser Leu Ala Asp Leu Leu Lys Tyr Ser  
175 180 185  
ttc tac ctg ccc ttc ttc ttc ttc ggg ccc atc atg acc ttt gat cgc 787

Phe	Tyr	Leu	Pro	Phe	Phe	Phe	Phe	Gly	Pro	Ile	Met	Thr	Phe	Asp	Arg	
		190					195				200					
ttc	cat	gct	cag	gtg	agc	cag	gtg	gag	cca	gtg	aga	cgc	gag	ggg	gag	835
Phe	His	Ala	Gln	Val	Ser	Gln	Val	Glu	Pro	Val	Arg	Arg	Glu	Gly	Glu	
	205					210					215					
ctg	tgg	cac	atc	cga	gcc	cag	gca	ggc	cta	agc	gtg	gtg	gcc	atc	atg	883
Leu	Trp	His	Ile	Arg	Ala	Gln	Ala	Gly	Leu	Ser	Val	Val	Ala	Ile	Met	
	220				225					230					235	
gcc	gtc	gac	atc	ttc	ttt	cac	ttc	ttc	tac	atc	ctc	act	atc	ccc	agc	931
Ala	Val	Asp	Ile	Phe	Phe	His	Phe	Phe	Tyr	Ile	Leu	Thr	Ile	Pro	Ser	
				240				245						250		
gac	ctc	aag	ttc	gcc	aac	cgc	ctc	cca	gac	att	gcc	ctc	gct	ggc	cta	979
Asp	Leu	Lys	Phe	Ala	Asn	Arg	Leu	Pro	Asp	Ile	Ala	Leu	Ala	Gly	Leu	
			255				260						265			
gcc	tat	tca	aac	ctg	gtg	tat	gac	tgg	gtg	aag	gcg	gcc	gtc	ctc	ttt	1027
Ala	Tyr	Ser	Asn	Leu	Val	Tyr	Asp	Trp	Val	Lys	Ala	Ala	Val	Leu	Phe	
	270					275					280					
ggg	gtt	gtc	aac	act	gtg	gca	tgc	ctc	gac	cac	ctg	gac	cca	ccc	cag	1075
Gly	Val	Val	Asn	Thr	Val	Ala	Cys	Leu	Asp	His	Leu	Asp	Pro	Pro	Gln	
	285					290				295						
cct	ccc	aag	tgc	atc	acc	gca	ctc	tac	gtc	ttt	gcg	gaa	acg	cac	ttt	1123
Pro	Pro	Lys	Cys	Ile	Thr	Ala	Leu	Tyr	Val	Phe	Ala	Glu	Thr	His	Phe	
	300				305				310						315	
gac	cgt	ggc	atc	aac	gac	tgg	ctt	tgc	aaa	tat	gtg	tat	aac	cac	att	1171
Asp	Arg	Gly	Ile	Asn	Asp	Trp	Leu	Cys	Lys	Tyr	Val	Tyr	Asn	His	Ile	
				320			325							330		
ggg	ggg	gag	cat	tcc	gct	gtg	atc	cca	gag	ctg	gca	gcc	aca	gtg	gcc	1219
Gly	Gly	Glu	His	Ser	Ala	Val	Ile	Pro	Glu	Leu	Ala	Ala	Thr	Val	Ala	
			335				340						345			
aca	ttt	gcc	atc	acc	aca	ctg	tgg	ctt	ggg	cct	tgt	gac	att	gtc	tac	1267
Thr	Phe	Ala	Ile	Thr	Thr	Leu	Trp	Leu	Gly	Pro	Cys	Asp	Ile	Val	Tyr	
		350				355					360					
ctg	tgg	tca	ttc	ctt	aac	tgc	ttt	ggc	ctc	aac	ttt	gag	ctc	tgg	atg	1315
Leu	Trp	Ser	Phe	Leu	Asn	Cys	Phe	Gly	Leu	Asn	Phe	Glu	Leu	Trp	Met	
	365				370						375					
caa	aaa	ctg	gca	gag	tgg	ggg	ccc	cta	gca	cga	att	gag	gcc	tct	ctg	1363
Gln	Lys	Leu	Ala	Glu	Trp	Gly	Pro	Leu	Ala	Arg	Ile	Glu	Ala	Ser	Leu	
	380				385					390					395	
tca	gtg	cag	atg	tcc	cgt	agg	gtc	cgg	gcc	ctg	ttt	gga	gcc	atg	aac	1411
Ser	Val	Gln	Met	Ser	Arg	Arg	Val	Arg	Ala	Leu	Phe	Gly	Ala	Met	Asn	
				400				405						410		
ttc	tgg	gcc	atc	atc	atg	tac	aac	ctt	gtg	agc	ctg	aac	agc	ctc	aaa	1459
Phe	Trp	Ala	Ile	Ile	Met	Tyr	Asn	Leu	Val	Ser	Leu	Asn	Ser	Leu	Lys	
			415				420							425		
ttc	aca	gag	ctg	gtt	gcc	cgg	cgc	ctg	cta	ctc	aca	ggg	ttc	ccc	cag	1507
Phe	Thr	Glu	Leu	Val	Ala	Arg	Arg	Leu	Leu	Leu	Thr	Gly	Phe	Pro	Gln	
		430				435					440					
acc	acg	ctg	tcc	atc	ctg	ttt	gtc	acc	tac	tgt	ggc	gtc	cag	ctg	gta	1555
Thr	Thr	Leu	Ser	Ile	Leu	Phe	Val	Thr	Tyr	Cys	Gly	Val	Gln	Leu	Val	
	445				450					455						
aag	gag	cgt	gag	cga	acc	ttg	gca	ctg	gag	gag	gag	cag	aag	cag	gac	1603
Lys	Glu	Arg	Glu	Arg	Thr	Leu	Ala	Leu	Glu	Glu	Glu	Gln	Lys	Gln	Asp	
	460				465				470					475		
aaa	gag	aag	ccg	gag	taggaggggag	cgggtagagg	gatgggctct	gctcagctat								1658
Lys	Glu	Lys	Pro	Glu												
			480													
tcttggggcca	gatggggcct	gaccgataga	ataaaagact	tttctacaac	aaaaaaaaaa											1718
aaaaaaaaa																1725

<210> 139  
 <211> 1474  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 16..471

<220>  
 <221> sig\_peptide  
 <222> 16..93  
 <223> Von Heijne matrix  
 score 5.809301698725  
 seq FCVCVIAIGVVQA/LI

<400> 139  
 tacacgtttt cgtta atg gtg acc ttc cct gat gtg cct ctg ggc atc ttc 51  
 Met Val Thr Phe Pro Asp Val Pro Leu Gly Ile Phe  
 -25 -20 -15  
 ttg ttc tgt gtg tgt gtg atc gcc atc ggg gtc gtg cag gca ctg att 99  
 Leu Phe Cys Val Cys Val Ile Ala Ile Gly Val Val Gln Ala Leu Ile  
 -10 -5 1  
 gta ggg tac gca ttc cac ttc ccg cac ctg ctg agc ccg cag atc cag 147  
 Val Gly Tyr Ala Phe His Phe Pro His Leu Leu Ser Pro Gln Ile Gln  
 5 10 15  
 cgc tct gcc cac agg gct ctg tac cga cga cac gtc ctg ggc atc gtc 195  
 Arg Ser Ala His Arg Ala Leu Tyr Arg Arg His Val Leu Gly Ile Val  
 20 25 30  
 ctc caa ggc ccg gcc ctg tgc ttt gca gcg gcc atc ttc tct ctc ttc 243  
 Leu Gln Gly Pro Ala Leu Cys Phe Ala Ala Ala Ile Phe Ser Leu Phe  
 35 40 45 50  
 ttt gtc ccc ttg tct tac ctg ctg atg gtg act gtc atc ctc ctc ccc 291  
 Phe Val Pro Leu Ser Tyr Leu Leu Met Val Thr Val Ile Leu Leu Pro  
 55 60 65  
 tat gtc agc aag gtc acc ggc tgg tgc aga gac agg ctc ctg ggc cac 339  
 Tyr Val Ser Lys Val Thr Gly Trp Cys Arg Asp Arg Leu Leu Gly His  
 70 75 80  
 agg gag ccc tcg gct cac cca gtg gaa gtc ttc tcg ttt gac ctc cac 387  
 Arg Glu Pro Ser Ala His Pro Val Glu Val Phe Ser Phe Asp Leu His  
 85 90 95  
 gag cca ctc agc aag gag cgc gtg gaa gcc ttc agc gac gga gtc tac 435  
 Glu Pro Leu Ser Lys Glu Arg Val Glu Ala Phe Ser Asp Gly Val Tyr  
 100 105 110  
 gcc atc gtg gcc acg ctt ctc atc ctg gac atc tgg tgaggacccc 481  
 Ala Ile Val Ala Thr Leu Leu Ile Leu Asp Ile Trp  
 115 120 125  
 gcgtcacctg cccagctat caggtggcca atgtgtcttg agtccctggc gtctcactct 541  
 ggaaccccca gaaaggcaca ggggtcttgg ctccaccctc ctctggatgc cttagagtttt 601  
 gtgtgaggtc agggcagccc ccacttcagg gaggacaacc ttcccgccgg cccctccctt 661  
 cccagcggcc cctcccttcc cagaggctcc caccccaagc acagccgagg atggggtgcc 721  
 aggggtgaggt cagcaccagc agccaaactgc tctcctcact cctctcagag gggctcagca 781  
 gccatgggta tccccctgcc ccaggcctca cccctgcccc aacaccagcc cctcctagtc 841  
 cctagtcctt cccattccct ccggctccct cccagtcccc cccatcgctt cgcagccctt 901  
 tctgtctcct ttggctggct gttgcttctt tccagcgtct gctcctccgc ggcctcatct 961  
 gcctcttcgt ctgttagagc gcgcgtctcg tctcagtcgt cacgtttttg gtttttgtgg 1021  
 ggtttttttt tttttttttt tttgagacag tcctgctgtg tcgcccaggc tggagtatag 1081

```

tggctcaagc tcagctcaact gcaacctccg cctcccaggt tcaagcaatt ctctcgctc 1141
agcctcccaa gtagttggga ttacaagcac ccaccaccat gccagctaa ctttttgcac 1201
ttttaataga gatgagggtt caccaagttg gccaggctgg tcttgaactc ctgacctcag 1261
gtgatctgcc cacctcggcc tcccaaagtg ctgggattac aggtgtaagc caccgtgccc 1321
ggccatcgta atgtttgaat ttgctttttt acatcttcca tccttttgga gtgtcttggt 1381
ccctcgatcat agttcagcac tgtgaccacc ttgggggttag acactatggt tttatatcct 1441
gtacttgata ttctccaaaa aaaaaaaaaa aaa 1474

```

```

<210> 140
<211> 653
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 222..374

```

```

<220>
<221> sig_peptide
<222> 222..299
<223> Von Heijne matrix
      score 4.28353322771141
      seq ILFKFSLCPYAAA/LS

```

```

<400> 140
taataatggt gttaaattat tgccttctca tctgcgtgtc tcttatgttc tgcttaaaga 60
gattgtcagt ttgttcaagc tcttttttagt tgttgctcct ccagtgccta gctttgagct 120
ttgtacacgg tagttattga gttgagtaac atagtttggt ctgagtcatt tgttccacat 180
gcttgaagac ttggcttaac ctagtagata ataggaaaga a atg gaa atg ctc ttt 236
                                     Met Glu Met Leu Phe
                                     -25

```

```

gat gaa aga gcc cct ctc tta ttc atc ctt ttt aaa ttt tct ttg tgc 284
Asp Glu Arg Ala Pro Leu Leu Phe Ile Leu Phe Lys Phe Ser Leu Cys
-20 -15 -10
cca tat gca gca gct ctc agc aaa cct ata ttt ggc agt gtg gcc tgt 332
Pro Tyr Ala Ala Ala Leu Ser Lys Pro Ile Phe Gly Ser Val Ala Cys
-5 1 5 10
atg act aaa gaa atc ctg gcc agg cac ggt ggc tca cgc ctg 374
Met Thr Lys Glu Ile Leu Ala Arg His Gly Gly Ser Arg Leu
15 20 25

```

```

taatcccagc actttgggag gccgaggcgg gtggattacg aggtcaggag attgagacca 434
tcctgggctaa catggcgaaa ccccatctct acgaaaaata caaaaaaaaaa aattagccgg 494
gcatcatggc gggcgccctgt agtcttagct actcaggagg ctgaggcagg agaatggcgt 554
gaacccggga ggcggagctt gcagtgagcc gagattgcgc cactgcactc cagcctgggg 614
caacagagca agactccgtc tcaaaaaaaaa aaaaaaaaaa 653

```

```

<210> 141
<211> 1490
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 59..274

```

```

<220>
<221> sig_peptide
<222> 59..127

```

<223> Von Heijne matrix  
score 7.37647149292058  
seq LGLCSLLVGEAEA/PS

<400> 141  
agacagagggc agggccttgcg acggaagtgg cctctctgct tctgcagggc tggggaag 58  
atg ctg cgt cca gcg tta ccg tgg ctg tac ctt ggc ctc tgc agc ctc 106  
Met Leu Arg Pro Ala Leu Pro Trp Leu Tyr Leu Gly Leu Cys Ser Leu  
-20 -15 -10  
ctg gtg ggg gag gca gag gcc ccg agc ccc gtg gat ccg ctg gag cgg 154  
Leu Val Gly Glu Ala Glu Ala Pro Ser Pro Val Asp Pro Leu Glu Arg  
-5 1 5  
agc cgg ccg tac gcg gtg ctg cga ggg cag aac ctg gtg ttg atg gga 202  
Ser Arg Pro Tyr Ala Val Leu Arg Gly Gln Asn Leu Val Leu Met Gly  
10 15 20 25  
acc att ttc agc atc ctg ctg gtg act gtc atc ctt atg gca ttt tgt 250  
Thr Ile Phe Ser Ile Leu Leu Val Thr Val Ile Leu Met Ala Phe Cys  
30 35 40  
gtc tac aag ccc att cgg cgt cgg tgacagccag acaagttctt caatgagtat 304  
Val Tyr Lys Pro Ile Arg Arg Arg  
45  
ttggaatag gataagttgt gttgcacaca ggccagtggg gaagttggaa ccaaaacttt 364  
cctacttgga aatgaccttt ggtctggaca gttggtaaat gctaaatgaa ttagaagaaa 424  
acatgtacta gacattatth tttcctaaca ctgtagcgca aataattggc cctgagtgcc 484  
gcttctcagt gtttctgact gtacttgta aaagtaagac ctgaaagctc caaagggtcag 544  
tgtaaagatg gagtggtcat gagaaagaaa acatggtaac cttgtgagtg cctgtaagaa 604  
ccacactgta aagaactcat cattaatgct tgaaaatgtt attaagaagg agacttacca 664  
tgcagacatt ccctatttaa gaaccatttg gttacagtgg gttagaatc acagattttt 724  
ttttttaatc tcacctgagt tagcctagaa tgcgctgggt gcaaagtggg gtcagctgtg 784  
gggatcttgg gccctcggtc ctcacctgca tectgccttg cactcagggtg ctccccctga 844  
agtcagggtc acatcaggta gacctgttac tatatgcacc tttggcctgg aatgctctga 904  
agttggactg gaaatgttac taggttggtc tgttacaaaa aggaccccat cctgcttaaa 964  
cacattgatc tcccttgccc tgcatttgag tctttctagc ccacgggtctg aaacttgagg 1024  
cagctttcca gatttggaat gtaaaaggct cagtgggcac tctgttcatc cctgggtggg 1084  
gagggcccag ccaacagaag tgcattgtcca ctgtgcgggc cagtgtgtgt ttacacaaat 1144  
ttcatctcag ctttgaaaat gctgctatta gtttccactg ttggtgaact ggattttttc 1204  
ctcctattga aatgatactt tcatacttat aaagctgtcg tcaatattta tttcaagggtg 1264  
ctagatttaa ttttggtatt aaattgaaat gcttatcttg tgttcaagca cagcactgat 1324  
tttaacaacc tgcatttaac gtgaagtaac cgaagtagga tactgtaact gtgtaaggat 1384  
tttggttgta atcttgtaac attgaacct tgaaatgttc agttctttgc ttttgagcaa 1444  
aacgtcaatt aaaactaaag taaaatctta aaaaaaaaaa aaaaaa 1490

<210> 142  
<211> 661  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 158..442

<220>  
<221> sig\_peptide  
<222> 158..301  
<223> Von Heijne matrix  
score 7.53908709538105  
seq FVILLLLFIFTVVS/LV

```

<400> 142
aaaaacagac gataccatcg cttcagcagc atcctctcag acaagagcca ctatttctga      60
ttcagatcac ctgtcatcga agtttaaaga aggggaaaca ggagacagaa atacactgaa      120
ccaaaaagat tcaaaagagc aagtggaatc tctaaga atg gct tcc agc cac tgg      175
                               Met Ala Ser Ser His Trp
                               -45
aat gaa acc act acc tct gtt tat cag tac ctt ggt ttt caa gtt caa      223
Asn Glu Thr Thr Thr Ser Val Tyr Gln Tyr Leu Gly Phe Gln Val Gln
-40                               -35                               -30
aaa att tac cct ttc cat gac aac tgg aac act gcc tgc ttt gtc atc      271
Lys Ile Tyr Pro Phe His Asp Asn Trp Asn Thr Ala Cys Phe Val Ile
-25                               -20                               -15
ctg ctt tta ttt ata ttt aca gtg gta tct tta gtg gtg ctg gct ttc      319
Leu Leu Leu Phe Ile Phe Thr Val Val Ser Leu Val Val Leu Ala Phe
-10                               -5                               1                               5
ctt tat gaa gtg ctt gac tgc tgc tgc tgt gta aaa aac aaa acc gtg      367
Leu Tyr Glu Val Leu Asp Cys Cys Cys Cys Val Lys Asn Lys Thr Val
10                               15                               20
aaa gac ttg aaa agt gaa ccc aac cct ctt aga agt atg atg gac aac      415
Lys Asp Leu Lys Ser Glu Pro Asn Pro Leu Arg Ser Met Met Asp Asn
25                               30                               35
atc aga aaa cgt gaa act gaa gtg gtc taacactcta tagaagatga      462
Ile Arg Lys Arg Glu Thr Glu Val Val
40                               45
acaaaatctc tgaaagcagc tcaacctctt ctgagaaaaa aaatatattc tgaggccaac      522
tgttgctaca aaacaaattc tgactgaatg tttaaaacat ttctagtaga aggggaaaaa      582
aaagttaaac atgcactgtt tgtgtgtata gccatttcat taaatataca gtaaaacttc      642
ataaaaaaaaa aaaaaaaaaa      661

<210> 143
<211> 1789
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 5..454

<220>
<221> sig_peptide
<222> 5..64
<223> Von Heijne matrix
score 6.64507667657896
seq LLPLLSLLVGAWL/KL

<400> 143
cctg atg gcc cgg cat ggg tta ccg ctg ctg ccc ctg ctg tcg ctc ctg      49
Met Ala Arg His Gly Leu Pro Leu Leu Pro Leu Leu Ser Leu Leu
-20                               -15                               -10
gtc ggc gcg tgg ctc aag cta gga aat gga cag gct act agc atg gtc      97
Val Gly Ala Trp Leu Lys Leu Gly Asn Gly Gln Ala Thr Ser Met Val
-5                               1                               5                               10
caa ctg cag ggt ggg aga ttc ctg atg gga aca aat tct cca gac agc      145
Gln Leu Gln Gly Gly Arg Phe Leu Met Gly Thr Asn Ser Pro Asp Ser
15                               20                               25
aga gat ggt gaa ggg cct gtg cgg gag gcg aca gtg aaa ccc ttt gcc      193
Arg Asp Gly Glu Gly Pro Val Arg Glu Ala Thr Val Lys Pro Phe Ala
30                               35                               40

```

```

atc gac ata ttt cct gtc acc aac aaa gat ttc agg gat ttt gtc agg      241
Ile Asp Ile Phe Pro Val Thr Asn Lys Asp Phe Arg Asp Phe Val Arg
  45                      50                      55
gag aaa aag tat cgg aca gaa gct gag atg ttt gga tgg agc ttt gtc      289
Glu Lys Lys Tyr Arg Thr Glu Ala Glu Met Phe Gly Trp Ser Phe Val
  60                      65                      70                      75
ttt gag gac ttt gtc tct gat gag ctg aga aac aaa gcc acc cag cca      337
Phe Glu Asp Phe Val Ser Asp Glu Leu Arg Asn Lys Ala Thr Gln Pro
                      80                      85                      90
atg aag gtc aag ttt acc cat ggg gga act ggt tcc agc caa acc gca      385
Met Lys Val Lys Phe Thr His Gly Gly Thr Gly Ser Ser Gln Thr Ala
  95                      100                      105
cca acc tgt ggc agg gaa agt tcc cca agg gag aca aag ctg agg atg      433
Pro Thr Cys Gly Arg Glu Ser Ser Pro Arg Glu Thr Lys Leu Arg Met
  110                      115                      120
gct tcc atg gag tct ccc cag tgaatgcttt ccccgcccag aacaactacg      484
Ala Ser Met Glu Ser Pro Gln
  125                      130
ggctctatga cctcctgggg aacgtgtggg agtggacagc atcacctgtac caggctgctg      544
agcaggacat gcgcgtcctc cgggggggcat cctggatcga cacagctgat ggctctgcca      604
atcacccggc ccgggtcacc accaggatgg gcaacactcc agattcagcc tcagacaacc      664
tcggtttccg ctgtgctgca gacgcaggcc ggccgcccagg ggagctgtaa gcagccgggt      724
ggtgacaagg agaaaagcct tctaggggtca ctgtcattcc ctggccatgt tgcaaacagc      784
gcaattccaa gctcgagagc ttcagcctca ggaaagaact tccccctccc tgtctcccat      844
ccctctgtgg caggcgccctc tcaccagggc aggagaggac tcagcctcct gtgttttgga      904
gaagggggccc aatgtgtgtt gacgatggct gggggccagg tgtttctgtt agaggccaag      964
tattattgac acaggattgc aaacacacaa acaattggaa cagagcactc tgaaaggcca      1024
ttttttaagc attttaaaat ctattctctc cccctttctc cctggatgat tcaggaagct      1084
gacattgttt cctcaaggca gaattttcct gggtctgttt tctcagccag ttgctgtgga      1144
aggagaatgc tttctttgtg gcctcatctg tggtttcgtg tccctctgaa ggaaactagt      1204
ttccactgtg taacaggcag acatgtaact atttaaagca cagttcagtc ctaaaagggt      1264
ctgggagaac cagatgatgt actaggtgaa gcattgcatt gtgggaatca caaagcaaatt      1324
agtactccag aaagacaaat atcagaagct tcctattctt tttttttttt tttttttttt      1384
ttgagacagg gtctttctct gttgcccagg ctagagtgca ctgggtgatca cggctcactc      1444
tagccttgaa ttcttgggcc caagcaattc tcccacctca gcctcctgag tagctgggac      1504
tacaagtgtg caccaccatg cctggctaatt tttttgaatt tttgtagtga tgggatctcg      1564
ctctgttgcc cagggtgggtc tcgaactcct ggccctcaagc gatcctccca cctcgacctc      1624
ccaaagtgtc gggattacag gtgtgagcca cctcgccctgg gcccccttct ccatatgcct      1684
ccaaaaacat gtccctggag agtagcctgc tcccacactg tcaactggatg tcatggggcc      1744
aataaaatct cctgcaattg tgtatctcaa aaaaaaaaaa aaaaaa      1789

```

<210> 144  
 <211> 2006  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 241..1302

```

<400> 144
tagtgccgga gccccgccag agccccgactt cagccccagc cagatcccgc gtcaacggag      60
gcggaacggc ggaccccgtg ccttggcagc atcggagcac cggcggggtga aggcaagggtc      120
cctggactgg tcatatacct cttgtggccc tggcagaatc aagatgaggc cctgtcatgc      180
ctccccagtg aggccctacag tctgagcaga cagcatggcc tgccactggc agtgaacacc      240
atg tct gca gga ggt ggc cgg gcc ttt gct tgg caa gtg ttc ccc ccc      288
Met Ser Ala Gly Gly Arg Ala Phe Ala Trp Gln Val Phe Pro Pro
  1                      5                      10                      15

```

atg	ccc	act	tgc	cgg	gtc	tat	ggc	aca	gtg	gca	cac	caa	gat	ggg	cac	336
Met	Pro	Thr	Cys	Arg	Val	Tyr	Gly	Thr	Val	Ala	His	Gln	Asp	Gly	His	
			20					25					30			
ctg	ctg	gtg	ttg	ggg	ggg	tgt	ggc	cgg	gct	gga	ctg	ccc	ctg	gac	act	384
Leu	Leu	Val	Leu	Gly	Gly	Cys	Gly	Arg	Ala	Gly	Leu	Pro	Leu	Asp	Thr	
		35					40					45				
gct	gag	aca	ctg	gac	atg	gcc	tcg	cac	aca	tgg	ctg	gca	ctg	gca	ccc	432
Ala	Glu	Thr	Leu	Asp	Met	Ala	Ser	His	Thr	Trp	Leu	Ala	Leu	Ala	Pro	
	50					55					60					
ctg	ccc	act	gcc	cgg	gct	ggg	gca	gct	gcg	gta	gtt	ctg	ggc	aag	cag	480
Leu	Pro	Thr	Ala	Arg	Ala	Gly	Ala	Ala	Ala	Val	Val	Leu	Gly	Lys	Gln	
	65				70					75				80		
gtg	cta	gtg	gtg	tgt	ggg	gtg	gat	gag	gtc	cag	agc	ccg	gta	gct	gct	528
Val	Leu	Val	Val	Cys	Gly	Val	Asp	Glu	Val	Gln	Ser	Pro	Val	Ala	Ala	
				85					90					95		
gta	gag	gcc	ttc	ctg	atg	gat	gag	ggc	cgc	tgg	gag	cgt	cgg	gcc	acc	576
Val	Glu	Ala	Phe	Leu	Met	Asp	Glu	Gly	Arg	Trp	Glu	Arg	Arg	Ala	Thr	
			100					105					110			
ctc	cct	caa	gca	gcc	atg	ggg	gtt	gca	act	gtg	gag	aga	gat	ggg	atg	624
Leu	Pro	Gln	Ala	Ala	Met	Gly	Val	Ala	Thr	Val	Glu	Arg	Asp	Gly	Met	
		115					120					125				
gtg	tat	gct	ctg	ggg	gga	atg	ggc	cct	gac	acg	gcc	ccc	cag	gcc	cag	672
Val	Tyr	Ala	Leu	Gly	Gly	Met	Gly	Pro	Asp	Thr	Ala	Pro	Gln	Ala	Gln	
	130					135					140					
gta	cgt	gtg	tat	gac	ccc	cgt	cgg	gac	tgc	tgg	ctt	tcg	cta	ccc	tcc	720
Val	Arg	Val	Tyr	Asp	Pro	Arg	Arg	Asp	Cys	Trp	Leu	Ser	Leu	Pro	Ser	
	145				150				155					160		
atg	ccc	aca	ccc	tgc	tat	ggg	gcc	tcc	acc	ttc	ctg	cac	ggg	aac	aag	768
Met	Pro	Thr	Pro	Cys	Tyr	Gly	Ala	Ser	Thr	Phe	Leu	His	Gly	Asn	Lys	
				165					170					175		
atc	tat	gtc	ctg	ggg	ggc	cgc	cag	ggc	aag	ctc	ccg	gtg	act	gct	ttt	816
Ile	Tyr	Val	Leu	Gly	Gly	Arg	Gln	Gly	Lys	Leu	Pro	Val	Thr	Ala	Phe	
			180					185					190			
gaa	gcc	ttt	gat	ctg	gag	gcc	cgt	aca	tgg	acc	cgg	cat	cca	agc	cta	864
Glu	Ala	Phe	Asp	Leu	Glu	Ala	Arg	Thr	Trp	Thr	Arg	His	Pro	Ser	Leu	
		195				200					205					
ccc	agc	cgt	cgg	gcc	ttt	gct	ggc	tgc	gcc	atg	gct	gaa	ggc	agc	gtc	912
Pro	Ser	Arg	Arg	Ala	Phe	Ala	Gly	Cys	Ala	Met	Ala	Glu	Gly	Ser	Val	
		210				215					220					
ttt	agc	ctg	ggg	ggc	ctg	cag	cag	cct	ggg	ccc	cac	aac	ttc	tac	tct	960
Phe	Ser	Leu	Gly	Gly	Leu	Gln	Gln	Pro	Gly	Pro	His	Asn	Phe	Tyr	Ser	
		225			230				235					240		
cgc	cca	cac	ttt	gtc	aac	act	gtg	gag	atg	ttt	gac	ctg	gag	cat	ggg	1008
Arg	Pro	His	Phe	Val	Asn	Thr	Val	Glu	Met	Phe	Asp	Leu	Glu	His	Gly	
				245					250					255		
tcc	tgg	acc	aaa	ttg	ccc	cgc	agc	ctg	cgc	atg	agg	gat	aag	agg	gca	1056
Ser	Trp	Thr	Lys	Leu	Pro	Arg	Ser	Leu	Arg	Met	Arg	Asp	Lys	Arg	Ala	
			260					265					270			
gac	ttt	gtg	gtt	ggg	tcc	ctt	ggg	ggc	cac	att	gtg	gcc	att	ggg	ggc	1104
Asp	Phe	Val	Val	Gly	Ser	Leu	Gly	Gly	His	Ile	Val	Ala	Ile	Gly	Gly	
		275					280					285				
ctt	gga	aac	cag	cca	tgt	cct	ttg	ggc	tct	gtg	gag	agc	ttt	agc	ctt	1152
Leu	Gly	Asn	Gln	Pro	Cys	Pro	Leu	Gly	Ser	Val	Glu	Ser	Phe	Ser	Leu	
		290				295					300					
gca	cgg	cgg	cgc	tgg	gag	gca	ttg	cct	gcc	atg	ccc	act	gcc	cgc	tgc	1200
Ala	Arg	Arg	Arg	Trp	Glu	Ala	Leu	Pro	Ala	Met	Pro	Thr	Ala	Arg	Cys	
					310					315					320	
tcc	tgc	tct	agt	ctg	cag	gct	ggg	ccc	cgg	ctg	ttt	gtt	att	ggg	ggg	1248



Ser Cys Ser Ser Leu Gln Ala Gly Pro Arg Leu Phe Val Ile Gly Gly	
325 330 335	
gtg gcc cag ggc ccc agt caa gcc gtg gag gca ctg tgt ctg cgt gat	1296
Val Ala Gln Gly Pro Ser Gln Ala Val Glu Ala Leu Cys Leu Arg Asp	
340 345 350	
ggg gtc tgaaggcttg gtgggagctg tccactggag cagctcattg ccagagggcag	1352
Gly Val	
ctattttctat ggctcctttt gctgctgagg acactcactg tggctctgtg ggatgagaga	1412
ggcatggggg tgagcacttg aaacactgcc ttggggcctt gggttagggg agcctttgtc	1472
tttagtgtag gacacacata tgcttacacc tacctttatc accattcgtt catgaatcat	1532
gcctagctcc atccttgccc tgggacctac taggccttcc atccaactgg gaaatgggga	1592
gaagcaaagc tggcctcatg ctcttcaggg tcagttccta tctggagttg accaggccta	1652
ccccagttgc cattcctgaa aaatctcagc tgccaggctg cctttagggt ccctgcagac	1712
ccaggagagt tgagaggggt ggggacacac acagaataga gaggatgtgg gaactgccag	1772
agggccggag cgcaggagtt caagtggagg aatgctggct ttgagccctc tacactgctg	1832
gttgtagtag cttggacaag tcacttcacc tctctgtgcc tcagcatcct catctataaa	1892
tggggatctc tgaaaccttc ctaccctacc tacctcacag ggctgttgtg aggaccagg	1952
gagtttggtg gtggaagtaa aagtgtgtgt aaaaccgaaa aaaaaaaaaa aaaa	2006
<210> 145	
<211> 1096	
<212> DNA	
<213> Homo sapiens	
<220>	
<221> CDS	
<222> 15..635	
<400> 145	
atccaaggcg caag atg gcg ctg ctt ttt gca cgt tct ttg cgc ttg tgc	50
Met Ala Leu Leu Phe Ala Arg Ser Leu Arg Leu Cys	
1 5 10	
cgc tgg gga gcc aaa cga ttg gga gtt gcc tcc aca gag gcc cag aga	98
Arg Trp Gly Ala Lys Arg Leu Gly Val Ala Ser Thr Glu Ala Gln Arg	
15 20 25	
ggc gtc agt ttc aaa ctg gaa gaa aaa acc gcc cac agc agc ctg gca	146
Gly Val Ser Phe Lys Leu Glu Glu Lys Thr Ala His Ser Ser Leu Ala	
30 35 40	
ctc ttc aga gat gat acg ggt gtc aaa tat ggc ttg gtg gga ttg gag	194
Leu Phe Arg Asp Asp Thr Gly Val Lys Tyr Gly Leu Val Gly Leu Glu	
45 50 55 60	
ccc acc aag gtg gcc ttg aat gtg gag cgc ttc cgg gag tgg gca gtg	242
Pro Thr Lys Val Ala Leu Asn Val Glu Arg Phe Arg Glu Trp Ala Val	
65 70 75	
gtg ctg gca gac aca gcg gtc acc agt ggc aga cac tac tgg gaa gtg	290
Val Leu Ala Asp Thr Ala Val Thr Ser Gly Arg His Tyr Trp Glu Val	
80 85 90	
aca gtg aag cgc tcc cag cag ttc cgg ata gga gtg gca gat gtg gac	338
Thr Val Lys Arg Ser Gln Gln Phe Arg Ile Gly Val Ala Asp Val Asp	
95 100 105	
atg tcc cgg gat agc tgc att ggt gtt gat gat cgt tcc tgg gtg ttc	386
Met Ser Arg Asp Ser Cys Ile Gly Val Asp Asp Arg Ser Trp Val Phe	
110 115 120	
acc tat gcc cag cgc aag tgg tac acc atg ttg gcc aac gag aaa gcc	434
Thr Tyr Ala Gln Arg Lys Trp Tyr Thr Met Leu Ala Asn Glu Lys Ala	
125 130 135 140	
cca gtt gag ggt att ggg cag cca gag aag gtg ggg ctg ttg ctg gag	482
Pro Val Glu Gly Ile Gly Gln Pro Glu Lys Val Gly Leu Leu Leu Glu	

	145	150	155	
tat gag gcc cag aag ctg agc ctg gtg gat gtg agc cag gtc tct gtg				530
Tyr Glu Ala Gln Lys Leu Ser Leu Val Asp Val Ser Gln Val Ser Val				
	160	165	170	
gtt cac acg cta cag aca gat ttc cgg ggt cca gtg gtg cct gcc ttt				578
Val His Thr Leu Gln Thr Asp Phe Arg Gly Pro Val Val Pro Ala Phe				
	175	180	185	
gct ctc tgg gat ggg gag ctg ctg acc cat tca ggg ctt gag gtg ccc				626
Ala Leu Trp Asp Gly Glu Leu Leu Thr His Ser Gly Leu Glu Val Pro				
	190	195	200	
gag ggc ctc tagtatgtcc attactggag tccctaataca cgcctttggc				675
Glu Gly Leu				
205				
cagcctcctt ttgaaagtgt ccgaagcctt tttactttgc ctcaagcaac ctctagctcc				735
cacaattcag tggtgggtcc tctgtgcaat atcatgatca tcttctcat cccctacctt				795
gtgaaagcta ggcatacagc caaacctcc ttttccccac ccaccaacac tactgccaat				855
ttcctaggct accatgggtg tatcttcctt gacctgttc cttcagtcct tctgcctccc				915
tttgcccagg cctttctcag actgtattcc atcctgggggt cttatcattc agctttgttt				975
gaatttatta atcaccatga tacctctccc tccctttgtc cacatgtaac ttgttcttgg				1035
ggctctacca gatggctgaa gagtaaattcc tttctacctc tggcaaaaaa aaaaaaaaaa				1095
a				1096
<210>	146			
<211>	1666			
<212>	DNA			
<213>	Homo sapiens			
<220>				
<221>	CDS			
<222>	109..738			
<400>	146			
cccagcgttc ctctcccgcc cccaggtcac cgccagcacg cgcctgcttc ccgtctgcgc				60
gagtccacgc agtccccag gcccttcacc agcacagcag cagcaggc atg gca gca				117
			Met Ala Ala	
			1	
agc gtg gag cag cgc gag ggc acc atc cag gtg cag ggc cag gcc ctc				165
Ser Val Glu Gln Arg Glu Gly Thr Ile Gln Val Gln Gly Gln Ala Leu				
	5	10	15	
ttc ttc cga gag gcc ctg ccc ggc agt ggg cag gct cgc ttc tct gta				213
Phe Phe Arg Glu Ala Leu Pro Gly Ser Gly Gln Ala Arg Phe Ser Val				
	20	25	30	35
ctg ctg ctg cat ggt att cgc ttc tcc tcc gag acc tgg cag aac ctg				261
Leu Leu Leu His Gly Ile Arg Phe Ser Ser Glu Thr Trp Gln Asn Leu				
	40	45	50	
ggt aca ctg cac agg ctg gcc cag gct ggc tac cgg gct gtg gcc att				309
Gly Thr Leu His Arg Leu Ala Gln Ala Gly Tyr Arg Ala Val Ala Ile				
	55	60	65	
gac ctg cca ggt ctg ggg cac tcc aag gaa gca gca gcc cct gcc cct				357
Asp Leu Pro Gly Leu Gly His Ser Lys Glu Ala Ala Ala Pro Ala Pro				
	70	75	80	
att ggg gag ctg gcc cct ggc agc ttc ctg gcg gct gtg gtg gat gcc				405
Ile Gly Glu Leu Ala Pro Gly Ser Phe Leu Ala Ala Val Val Asp Ala				
	85	90	95	
ttg gag ctg ggc ccc ccg gtt gtg atc agt cca tca ctg agt ggc atg				453
Leu Glu Leu Gly Pro Pro Val Val Ile Ser Pro Ser Leu Ser Gly Met				
	100	105	110	115
tac tcc ctg ccc ttc ctc acg gcc cct ggc tcc cag ctc ccg ggc ttt				501

Tyr	Ser	Leu	Pro	Phe	Leu	Thr	Ala	Pro	Gly	Ser	Gln	Leu	Pro	Gly	Phe	
				120					125					130		
gtg	cca	gtg	gcc	ccc	atc	tgc	act	gac	aaa	atc	aat	gct	gcc	aac	tat	549
Val	Pro	Val	Ala	Pro	Ile	Cys	Thr	Asp	Lys	Ile	Asn	Ala	Ala	Asn	Tyr	
			135					140					145			
gcc	agt	gtg	aag	act	cca	gct	ctg	att	gta	tat	gga	gac	cag	gac	ccc	597
Ala	Ser	Val	Lys	Thr	Pro	Ala	Leu	Ile	Val	Tyr	Gly	Asp	Gln	Asp	Pro	
			150				155					160				
atg	ggt	cag	acc	agc	ttt	gag	cac	ctg	aag	cag	ctg	ccc	aac	cac	cgg	645
Met	Gly	Gln	Thr	Ser	Phe	Glu	His	Leu	Lys	Gln	Leu	Pro	Asn	His	Arg	
	165					170					175					
gtg	ctg	atc	atg	aag	ggg	gcg	ggg	cac	ccc	tgt	tac	ctg	gac	aaa	cca	693
Val	Leu	Ile	Met	Lys	Gly	Ala	Gly	His	Pro	Cys	Tyr	Leu	Asp	Lys	Pro	
	180				185					190					195	
gag	gag	tgg	cat	aca	ggg	ctg	ctg	gac	ttc	ctg	cag	ggg	ctc	cag		738
Glu	Glu	Trp	His	Thr	Gly	Leu	Leu	Asp	Phe	Leu	Gln	Gly	Leu	Gln		
			200					205					210			
tgaagcccag	cactgctgca	gggggtgggc	tgcctgcctg	ctctgagctc	tctcttgcac											798
gctctctctt	ctctcccagg	ctctggctca	tgcacatgca	acaggtgcgt	ctgtctatat											858
gtctgggttc	ttgtcttttg	tggctctgtt	gtcttttcta	cctctttctc	ttgcagtgat											918
agactgaggg	ggtaaaatca	agagaaaaaa	ctctcaggaa	tcaaggaaca	taatcctgtg											978
gagggtaaat	cattacatga	gcttctcctg	ttcttccact	ttctgacctg	gctttcactc											1038
cttccccctgc	tctgcccagc	ctttccctcc	cacccactcc	tacttctgca	aatgccctga											1098
aggccagccc	ttaccccaac	accactttcc	ccacctcctt	aggccccaga	tacatacatg											1158
cccacatgca	cgcttacatg	tttagagcca	tccttggttc	caaatatgac	ccttcgcttg											1218
agggcaactg	cataggtaca	tctaactctg	gactggcatg	cacattgtca	tgtgcagctt											1278
tgcataataca	cacatgcata	catgagcctc	cacacaagca	cttgccacaca	tgtggactcc											1338
taaccatgct	aacctcactg	gctgggaagg	tggggacccc	atggggccagc	ccttgcagga											1398
ggcccttttg	caaggcttag	ggtgtggcca	gccctgaaag	ctacttggac	acaggtttca											1458
gctggcccca	gccccaagt	gaccccgaga	aagggagggc	caccgctttg	ccccctgctt											1518
ttaccctttcc	ttctgggtgc	tctacacctc	aggttaccag	gcctgaggca	tctcagccaa											1578
gcttggtttcc	tgtctgtagg	cttgtggggg	gggagccaga	gtggaggtcg	gtgaaataaaa											1638
gtgatgcaat	taaaaaaaaa	aaaaaaaaa														1666

<210> 147

<211> 1687

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 21..1145

<400> 147

gtttctccgg	acttcgagcc	atg	gcg	gtg	acg	gaa	gcg	agc	ctg	ttg	cgc	cag				53
		Met	Ala	Val	Thr	Glu	Ala	Ser	Leu	Leu	Arg	Gln				
		1					5					10				
tgc	ccc	ctg	ctt	ctg	ccc	cag	aac	cgg	tgc	aaa	acc	gtg	tat	gag	gga	101
Cys	Pro	Leu	Leu	Leu	Pro	Gln	Asn	Arg	Ser	Lys	Thr	Val	Tyr	Glu	Gly	
		15					20					25				
ttc	atc	tgc	gct	cag	gga	aga	gac	ttc	cac	ctt	agg	ata	gtg	ttg	cct	149
Phe	Ile	Ser	Ala	Gln	Gly	Arg	Asp	Phe	His	Leu	Arg	Ile	Val	Leu	Pro	
		30				35					40					
gaa	gat	tta	caa	ctg	aag	aat	gca	aga	tta	tta	tgt	att	tgg	cag	ctg	197
Glu	Asp	Leu	Gln	Leu	Lys	Asn	Ala	Arg	Leu	Leu	Cys	Ile	Trp	Gln	Leu	
	45					50					55					
aga	aca	ata	ctt	agt	gga	tac	cat	cga	ata	gta	caa	cag	aga	atg	cag	245
Arg	Thr	Ile	Leu	Ser	Gly	Tyr	His	Arg	Ile	Val	Gln	Gln	Arg	Met	Gln	

60	65								70					75					
cac	tct	cct	gat	cta	atg	agc	ttt	atg	atg	gag	ttg	aag	atg	ctt	ttg	293			
His	Ser	Pro	Asp	Leu	Met	Ser	Phe	Met	Met	Glu	Leu	Lys	Met	Leu	Leu				
				80					85					90					
gaa	gtt	gcc	tta	aag	aat	aga	caa	gag	ctg	tat	gca	cta	cct	cct	cct	341			
Glu	Val	Ala	Leu	Lys	Asn	Arg	Gln	Glu	Leu	Tyr	Ala	Leu	Pro	Pro	Pro				
			95					100					105						
ccc	cag	ttc	tac	tca	agc	ctt	att	gaa	gag	ata	gga	act	ctt	ggg	tgg	389			
Pro	Gln	Phe	Tyr	Ser	Ser	Leu	Ile	Glu	Glu	Ile	Gly	Thr	Leu	Gly	Trp				
		110					115					120							
gat	aaa	ctt	gtg	tat	gcg	gat	acc	tgc	ttc	agt	acc	atc	aag	tta	aaa	437			
Asp	Lys	Leu	Val	Tyr	Ala	Asp	Thr	Cys	Phe	Ser	Thr	Ile	Lys	Leu	Lys				
	125					130					135								
gca	gaa	gat	gct	tct	ggg	aga	gag	cat	tta	atc	act	ctc	aag	ttg	aag	485			
Ala	Glu	Asp	Ala	Ser	Gly	Arg	Glu	His	Leu	Ile	Thr	Leu	Lys	Leu	Lys				
140					145					150					155				
gca	aag	tat	cct	gca	gaa	tca	cca	gat	tat	ttt	gtg	gat	ttt	cct	gtt	533			
Ala	Lys	Tyr	Pro	Ala	Glu	Ser	Pro	Asp	Tyr	Phe	Val	Asp	Phe	Pro	Val				
			160						165				170						
cca	ttt	tgt	gcc	tcc	tgg	aca	cct	cag	agc	tcc	tta	ata	agc	att	tat	581			
Pro	Phe	Cys	Ala	Ser	Trp	Thr	Pro	Gln	Ser	Ser	Leu	Ile	Ser	Ile	Tyr				
			175					180					185						
agt	cag	ttt	ttg	gca	gca	ata	gaa	tca	cta	aag	gca	ttc	tgg	gat	gtt	629			
Ser	Gln	Phe	Leu	Ala	Ala	Ile	Glu	Ser	Leu	Lys	Ala	Phe	Trp	Asp	Val				
		190					195					200							
atg	gat	gaa	atc	gat	gag	aag	acc	tgg	gta	ctt	gag	cca	gaa	aaa	cct	677			
Met	Asp	Glu	Ile	Asp	Glu	Lys	Thr	Trp	Val	Leu	Glu	Pro	Glu	Lys	Pro				
	205					210					215								
cca	cgg	agt	gca	aca	gca	cgc	aga	att	gca	tta	ggg	aat	aat	gtt	tcc	725			
Pro	Arg	Ser	Ala	Thr	Ala	Arg	Arg	Ile	Ala	Leu	Gly	Asn	Asn	Val	Ser				
220					225					230					235				
ata	aat	ata	gag	gta	gac	ccc	agg	cat	cct	act	atg	ctt	cct	gag	tgc	773			
Ile	Asn	Ile	Glu	Val	Asp	Pro	Arg	His	Pro	Thr	Met	Leu	Pro	Glu	Cys				
			240						245					250					
ttc	ttt	ctt	gga	gct	gac	cat	gtg	gta	aaa	ccc	ctg	gga	att	aag	ctg	821			
Phe	Phe	Leu	Gly	Ala	Asp	His	Val	Val	Lys	Pro	Leu	Gly	Ile	Lys	Leu				
			255					260					265						
agc	agg	aac	ata	cat	ttg	tgg	gat	cca	gaa	aat	agt	gtg	tta	caa	aat	869			
Ser	Arg	Asn	Ile	His	Leu	Trp	Asp	Pro	Glu	Asn	Ser	Val	Leu	Gln	Asn				
		270					275												



Ser	Asn	Ile	Leu	Val	Phe	Lys	Leu	Gly	Gly	Thr	Ser	Leu	Ser	Leu	Ser	
				195					200					205		
gtc	atg	gaa	gtt	aac	agt	gga	ata	tat	cgg	gtt	ctt	tca	aca	aac	act	735
Val	Met	Glu	Val	Asn	Ser	Gly	Ile	Tyr	Arg	Val	Leu	Ser	Thr	Asn	Thr	
			210					215						220		
gat	gat	aac	atc	ggt	ggt	gca	cat	ttc	aca	gaa	acc	tta	gca	cag	tat	783
Asp	Asp	Asn	Ile	Gly	Gly	Ala	His	Phe	Thr	Glu	Thr	Leu	Ala	Gln	Tyr	
		225					230						235			
cta	gct	tct	gag	ttc	caa	aga	tcc	ttc	aaa	cat	gat	gtg	aga	gga	aat	831
Leu	Ala	Ser	Glu	Phe	Gln	Arg	Ser	Phe	Lys	His	Asp	Val	Arg	Gly	Asn	
	240					245					250					
gcg	cga	gcc	atg	atg	aaa	tta	acg	aac	agt	gct	gaa	gta	gcg	aaa	cat	879
Ala	Arg	Ala	Met	Met	Lys	Leu	Thr	Asn	Ser	Ala	Glu	Val	Ala	Lys	His	
	255				260					265					270	
tct	ttg	tca	acc	ttg	gga	agt	gcc	aac	tgt	ttt	ctt	gac	tca	tta	tat	927
Ser	Leu	Ser	Thr	Leu	Gly	Ser	Ala	Asn	Cys	Phe	Leu	Asp	Ser	Leu	Tyr	
				275					280					285		
gaa	ggt	caa	gat	ttt	gat	tgc	aat	gtg	tcc	aga	gca	aga	ttt	gaa	ctt	975
Glu	Gly	Gln	Asp	Phe	Asp	Cys	Asn	Val	Ser	Arg	Ala	Arg	Phe	Glu	Leu	
			290					295					300			
ctt	tgt	tct	cca	ctt	ttt	aat	aag	tgt	ata	gaa	gca	atc	aga	gga	ctc	1023
Leu	Cys	Ser	Pro	Leu	Phe	Asn	Lys	Cys	Ile	Glu	Ala	Ile	Arg	Gly	Leu	
		305					310					315				
tta	gat	caa	aat	gga	ttt	aca	aca	gat	gat	atc	aac	aag	gtt	gtc	ctt	1071
Leu	Asp	Gln	Asn	Gly	Phe	Thr	Thr	Asp	Asp	Ile	Asn	Lys	Val	Val	Leu	
	320					325					330					
tgt	gga	ggg	tct	tct	cga	atc	cca	aag	cta	cag	caa	ctg	att	aaa	gat	1119
Cys	Gly	Gly	Ser	Ser	Arg	Ile	Pro	Lys	Leu	Gln	Gln	Leu	Ile	Lys	Asp	
	335				340					345				350		
ctt	ttc	cca	gct	gtt	gag	ctt	ctc	aat	tct	atc	cct	cct	gat	gaa	gtg	1167
Leu	Phe	Pro	Ala	Val	Glu	Leu	Leu	Asn	Ser	Ile	Pro	Pro	Asp	Glu	Val	
				355					360					365		
atc	cct	att	ggt	gca	gct	ata	gaa	gca	gga	att	ctt	att	ggg	aaa	gaa	1215
Ile	Pro	Ile	Gly	Ala	Ala	Ile	Glu	Ala	Gly	Ile	Leu	Ile	Gly	Lys	Glu	
			370					375					380			
aac	ctg	ttg	gtg	gaa	gac	tct	ctt	atg	ata	gag	tgt	tca	gcc	aga	gat	1263
Asn	Leu	Leu	Val	Glu	Asp	Ser	Leu	Met	Ile	Glu	Cys	Ser	Ala	Arg	Asp	
		385					390					395				
att	tta	ggt	aag	ggt	gtg	gac	gaa	tca	gga	gcc	agt	aga	ttc	aca	gtg	1311
Ile	Leu	Val	Lys	Gly	Val	Asp	Glu	Ser	Gly	Ala	Ser	Arg	Phe	Thr	Val	
	400					405					410					
ctg	ttt	cca	tca	ggg	act	cct	ttg	cca	gct	cga	aga	caa	cac	aca	ttg	1359
Leu	Phe	Pro	Ser	Gly	Thr	Pro	Leu	Pro	Ala	Arg	Arg	Gln	His	Thr	Leu	
	415				420					425					430	
caa	gcc	cct	gga	agc	ata	tct	tca	gtg	tgc	ctt	gaa	ctc	tat	gag	tct	1407
Gln	Ala	Pro	Gly	Ser	Ile	Ser	Ser	Val	Cys	Leu	Glu	Leu	Tyr	Glu	Ser	
				435					440					445		
gat	ggg	aag	aac	tct	gcc	aaa	gag	gaa	acc	aag	ttt	gca	cag	gtt	gta	1455
Asp	Gly	Lys	Asn	Ser	Ala	Lys	Glu	Glu	Thr	Lys	Phe	Ala	Gln	Val	Val	
			450					455					460			
ctc	cag	gat	tta	gat	aaa	aaa	gaa	aat	gga	tta	cgt	gat	ata	tta	gct	1503
Leu	Gln	Asp	Leu	Asp	Lys	Lys	Glu	Asn	Gly	Leu	Arg	Asp	Ile	Leu	Ala	
		465					470					475				
gtt	ctt	act	atg	aaa	agg	gat	gga	tct	tta	cat	gtg	aca	tgc	aca	gat	1551
Val	Leu	Thr	Met	Lys	Arg	Asp	Gly	Ser	Leu	His	Val	Thr	Cys	Thr	Asp	
	480					485					490					
caa	gaa	act	gga	aaa	tgt	gaa	gca	atc	tct	att	gag	ata	gca	tct		1596
Gln	Glu	Thr	Gly	Lys	Cys	Glu	Ala	Ile	Ser	Ile	Glu	Ile	Ala	Ser		



```

att gaa aac aac atc gtg gtt ttt gaa aac ttc tgg gaa gga ctg tgg      261
Ile Glu Asn Asn Ile Val Val Phe Glu Asn Phe Trp Glu Gly Leu Trp
      40                                45                                50
atg aat tgc gtg agg cag gct aac atc agg atg cag tgc aaa atc tat      309
Met Asn Cys Val Arg Gln Ala Asn Ile Arg Met Gln Cys Lys Ile Tyr
      55                                60                                65
gat tcc ctg ctg gct ctt tct ccg gac cta cag gca gcc aga gga ctg      357
Asp Ser Leu Leu Ala Leu Ser Pro Asp Leu Gln Ala Ala Arg Gly Leu
      70                                75                                80
atg tgt gct gct tcc gtg atg tcc ttc ttg gct ttc atg atg gcc atc      405
Met Cys Ala Ala Ser Val Met Ser Phe Leu Ala Phe Met Met Ala Ile
      85                                90                                95
ctt ggc atg aaa tgc acc agg tgc acg ggg gac aat gag aag gtg aag      453
Leu Gly Met Lys Cys Thr Arg Cys Thr Gly Asp Asn Glu Lys Val Lys
      100                                105                                110                                115
gct cac att ctg ctg acg gct gga atc atc ttc atc atc acg ggc atg      501
Ala His Ile Leu Leu Thr Ala Gly Ile Ile Phe Ile Ile Thr Gly Met
      120                                125                                130
gtg gtg ctc atc cct gtg agc tgg gtt gcc aat gcc atc atc aga gat      549
Val Val Leu Ile Pro Val Ser Trp Val Ala Asn Ala Ile Ile Arg Asp
      135                                140                                145
ttc tat aac cca ata gtg aat gtt gcc caa aaa cgt gag ctt gga      594
Phe Tyr Asn Pro Ile Val Asn Val Ala Gln Lys Arg Glu Leu Gly
      150                                155                                160
taagctctct acttaggatg gaccacggca ctggtgctga ttgttggagg agctctgttc      654
tgctgcgttt tttgttgcaa cgaaaagagc agtagctaca gatactcgat accttcccat      714
cgcacaaccc aaaaaagtta tcacaccgga aagaagtcac cgagcgtcta ctccagaagt      774
cagtatgtgt agttgtgtat gtttttttaa ctttactata aagccatgca aatgacaaaa      834
atctatatta ctttctcaaa atggacccca aagaaacttt gatttactgt tcttaactgc      894
ctaactctaa ttacaggaac tgtgcatcag ctatttatga ttctataagc tatttcagca      954
gaatgagata ttaaatccaa tgctttgatt gttctagaaa gtatagtaat ttgttttcta      1014
aggtgggttca agcatctact ctttttatca tttacttcaa aatgacattg ctaaagactg      1074
cattatttta ctactgtaat ttctccacga catagcatta tgtacataga tgagtgtaac      1134
atztatatct cacatagaga catgcttata tggttttatt taaaatgaaa tgccagtcca      1194
ttacactgaa taaatagaac tcaactattg cttttcaggg aaatcatgga taggggtgaa      1254
gaaggttact attaattggt taaaaacagc ttagggatta atgtcctcca tttataatga      1314
agattaaaaa gaaggcttta atcagcattg taaaggaaat tgaatggctt tctgatatgc      1374
tggttttttg cctaggagtt agaaatccta acttctttat cctcttctcc cagaggcttt      1434
ttttttcttg tgtattaaat taacattttt aaaaagcaga tattttgtca aggggctttg      1494
cattcaaaact gcttttccag ggctatactc agaagaaaga taaaagtgtg atctaagaaa      1554
aagtgatggt tttaggaaag tgaaaaatatt tttgtttttg tatttgaaga agaatgatgc      1614
attttgacaa gaaatcatat atgtatggat atattttaat aagtatttga gtacagactt      1674
tgaggtttca tcaatataaa taaaagagca gaaaaatatg tcttggtttt catttgctta      1734
ccaaaaaaac aacaacaaaa aaagttgtcc tttgagaact tcacctgctc ctatgtgggt      1794
acctgagtca aaattgtcat ttttgttctg tgaaaaataa atttccttct tgtaccattt      1854
ctggttagtt ttactaaaat ctgtaaatac tgtatttttc tgtttattcc aaatttgatg      1914
aaactgacaa tccaatttga aagtttgtgt cgacgtctgt ctagcttaaa tgaatgtgtt      1974
ctatttgctt tatacattta tattaataaa ttgtacattt ttctaattat ttggaaaaaa      2034
aaaaaaaaaa a
      2045

```

<210> 151  
 <211> 788  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 150..587



```

<400> 151
attttcaaatt ttaccctctt gtgacttgta agccatgcaa ttcgtagggc taaatatgca      60
gttgttcgat ttacacgggtt ggaatctctt gtcaagggac tgggactctt caattaatct      120
gacatttcac aaatccaaaaa ttgccgtgg atg aac tct tta ctt cac ttc ggg      173
                               Met Asn Ser Leu Leu His Phe Gly
                               1           5

ata ttg ctg gag ctg agt ctc ctg aaa cag ttt aag tct gta tat gtt      221
Ile Leu Leu Glu Leu Ser Leu Leu Lys Gln Phe Lys Ser Val Tyr Val
    10           15           20
cct gga aat cat acc cac cag gca tct tat aag cca ttg ttg aag caa      269
Pro Gly Asn His Thr His Gln Ala Ser Tyr Lys Pro Leu Leu Lys Gln
    25           30           35           40
gtt gtg gag gaa ata ttt cat ccc gag agg cca gat tcc gtt gat att      317
Val Val Glu Glu Ile Phe His Pro Glu Arg Pro Asp Ser Val Asp Ile
           45           50           55
gaa cac atg tct tca ggc ctc act gat ctc ctt aaa act gga ttt agc      365
Glu His Met Ser Ser Gly Leu Thr Asp Leu Leu Lys Thr Gly Phe Ser
           60           65           70
atg ttc atg aag gtg agc cgg cct cat cct agt gac tac ccc ctc ctg      413
Met Phe Met Lys Val Ser Arg Pro His Pro Ser Asp Tyr Pro Leu Leu
           75           80           85
atc ctc ttt gtg gta ggt ggg gtc aca gtc tct gaa gtg aaa atg gtc      461
Ile Leu Phe Val Val Gly Gly Val Thr Val Ser Glu Val Lys Met Val
           90           95           100
aaa gat ctt gtg gca tcg ttg aag cca gga acc cag gta atc gtg ctg      509
Lys Asp Leu Val Ala Ser Leu Lys Pro Gly Thr Gln Val Ile Val Leu
           105           110           115           120
tcc aca cga ctc ctg aag cca ctt aac att cct gag ctg tta ttt gca      557
Ser Thr Arg Leu Leu Lys Pro Leu Asn Ile Pro Glu Leu Leu Phe Ala
           125           130           135
act gac cga ctg cat cca gac ctt ggc ttc tgagcatccg ctaagaagat      607
Thr Asp Arg Leu His Pro Asp Leu Gly Phe
           140           145
aagacctact caagctggaa atgccgatgc aattttctgc caccactcca aatactctc      667
cacaaccagc gtccctgtca ctaattgcga gaatgatgga attctgcctg aagggtcttg      727
atacctactc agtgaggtac stttgcttgg attgctgtga ttccaaaaaa aaaaaaaaaa      787
a                                                                                   788

```

<210> 152  
 <211> 1931  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 173..847

```

<400> 152
actggatact atctggccag aagtagcaaa gcagctctta tttgaaaaac cactgggttc      60
cgagttcatt actacaggaa aaactgttct cttctgtggc acagagaacc ctgcttcaaa      120
gcagaagtag cagttccgga gtccagctgg ctaaaactca tcccagagga ta atg gca      178
                               Met Ala
                               1

acc cat gcc tta gaa atc gct ggg ctg ttt ctt ggt ggt gtt gga atg      226
Thr His Ala Leu Glu Ile Ala Gly Leu Phe Leu Gly Gly Val Gly Met
           5           10           15
gtg ggc aca gtg gct gtc act gtc atg cct cag tgg aga gtg tcg gcc      274

```

Val	Gly	Thr	Val	Ala	Val	Thr	Val	Met	Pro	Gln	Trp	Arg	Val	Ser	Ala		
20						25					30						
ttc	att	gaa	aac	aac	atc	gtg	ggt	ttt	gaa	aac	ttc	tgg	gaa	gga	ctg	322	
Phe	Ile	Glu	Asn	Asn	Ile	Val	Val	Phe	Glu	Asn	Phe	Trp	Glu	Gly	Leu		
35					40				45						50		
tgg	atg	aat	tgc	gtg	agg	cag	gct	aac	atc	agg	atg	cag	tgc	aaa	atc	370	
Trp	Met	Asn	Cys	Val	Arg	Gln	Ala	Asn	Ile	Arg	Met	Gln	Cys	Lys	Ile		
			55					60						65			
tat	gat	tcc	ctg	ctg	gct	ctt	tct	ccg	gac	cta	cag	gca	gcc	aga	gga	418	
Tyr	Asp	Ser	Leu	Leu	Ala	Leu	Ser	Pro	Asp	Leu	Gln	Ala	Ala	Arg	Gly		
			70					75					80				
ctg	atg	tgt	gct	gct	tcc	gtg	atg	tcc	ttc	ttg	gct	ttc	atg	atg	gcc	466	
Leu	Met	Cys	Ala	Ala	Ser	Val	Met	Ser	Phe	Leu	Ala	Phe	Met	Met	Ala		
		85				90					95						
atc	ctt	ggc	atg	aaa	tgc	acc	agg	tgc	acg	ggg	gac	aat	gag	aag	gtg	514	
Ile	Leu	Gly	Met	Lys	Cys	Thr	Arg	Cys	Thr	Gly	Asp	Asn	Glu	Lys	Val		
100						105					110						
aag	gct	cac	att	ctg	ctg	acg	gct	gga	atc	atc	ttc	atc	atc	gcg	ggc	562	
Lys	Ala	His	Ile	Leu	Leu	Thr	Ala	Gly	Ile	Ile	Phe	Ile	Ile	Ala	Gly		
115					120					125					130		
atg	gtg	gtg	ctc	atc	cct	gtg	agc	tgg	ggt	gcc	aat	gcc	atc	atc	aga	610	
Met	Val	Val	Leu	Ile	Pro	Val	Ser	Trp	Val	Ala	Asn	Ala	Ile	Ile	Arg		
			135					140						145			
gat	ttc	tat	aac	cca	ata	gtg	aat	gtt	gcc	caa	aaa	cgt	gag	ctt	gga	658	
Asp	Phe	Tyr	Asn	Pro	Ile	Val	Asn	Val	Ala	Gln	Lys	Arg	Glu	Leu	Gly		
			150					155					160				
gaa	gct	ctc	tac	tta	gga	tgg	acc	acg	gca	ctg	gtg	ctg	att	gtt	gga	706	
Glu	Ala	Leu	Tyr	Leu	Gly	Trp	Thr	Thr	Ala	Leu	Val	Leu	Ile	Val	Gly		
		165				170					175						
gga	gct	ctg	ttc	tgc	tgc	gtt	ttt	tgt	tgc	aac	gaa	aag	agc	agt	agc	754	
Gly	Ala	Leu	Phe	Cys	Cys	Val	Phe	Cys	Cys	Asn	Glu	Lys	Ser	Ser	Ser		
		180				185					190						
tac	aga	tac	tcg	ata	cct	tct	cat	cgc	aca	acc	caa	aaa	agt	tat	cac	802	
Tyr	Arg	Tyr	Ser	Ile	Pro	Ser	His	Arg	Thr	Thr	Gln	Lys	Ser	Tyr	His		
195					200					205					210		
acc	gga	aag	aag	tca	ccg	agc	gtc	tac	tcc	aga	agt	cag	tat	gtg		847	
Thr	Gly	Lys	Lys	Ser	Pro	Ser	Val	Tyr	Ser	Arg	Ser	Gln	Tyr	Val			
			215					220					225				
tagttgtgta	tgttttttta	acttttactat	aaagctatgc	aaatgacaaa	aatctatatatt											907	
acttttctcaa	aatggacccc	aaagaaaactt	tgattttactg	ttcttaactg	cctaacttta											967	
attacaggaa	ctgtgcatca	gctattttatg	attctataag	ctattttcagc	agaatgagat											1027	
attaaatcca	atgctttgat	tggtctagaa	agtatagtaa	tttgttttct	aagggtggttc											1087	
aagcatctac	tctttttatc	atttacttca	aaatgacatt	gctaaagact	gcattatttt											1147	
actactgtaa	tttctccatg	acatagcatt	atgtacatag	atgagtgtaa	catttatatc											1207	
tcacatagag	acatgcttat	atggttttat	ttaaaatgaa	atgccagtc	attacactga											1267	
ataaaatagaa	ctcaactatt	gctttttcagg	gaaatcatgg	atagggttga	agaaggttac											1327	
tattaattgt	ttaaaaacag	cttagggatt	aatgtctctc	atttataatg	aagattaaaa											1387	
tgaaggcttt	aatcagcatt	gtaaaaggaaa	ttgaatggct	ttctgatatg	ctgttttttta											1447	
gcctaggagt	tagaaatcct	aacttcttta	tcctcttctc	ccagaggctt	tttttttctt											1507	
gtgtattaaa	ttaacatttt	taaaaagcag	atattttgtc	aaggggcttt	gcattcaaac											1567	
tgcttttcca	gggctatact	cagaagaaag	ataaaagtgt	gatctaagaa	aaagtgtatg											1627	
ttttaggaaa	gtgaaaatat	ttttgttttt	gtattttgaag	aagaatgatg	catttttgaca											1687	
agaaatcata	tatgtatgga	tatattttta	taagtatttg	agtacagact	ttgagggttc											1747	
atcaatataa	ataaaagagc	agaaaaatat	gtctttgggtt	tcattttgctt	acaaaaaaaa											1807	
caacaacaaa	aaaagttgtc	ctttgagaac	ttcacctgct	cctatgtggg	tacctgagtc											1867	
aaaattgtca	tttttgttct	gtgaaaaata	aatttccttc	ttgtacacaaa	aaaaaaaaaa											1927	
aaaa																1931	

<210> 153  
 <211> 514  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 100..441

<400> 153  
 ataccaggca ctttagaacc agagactctg ctgcttttcc tgggcagggc ctgcttgctc 60  
 cagctctcaa gtctgacttg catctacact gcgggcaag atg cgg ctg caa gac 114  
 Met Arg Leu Gln Asp  
 1 5  
 cgc atc gcc acg ttc ttc ttc cca aaa ggc atg atg ctc acc acg gct 162  
 Arg Ile Ala Thr Phe Phe Phe Pro Lys Gly Met Met Leu Thr Thr Ala  
 10 15 20  
 gcg ctg atg ctc ttc ttc tta cac ctg ggc atc ttc atc aga gac gtg 210  
 Ala Leu Met Leu Phe Phe Leu His Leu Gly Ile Phe Ile Arg Asp Val  
 25 30 35  
 cac aac ttc tgc atc acc tac cac tat gac cac atg agc ttt cac tac 258  
 His Asn Phe Cys Ile Thr Tyr His Tyr Asp His Met Ser Phe His Tyr  
 40 45 50  
 acg gtc gtc ctg atg ttc tcc cag gtg atc agc atc tgc tgg gct gcc 306  
 Thr Val Val Leu Met Phe Ser Gln Val Ile Ser Ile Cys Trp Ala Ala  
 55 60 65  
 atg ggg tca ctc tat gct gag atg aca gaa aac aat gct caa cgg agc 354  
 Met Gly Ser Leu Tyr Ala Glu Met Thr Glu Asn Asn Ala Gln Arg Ser  
 70 75 80 85  
 cat gtt ctt caa ccg cct gtc ctt gga gtt tct ggc cat cga gta ccg 402  
 His Val Leu Gln Pro Pro Val Leu Gly Val Ser Gly His Arg Val Pro  
 90 95 100  
 gga gga gca cca ctg agg cct ggg gag tcg gaa cag ggc taaggagggg 451  
 Gly Gly Ala Pro Leu Arg Pro Gly Glu Ser Glu Gln Gly  
 105 110  
 gaagcaaaag gctgcctcgg gtgttttaat aaagttgttg tttattccaa aaaaaaaaaa 511  
 aaa 514

<210> 154  
 <211> 1183  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 32..1132

<400> 154  
 acttctttcc tgccctctgat tccgggctgt c atg gcg acc ccc aac aat ctg 52  
 Met Ala Thr Pro Asn Asn Leu  
 1 5  
 acc ccc acc aac tgc agc tgg tgg ccc atc tcc gcg ctg gag agc gat 100  
 Thr Pro Thr Asn Cys Ser Trp Trp Pro Ile Ser Ala Leu Glu Ser Asp  
 10 15 20  
 gcg gcc aag cca gcg gag gcc ccc gac gct ccc gag gcg gcc agc ccc 148  
 Ala Ala Lys Pro Ala Glu Ala Pro Asp Ala Pro Glu Ala Ala Ser Pro  
 25 30 35  
 gcc cat tgg ccc agg gag agc ctg gtt ctg tac cac tgg acc cag tcc 196

Ala	His	Trp	Pro	Arg	Glu	Ser	Leu	Val	Leu	Tyr	His	Trp	Thr	Gln	Ser	
40					45				50						55	
ttc	agc	tcg	cag	aag	gtg	cgg	ctg	gtg	atc	gcc	gag	aag	ggc	ctg	gtg	244
Phe	Ser	Ser	Gln	Lys	Val	Arg	Leu	Val	Ile	Ala	Glu	Lys	Gly	Leu	Val	
				60					65					70		
tgc	gag	gag	cgg	gac	gtg	agc	ctg	cca	cag	agc	gag	cac	aag	gag	ccc	292
Cys	Glu	Glu	Arg	Asp	Val	Ser	Leu	Pro	Gln	Ser	Glu	His	Lys	Glu	Pro	
			75					80					85			
tgg	ttc	atg	cgg	ctc	aac	ctg	ggc	gag	gag	gtg	ccc	gtc	atc	atc	cac	340
Trp	Phe	Met	Arg	Leu	Asn	Leu	Gly	Glu	Glu	Val	Pro	Val	Ile	Ile	His	
		90					95					100				
cgc	gac	aac	atc	atc	agt	gac	tat	gac	cag	atc	att	gac	tat	gtg	gag	
Arg	Asp	Asn	Ile	Ile	Ser	Asp	Tyr	Asp	Gln	Ile	Ile	Asp	Tyr	Val	Glu	388
	105					110					115					
cgc	acc	ttc	aca	gga	gag	cac	gtg	gtg	gcc	ctg	atg	ccc	gag	gtg	ggc	436
Arg	Thr	Phe	Thr	Gly	Glu	His	Val	Val	Ala	Leu	Met	Pro	Glu	Val	Gly	
120					125				130						135	
agc	ctg	cag	cac	gca	cgg	gtg	ctg	cag	tac	cgg	gag	ctg	ctg	gac	gca	484
Ser	Leu	Gln	His	Ala	Arg	Val	Leu	Gln	Tyr	Arg	Glu	Leu	Leu	Asp	Ala	
				140					145					150		
ctg	ccc	atg	gat	gcc	tac	acg	cat	ggc	tgc	atc	ctg	cat	ccc	gag	ctc	532
Leu	Pro	Met	Asp	Ala	Tyr	Thr	His	Gly	Cys	Ile	Leu	His	Pro	Glu	Leu	
			155					160						165		
acc	acc	gac	tcc	atg	atc	ccc	aag	tac	gcc	acg	gcc	gag	atc	cgc	aga	580
Thr	Thr	Asp	Ser	Met	Ile	Pro	Lys	Tyr	Ala	Thr	Ala	Glu	Ile	Arg	Arg	
		170					175					180				
cat	tta	gcc	aat	gcc	acc	acg	gac	ctc	atg	aaa	ctg	gac	cat	gaa	gag	628
His	Leu	Ala	Asn	Ala	Thr	Thr	Asp	Leu	Met	Lys	Leu	Asp	His	Glu	Glu	
	185					190					195					
gag	ccc	cag	ctc	tcc	gag	ccc	tac	ctt	tct	aaa	caa	aag	aag	ctc	atg	676
Glu	Pro	Gln	Leu	Ser	Glu	Pro	Tyr	Leu	Ser	Lys	Gln	Lys	Lys	Leu	Met	
200					205					210					215	
gtc	aag	atc	ttg	gag	cat	gat	gat	gtg	agc	tac	ctg	aag	aag	atc	ctc	724
Val	Lys	Ile	Leu	Glu	His	Asp	Asp	Val	Ser	Tyr	Leu	Lys	Lys	Ile	Leu	
				220					225					230		
ggg	gaa	ctg	gcc	atg	gtg	ctg	gac	cag	att	gag	gag	gag	ctg	gag	aag	772
Gly	Glu	Leu	Ala	Met	Val	Leu	Asp	Gln	Ile	Glu	Ala	Glu	Leu	Glu	Lys	
			235					240					245			
agg	aag	ctg	gag	aac	gag	ggg	cag	aaa	tgc	gag	ctg	tgg	ctc	tgt	ggc	820
Arg	Lys	Leu	Glu	Asn	Glu	Gly	Gln	Lys	Cys	Glu	Leu	Trp	Leu	Cys	Gly	
		250					255					260				
tgt	gcc	ttc	acc	ctc	gct	gat	gtc	ctc	ctg	gga	gcc	acc	ctg	cac	cgc	868
Cys	Ala	Phe	Thr	Leu	Ala	Asp	Val	Leu	Leu	Gly	Ala	Thr	Leu	His	Arg	
	265					270					275					
ctc	aag	ttc	ctg	gga	ctg	tcc	aag	aaa	tac	tgg	gaa	gat	ggc	agc	cgg	916
Leu	Lys	Phe	Leu	Gly	Leu	Ser	Lys	Lys	Tyr	Trp	Glu	Asp	Gly	Ser	Arg	
280					285					290					295	
ccc	aac	ctg	cag	tcc	ttc	ttt	gag	agg	gtc	cag	aga	cgc	ttt	gcc	ttc	964
Pro	Asn	Leu	Gln	Ser	Phe	Phe	Glu	Arg	Val	Gln	Arg	Arg	Phe	Ala	Phe	
				300					305					310		
cgg	aaa	gtc	ctg	ggt	gac	atc	cac	acc	acc	ctg	ctg	tcg	gcc	gtc	atc	1012
Arg	Lys	Val	Leu	Gly	Asp	Ile	His	Thr	Thr	Leu	Leu	Ser	Ala	Val	Ile	
			315					320					325			
ccc	aat	gct	ttc	cgg	ctg	gtc	aag	agg	aaa	ccc	cca	tcc	ttc	ttc	ggg	1060
Pro	Asn	Ala	Phe	Arg	Leu	Val	Lys	Arg	Lys	Pro	Pro	Ser	Phe	Phe	Gly	
		330					335					340				
gcg	tcc	ttc	ctc	atg	ggc	tcc	ctg	ggt	ggg	atg	ggc	tac	ttt	gcc	tac	1108
Ala	Ser	Phe	Leu	Met	Gly	Ser	Leu	Gly	Gly	Met	Gly	Tyr	Phe	Ala	Tyr	

```

      345              350              355
tgg tac ctc aag aaa aaa tac atc tagggccagg cctggggcctt ggtgtctgac 1162
Trp Tyr Leu Lys Lys Lys Tyr Ile
360              365
tgtcaaaaaa aaaaaaaaaa a 1183

<210> 155
<211> 1545
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 160..996

<400> 155
acacagcatg catttcttca acaagcgact cagaaggcac ttgcacatcg ttgctgttct 60
gcctcttttg ttcagcatga ttaccagag gcgcaccgct gccgtggcct gcccgctcgtc 120
tatgcacccg tgctgtggcg tgcccgtcgt ctgtgtggc atg cct gtc tgt gca 174
                                Met Pro Val Cys Ala
                                1              5
ccc gtg ctg tgg cgt gcc cgt cgt ctg tgt ggc atg cct gtc tgt gca 222
Pro Val Leu Trp Arg Ala Arg Arg Leu Cys Gly Met Pro Val Cys Ala
                                10              15              20
ccc gtg ccg tgg cgt gcc cgt cgt ctg tgc acc cgt gct gtg gtg tgc 270
Pro Val Pro Trp Arg Ala Arg Arg Leu Cys Thr Arg Ala Val Val Cys
                                25              30              35
cct tcg tct gtt cct ttt att gcc ggg cag ggt tgc acc cac atg tgc 318
Pro Ser Ser Val Pro Phe Ile Ala Gly Gln Gly Cys Thr His Met Cys
                                40              45              50
aag cca gcg acg gac ccc agg ttc acc cgt tca ccg ctg gct gga ggc 366
Lys Pro Ala Thr Asp Pro Arg Phe Thr Arg Ser Pro Leu Ala Gly Gly
                                55              60              65
gtg atc ctg ggt gtg gcc ctg tgg ctc cgc cat gac ccg cag acc acc 414
Val Ile Leu Gly Val Ala Leu Trp Leu Arg His Asp Pro Gln Thr Thr
                                70              75              80              85
aac ctc ctg tat ctg gag ctg gga gac aag ccc gcg ccc aac acc ttc 462
Asn Leu Leu Tyr Leu Glu Leu Gly Asp Lys Pro Ala Pro Asn Thr Phe
                                90              95              100
tat gta ggc atc tac atc ctc atc gct gtg ggc gct gtc atg atg ttc 510
Tyr Val Gly Ile Tyr Ile Leu Ile Ala Val Gly Ala Val Met Met Phe
                                105              110              115
gtt ggc ttc ctg ggc tgc tac ggg gcc atc cag gaa tcc cag tgc ctg 558
Val Gly Phe Leu Gly Cys Tyr Gly Ala Ile Gln Glu Ser Gln Cys Leu
                                120              125              130
ctg ggg acg ttc ttc act tgc ctg gtc atc ctg ttt gcc tgt gag gtg 606
Leu Gly Thr Phe Phe Thr Cys Leu Val Ile Leu Phe Ala Cys Glu Val
                                135              140              145
gcc gcc ggc atc tgg ggc ttt gtc aac aag gac cag atc gcc aag gat 654
Ala Ala Gly Ile Trp Gly Phe Val Asn Lys Asp Gln Ile Ala Lys Asp
                                150              155              160              165
gtg aag cag ttc tat gac cag gcc cta cag cag gcc gtg gtg gat gat 702
Val Lys Gln Phe Tyr Asp Gln Ala Leu Gln Gln Ala Val Val Asp Asp
                                170              175              180
gac gcc aac aac gcc aag gct gtg gtg aag acc ttc cac gag acg ctt 750
Asp Ala Asn Asn Ala Lys Ala Val Val Lys Thr Phe His Glu Thr Leu
                                185              190              195
gac tgc tgt ggc tcc agc aca ctg act gct ttg acc acc tca gtg ctc 798

```

```

Asp Cys Cys Gly Ser Ser Thr Leu Thr Ala Leu Thr Thr Ser Val Leu
      200      205      210
aag aac aat ttg tgt ccc tcg ggc agc aac atc atc agc aac ctc ttc      846
Lys Asn Asn Leu Cys Pro Ser Gly Ser Asn Ile Ile Ser Asn Leu Phe
      215      220      225
aag gag gac tgc cac cag aag atc gat gac ctc ttc tcc ggg aag ctg      894
Lys Glu Asp Cys His Gln Lys Ile Asp Asp Leu Phe Ser Gly Lys Leu
230      235      240      245
tac ctc atc ggc att gct gcc atc gtg gtc gct gtg atc atg atc ttc      942
Tyr Leu Ile Gly Ile Ala Ala Ile Val Val Ala Val Ile Met Ile Phe
      250      255      260
gag atg atc ctg agc atg gtg ctg tgc tgt ggc atc cgg aac agc tcc      990
Glu Met Ile Leu Ser Met Val Leu Cys Cys Gly Ile Arg Asn Ser Ser
      265      270      275
gtg tac tgaggccccg cagctctggc cacagggacc tctgcagtgc cccctaagtg      1046
Val Tyr
accgggacac ttccgagggg gccatcaccg cctgtgtata taacgtttcc ggtattactc      1106
tgctacacgt agccttttta cttttggggg tttgtttttg ttctgaactt tctgtttacc      1166
ttttcagggc tgacgtcaca tgtaggtggc gtgtatgagt ggagacgggc ctgggtcttg      1226
gggactggag ggcaggggtc cttctgcctt ggggtcccag ggtgctctgc ctgctcagcc      1286
aggcctctcc tgggagccac tcgccagag actcagcttg gccaaacttg ggggctgtgt      1346
ccaccagcc cgcccgctct gtgggctgca cagctcacct tgttccctcc tgccccggtt      1406
cgagagccga gtctgtgggc actctctgcc ttcatgcacc tgtcctttct aacacgtcgc      1466
cttcaactgt aatcacaca tcctgactcc gtcatttaat aaagaaggaa catcaggcat      1526
gcaaaaaaaaa aaaaaaaaaa      1545

<210> 156
<211> 1068
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 11..529

<400> 156
gaagcacgga atg tgt ctc ctg ctg ggg gcc acg ggc gtc ggg aag acg      49
      Met Cys Leu Leu Leu Gly Ala Thr Gly Val Gly Lys Thr
      1      5      10
ctg ctg gtg aaa cgg ctg cag gag gtg agc tcc cgg gat ggg aaa ggc      97
Leu Leu Val Lys Arg Leu Gln Glu Val Ser Ser Arg Asp Gly Lys Gly
      15      20      25
gac ctg ggg gag ccg ccc ccg aca cgg ccc acg gtg ggc acc aat ctt      145
Asp Leu Gly Glu Pro Pro Pro Thr Arg Pro Thr Val Gly Thr Asn Leu
      30      35      40      45
act gac atc gtg gca cag aga aag atc acc atc cgg gag ctt ggg ggg      193
Thr Asp Ile Val Ala Gln Arg Lys Ile Thr Ile Arg Glu Leu Gly Gly
      50      55      60
tgc atg ggc ccc atc tgg tcc agt tac tat gga aac tgc cgt tct ctc      241
Cys Met Gly Pro Ile Trp Ser Ser Tyr Tyr Gly Asn Cys Arg Ser Leu
      65      70      75
ctg ttt gtg atg gac gcc tct gac ccc acc cag ctc tct gca tcc tgt      289
Leu Phe Val Met Asp Ala Ser Asp Pro Thr Gln Leu Ser Ala Ser Cys
      80      85      90
gtg cag ctc tta ggt ctc ctt tct gca gaa caa ctt gca gaa gca tcg      337
Val Gln Leu Leu Gly Leu Ser Ala Glu Gln Leu Ala Glu Ala Ser
      95      100      105
gtg ctg ata ctc ttc aat aaa atc gac cta ccc tgt tac atg tcc acg      385

```

Val	Leu	Ile	Leu	Phe	Asn	Lys	Ile	Asp	Leu	Pro	Cys	Tyr	Met	Ser	Thr	
110					115				120					125		
gag	gag	atg	aag	tca	tta	atc	agg	ctt	cca	gac	atc	att	gct	tgt	gcc	433
Glu	Glu	Met	Lys	Ser	Leu	Ile	Arg	Leu	Pro	Asp	Ile	Ile	Ala	Cys	Ala	
				130					135					140		
aag	cag	aac	atc	acc	acg	gca	gaa	atc	agc	gcc	cgt	gaa	ggc	act	ggc	481
Lys	Gln	Asn	Ile	Thr	Thr	Ala	Glu	Ile	Ser	Ala	Arg	Glu	Gly	Thr	Gly	
			145					150					155			
tta	gca	ggg	gtg	ctg	gcc	tgg	ctc	cag	gcc	acc	cac	aga	gcc	aac	gat	529
Leu	Ala	Gly	Val	Leu	Ala	Trp	Leu	Gln	Ala	Thr	His	Arg	Ala	Asn	Asp	
		160					165					170				
tgactgcacg	gcagaggcgc	agctggcctg	agctgggggag	aggtggcaga	gggcagtatg											589
gctttgctgc	caatagtttc	ttctcacagg	ggcagaataa	cccaaagtaa	ccctacatga											649
tggggctctg	tgctgggatg	caatgatgtg	taaactgagg	catgtggaga	tggaaagtga											709
catctggcct	ctgaaaaaag	tgtccccagg	ggctaggcat	ggtggctcac	acctgtaatc											769
ccagcacttt	gagaggccga	ggcgggtgta	tcacctgagg	tcggggagttc	gagactagcc											829
tgaccaacat	ggagaaaacc	tgtctctact	aaaaatacaa	aattagctgg	gtgtgctgggt											889
gcatgcctgt	aatctcagct	acttggggagg	ctgagacagg	agaatccctt	gaacctggga											949
ggtggagggt	gcagtgagtc	gagatcatgc	cattgcactg	cacctgggca	acaagagtga											1009
aactccgtct	taaaaaatat	aagaaataaa	aaaataaaaa	cctaaaaaaaa	aaaaaaaaaa											1068
<210> 157																
<211> 1097																
<212> DNA																
<213> Homo sapiens																
<220>																
<221> CDS																
<222> 135..749																
<400> 157																
aacgaaacgg	taaccagccc	tgggaagccc	gcaagaggcc	tcagcgggtg	ccgtccgagc											60
gccgagaggt	gaggggtgcc	ccgcctcacc	tgcaagaggg	ccgttccggg	ctcgaacccg											120
gcaccttccg	gaaa	atg	gcg	gct	gcc	agg	ccc	agc	ctg	ggc	mga	gtc	ctc			170
	Met	Ala	Ala	Ala	Arg	Pro	Ser	Leu	Gly	Arg	Val	Leu				
	1				5						10					
cca	gga	tcc	tct	gtc	ctg	ttc	ctg	tgt	gac	atg	cag	gag	aag	ttc	cgc	218
Pro	Gly	Ser	Ser	Val	Leu	Phe	Leu	Cys	Asp	Met	Gln	Glu	Lys	Phe	Arg	
	15				20						25					
cac	aac	atc	gcc	tac	ttc	cca	cag	atc	gtc	tca	gtg	gct	gcc	cgc	atg	266
His	Asn	Ile	Ala	Tyr	Phe	Pro	Gln	Ile	Val	Ser	Val	Ala	Ala	Arg	Met	
	30				35						40					
ctc	aag	gtg	gcc	cgg	ctg	ctt	gag	gtg	cca	gtc	atg	ctg	acg	gag	cag	314
Leu	Lys	Val	Ala	Arg	Leu	Leu	Glu	Val	Pro	Val	Met	Leu	Thr	Glu	Gln	
	45				50					55					60	
tac	cca	caa	ggc	ctg	ggc	ccc	acg	gtg	ccc	gag	ctg	ggg	act	gag	ggc	362
Tyr	Pro	Gln	Gly	Leu	Gly	Pro	Thr	Val	Pro	Glu	Leu	Gly	Thr	Glu	Gly	
				65				70						75		
ctt	cgg	ccg														

```

Arg Gly Leu Gln Val His Val Val Val Asp Ala Cys Ser Ser Arg Ser
125          130          135          140
cag gtg gac cgt ctg gtg gct ctg gcc cgc atg aga cag agt ggt gcc      602
Gln Val Asp Arg Leu Val Ala Leu Ala Arg Met Arg Gln Ser Gly Ala
          145          150          155
ttc ctc tcc acc agc gaa ggg ctc att ctg cag ctt gtg ggc gat gcc      650
Phe Leu Ser Thr Ser Glu Gly Leu Ile Leu Gln Leu Val Gly Asp Ala
          160          165          170
gtc cac ccc cag ttc aag gag atc cag aaa ctc atc aag gag ccc gcc      698
Val His Pro Gln Phe Lys Glu Ile Gln Lys Leu Ile Lys Glu Pro Ala
          175          180          185
cca gac agc gga ctg ctg ggc ctc ttc caa ggc cag aac tcc ctc ctc      746
Pro Asp Ser Gly Leu Leu Gly Leu Phe Gln Gly Gln Asn Ser Leu Leu
          190          195          200
cac tgaactccaa ccctgccttg aggggaagacc accctcctgt caccgggacc      799
His
205
tcagtgggaag cccgttcccc ccatccctgg atcccaagag tgggtgcgac caccaggagt      859
gccgccccct tgtggggggg ggcagggtgc tgccttccca ttggacagct gctcccggaa      919
atgcaaataa gactcctgga aactgggtgg gaattggctg agccaagatg gaggcggggc      979
tcggccccgg gccacttcac ggggcgggaa ggggagggga agaagagtct cagactgtgg      1039
gacacgggact cgcagaataa acatatatgt ggctgtggac caaaaaaaaa aaaaaaaaa      1097

<210> 158
<211> 894
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 98..637

<400> 158
ctttggggcc gaagtgggcg tgcggctcgc gctgttcgcg gccttccttg tgacggagct      60
gctccccccg ttccagagac tcatccagcc ggaggag atg tgg ctc tac cgg aac      115
                               1                               5
ccc tac gtg gag gcg gag tat ttc ccc acc aag ccg atg ttt gtt att      163
Pro Tyr Val Glu Ala Glu Tyr Phe Pro Thr Lys Pro Met Phe Val Ile
          10          15          20
gca ttt ctc tct cca ctg tct ctg atc ttc ctg gcc aaa ttt ctc aag      211
Ala Phe Leu Ser Pro Leu Ser Leu Ile Phe Leu Ala Lys Phe Leu Lys
          25          30          35
aag gca gac aca aga gac agc aga caa gcc tgc ctg gct gcc agc ctt      259
Lys Ala Asp Thr Arg Asp Ser Arg Gln Ala Cys Leu Ala Ala Ser Leu
          40          45          50
gcc ctg gct ctg aat ggc gtc ttt acc aac aca ata aaa ctg atc gta      307
Ala Leu Ala Leu Asn Gly Val Phe Thr Asn Thr Ile Lys Leu Ile Val
          55          60          65          70
ggg agg cca cgc cca gat ttc ttc tac cgc tgc ttc cct gat ggg cta      355
Gly Arg Pro Arg Pro Asp Phe Phe Tyr Arg Cys Phe Pro Asp Gly Leu
          75          80          85
gcc cat tct gac ttg atg tgt aca ggg gat aag gac gtg gtg aat gag      403
Ala His Ser Asp Leu Met Cys Thr Gly Asp Lys Asp Val Val Asn Glu
          90          95          100
ggc cga aag agc ttc ccc agt gga cat tct tcc ttt gca ttt gct ggt      451
Gly Arg Lys Ser Phe Pro Ser Gly His Ser Ser Phe Ala Phe Ala Gly
          105          110          115

```



ctg gcc ttt gcg tcc ttc tac ctg gca ggg aag tta cac tgc ttc aca	499
Leu Ala Phe Ala Ser Phe Tyr Leu Ala Gly Lys Leu His Cys Phe Thr	
120 125 130	
cca caa ggc cgt ggg aaa tct tgg agg ttc tgt gcc ttt ctg tca cct	547
Pro Gln Gly Arg Gly Lys Ser Trp Arg Phe Cys Ala Phe Leu Ser Pro	
135 140 145 150	
cta ctt ttt gca gct gtg att gca ctg tcc cgc aca tgt gac tac aag	595
Leu Leu Phe Ala Ala Val Ile Ala Leu Ser Arg Thr Cys Asp Tyr Lys	
155 160 165	
cat cac tgg caa gat ctg ctc aaa tgc acc aac act gcc aag	637
His His Trp Cln Asp Leu Leu Lys Cys Thr Asn Thr Ala Lys	
170 175 180	
tgactaaggt agaaaagaaa aatgacaggt atcgatcatct gaaggacaga tgaatctttt	697
tctgccccctt cttcacaaatg gaataataagg aacaattatg ggatgtcatc agaatggatg	757
ccataggacc tacagctccc tttctcttta ttgtgattat actttaaata tgacattgtc	817
ttttatgtgt atgttcctat attttcaatg tatctttttc cttcagtaaa cctgatattc	877
aaaaaaaaa aaaaaaa	894
<210> 159	
<211> 703	
<212> DNA	
<213> Homo sapiens	
<220>	
<221> CDS	
<222> 221..670	
<400> 159	
aaggaagcgc cgcccccttcc tacggctacg ggaaggatcg tccagtggct gaggctggac	60
agagcacaga caaaagataa aaagcaagat ttgagagagg ttccctggatc aactggctca	120
atctgcttag ttctacaaag tggagtttct gggcatcatt cttcatttct gtacacaaag	180
tgctgtgaag ctcaagaaga aatagctctg cacaggaacg atg tgc act gcc cta	235
Met Cys Thr Ala Leu	
1 5	
ctg ctt ctt tat cta aga tgg tgt ttc aac tta aaa ctt gtg aat gtg	283
Leu Leu Leu Tyr Leu Arg Trp Cys Phe Asn Leu Lys Leu Val Asn Val	
10 15 20	
aaa tat gag cca aaa gac tct ctc ggc cct gaa atg acc ttt gta gca	331
Lys Tyr Glu Pro Lys Asp Ser Leu Gly Pro Glu Met Thr Phe Val Ala	
25 30 35	
gat gct gcc aga ggc ccc ctg tta tcc tcc ctg gac tct cca gct aac	379
Asp Ala Ala Arg Gly Pro Leu Leu Ser Ser Leu Asp Ser Pro Ala Asn	
40 45 50	
ctg atg tca act gcc agt gtg tgc atc tcc tta cct gag ggc tgt tct	427
Leu Met Ser Thr Ala Ser Val Cys Ile Ser Leu Pro Glu Gly Cys Ser	
55 60 65	
ggt ggc agg agt cct tgc tac tca cag aaa tgg cca cca gaa gtg cca	475
Gly Gly Arg Ser Pro Cys Tyr Ser Gln Lys Trp Pro Pro Glu Val Pro	
70 75 80 85	
gaa aaa tta acc tcc ctt ggc cag cag tcc tca acc agc tcc ctc act	523
Glu Lys Leu Thr Ser Leu Gly Gln Gln Ser Ser Thr Ser Ser Leu Thr	
90 95 100	
gac act gat gtg cag gtg tct cct atg ctg gtt gct gga gtc aac cac	571
Asp Thr Asp Val Gln Val Ser Pro Met Leu Val Ala Gly Val Asn His	
105 110 115	
agc agc agc ctt ctt gac aac ata ccc ttc act ggc tgc ctt cct ttc	619
Ser Ser Ser Leu Leu Asp Asn Ile Pro Phe Thr Gly Cys Leu Pro Phe	
120 125 130	

```

cat ctc tct tct tca ctc ccc tac cta tgt ctc cta ggc tct ccc ttc 667
His Leu Ser Ser Ser Leu Pro Tyr Leu Cys Leu Leu Gly Ser Pro Phe
135 140 145
aaa taaacagctt gcacttgaaa aaaaaaaaaa aaa 703
Lys
150

<210> 160
<211> 849
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 165..674

<400> 160
aaaactgagg cctgggagca ggaacctgta ggcagcgctt gagggtagcg ggatagcagc 60
tgcaagcgcg cgtgggaggg gggggctctg ggcggaacaa aaatcacagg atgtcagagg 120
atgtttcccg ggaagaactg ggataaagga aggggtcccag cacc atg gag gac ccg 176
Met Glu Asp Pro
1
aac cct gaa gag aac atg aag cag cag gat tca ccc aag gag aga agt 224
Asn Pro Glu Glu Asn Met Lys Gln Gln Asp Ser Pro Lys Glu Arg Ser
5 10 15 20
ccc cag agc cca gga ggc aac atc tgc cac ctg ggg gcc ccg aag tgc 272
Pro Gln Ser Pro Gly Gly Asn Ile Cys His Leu Gly Ala Pro Lys Cys
25 30 35
acc cgc tgc ctc atc acc ttc gca gat tcc aag ttc cag gag cgt cac 320
Thr Arg Cys Leu Ile Thr Phe Ala Asp Ser Lys Phe Gln Glu Arg His
40 45 50
atg aag cgg gag cac cca gcg gac ttc gtg gcc cag aag ctg cag ggg 368
Met Lys Arg Glu His Pro Ala Asp Phe Val Ala Gln Lys Leu Gln Gly
55 60 65
gtc ctc ttc atc tgc ttc acc tgc gcc cgc tcc ttc ccc tcc tcc aaa 416
Val Leu Phe Ile Cys Phe Thr Cys Ala Arg Ser Phe Pro Ser Ser Lys
70 75 80
gcc cta atc acc cac cag cgc agc cac ggt cca gcc gcc aag ccc acc 464
Ala Leu Ile Thr His Gln Arg Ser His Gly Pro Ala Ala Lys Pro Thr
85 90 95 100
ctg ccg gtt gca acc act act gcc cag ccc acc ttc cct tgt cct gac 512
Leu Pro Val Ala Thr Thr Thr Ala Gln Pro Thr Phe Pro Cys Pro Asp
105 110 115
tgt ggc aag acc ttt ggg cag gct gtt tct ctg agg cgg cac cgc cag 560
Cys Gly Lys Thr Phe Gly Gln Ala Val Ser Leu Arg Arg His Arg Gln
120 125 130
atg cat gag gtc cgt gcc cct cct gcc acc ttc gcc tgc aca gag tgc 608
Met His Glu Val Arg Ala Pro Pro Gly Thr Phe Ala Cys Thr Glu Cys
135 140 145
ggc cag gac ttt gct cag gaa gca ggg ctg cat caa cac tac att cgg 656
Gly Gln Asp Phe Ala Gln Glu Ala Gly Leu His Gln His Tyr Ile Arg
150 155 160
cat gcc cgg ggg gag ctc tgagtgcagc ttaagcctct ccacgggtgac 704
His Ala Arg Gly Glu Leu
165 170
gggtgggtct gtggctggta ggactcacc atgatatggg gtgcaggaac tctggggggc 764
ctgaaggatt tgcttccctc ccctgggaag gcagagggt cctaataaag aggaccacaga 824
agattctcaa aaaaaaaaaa aaaaaa 849

```

<210> 161  
 <211> 846  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 165..671

<400> 161  
 aaaactgagg cctgggagca ggaacctgta ggcagcgctt gagggtagcg ggatagcagc 60  
 tgcaagcgcg cgtgggagcg gggggctctg ggcggaacaa aaatcacagg atgtcagagg 120  
 atgtttcccg ggaagaactg ggataaagga aggggtcccag cacc atg gag gac ccg 176  
 Met Glu Asp Pro  
 1  
 aac cct gaa gag aac atg aag cag cag gat tca ccc aag gag aga agt 224  
 Asn Pro Glu Glu Asn Met Lys Gln Gln Asp Ser Pro Lys Glu Arg Ser  
 5 10 15 20  
 ccc cag ccc agg agg caa cat ctg cca cct ggg ggc ccc gaa gtg cac 272  
 Pro Gln Pro Arg Arg Gln His Leu Pro Gly Gly Pro Glu Val His  
 25 30 35  
 ccg ctg cct cat cac ctt cgc aga ttc caa gtt cca gga gcg tca cat 320  
 Pro Leu Pro His His Leu Arg Arg Phe Gln Val Pro Gly Ala Ser His  
 40 45 50  
 gaa gcg gga gca ccc agc gga ctt cgt ggc cca gaa gct gca ggg ggt 368  
 Glu Ala Gly Ala Pro Ser Gly Leu Arg Gly Pro Glu Ala Ala Gly Gly  
 55 60 65  
 cct ctt cat ctg ctt cac ctg cgc ccg ctc ctt ccc ctc ctc caa agc 416  
 Pro Leu His Leu Leu His Leu Arg Pro Leu Leu Pro Leu Leu Gln Ser  
 70 75 80  
 cct aat cac cca cca gcg cag cac ggt cca gcc gcc aag ccc acc ctg 464  
 Pro Asn His Pro Pro Ala Gln His Gly Pro Ala Ala Lys Pro Thr Leu  
 85 90 95 100  
 ccg gtt gca acc act act gcc cag ccc acc ttc cct tgt cct gac tgt 512  
 Pro Val Ala Thr Thr Thr Ala Gln Pro Thr Phe Pro Cys Pro Asp Cys  
 105 110 115  
 ggc aag acc ttt ggg cag gct gtt tct ctg agg cgg cac cgc cag atg 560  
 Gly Lys Thr Phe Gly Gln Ala Val Ser Leu Arg Arg His Arg Gln Met  
 120 125 130  
 cat gag gtc cgt gcc cct cct ggc acc ttc gcc tgc aca gag tgc ggt 608  
 His Glu Val Arg Ala Pro Pro Gly Thr Phe Ala Cys Thr Glu Cys Gly  
 135 140 145  
 cag gac ttt gct cag gaa gca ggg ctg cat caa cac tac att cgg cat 656  
 Gln Asp Phe Ala Gln Glu Ala Gly Leu His Gln His Tyr Ile Arg His  
 150 155 160  
 gcc cgg ggg gag ctc tgagtgcagc ttaagcctct ccacggtgac ggggtggtct 711  
 Ala Arg Gly Glu Leu  
 165  
 gtggctggta ggactcacc atgatatggg gtgcaggaac tctgggggcc ctgaaggatt 771  
 tgcttcctc ccctgggaag gcagagggt cttaataaag aggaccaga agattctcaa 831  
 aaaaaaaaaa aaaaa 846

<210> 162  
 <211> 1176  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 28..1128

<400> 162

```

ctttcttgcc tctgattccg ggctgtc atg gcg acc ccc aac aat ctg acc ccc      54
                        Met Ala Thr Pro Asn Asn Leu Thr Pro
                        1          5
acc aac tgc agc tgg tgg ccc atc tcc gcg ctg gag agc gat gcg gcc      102
Thr Asn Cys Ser Trp Trp Pro Ile Ser Ala Leu Glu Ser Asp Ala Ala
10          15          20          25
aag cca gcg gag gcc ccc gac gct ccc gag gcg gcc agc ccc gcc cat      150
Lys Pro Ala Glu Ala Pro Asp Ala Pro Glu Ala Ala Ser Pro Ala His
          30          35          40
tgg ccc agg gag agc ctg gtt ctg tac cac tgg acc cag tcc ttc agc      198
Trp Pro Arg Glu Ser Leu Val Leu Tyr His Trp Thr Gln Ser Phe Ser
          45          50          55
tcg cag aag gtg cgg ctg gtg atc gcc gag aag ggc ctg gtg tgc gag      246
Ser Gln Lys Val Arg Leu Val Ile Ala Glu Lys Gly Leu Val Cys Glu
60          65          70
gag cgg gac gtg agc ctg cca cag agc gag cac aag gag ccc tgg ttc      294
Glu Arg Asp Val Ser Leu Pro Gln Ser Glu His Lys Glu Pro Trp Phe
75          80          85
atg cgg ctc aac ctg ggc gag gag gtg ccc gtc atc atc cac cgc gac      342
Met Arg Leu Asn Leu Gly Glu Glu Val Pro Val Ile Ile His Arg Asp
90          95          100          105
aac atc atc agt gac tat gac cag atc att gac tat gtg gag cgc acc      390
Asn Ile Ile Ser Asp Tyr Asp Gln Ile Ile Asp Tyr Val Glu Arg Thr
110          115          120
ttc aca gga gag cac gtg gtg gcc ctg atg ccc gag gtg ggc agc ctg      438
Phe Thr Gly Glu His Val Val Ala Leu Met Pro Glu Val Gly Ser Leu
125          130          135
cag cac gca cgg gtg ctg cag tac cgg gag ctg ctg gac gca ctg ccc      486
Gln His Ala Arg Val Leu Gln Tyr Arg Glu Leu Leu Asp Ala Leu Pro
140          145          150
atg gat gcc tac acg cat ggc tgc atc ctg cat ctc gag ctc acc acc      534
Met Asp Ala Tyr Thr His Gly Cys Ile Leu His Leu Glu Leu Thr Thr
155          160          165
gac tcc atg atc ccc aag tac gcc acg gcc gag atc cgc aga cat tta      582
Asp Ser Met Ile Pro Lys Tyr Ala Thr Ala Glu Ile Arg Arg His Leu
170          175          180          185
gcc aat gcc acc acg gac ctc atg aaa ctg gac cat gaa gag gag ccc      630
Ala Asn Ala Thr Thr Asp Leu Met Lys Leu Asp His Glu Glu Glu Pro
190          195          200
cag ctc tcc gag ccc tac ctt tct aaa caa aag aag ctc atg gcc aag      678
Gln Leu Ser Glu Pro Tyr Leu Ser Lys Gln Lys Lys Leu Met Ala Lys
205          210          215
atc ttg gag cat gat gat gtg agc tac ctg aag aag atc ctc ggg gaa      726
Ile Leu Glu His Asp Asp Val Ser Tyr Leu Lys Lys Ile Leu Gly Glu
220          225          230
ctg gcc atg gtg ctg gac cag att gag gcg gag ctg gag aag agg aag      774
Leu Ala Met Val Leu Asp Gln Ile Glu Ala Glu Leu Glu Lys Arg Lys
235          240          245
ctg gag aac gag ggg cag aaa tgc gag ctg tgg ctc tgt ggc tgt gcc      822
Leu Glu Asn Glu Gly Gln Lys Cys Glu Leu Trp Leu Cys Gly Cys Ala
250          255          260          265
ttc acc ctc gct gat gtc ctc ctg gga gcc acc ctg cac cgc ctc aag      870
Phe Thr Leu Ala Asp Val Leu Leu Gly Ala Thr Leu His Arg Leu Lys

```

270	275	280	
ttc ctg gga ctg tcc aag aaa tac tgg gaa gat ggc agc cgg ccc aac			918
Phe Leu Gly Leu Ser Lys Lys Tyr Trp Glu Asp Gly Ser Arg Pro Asn			
285	290	295	
ctg cag tcc ttc ttt gag agg gtc cag aga cgc ttt gcc ttc cgg aaa			966
Leu Gln Ser Phe Phe Glu Arg Val Gln Arg Arg Phe Ala Phe Arg Lys			
300	305	310	
gtc ctg ggt gac atc cac acc acc ctg ctg tcg gcc gtc atc ccc aat			1014
Val Leu Gly Asp Ile His Thr Thr Leu Leu Ser Ala Val Ile Pro Asn			
315	320	325	
gct ttc cgg ctg gtc aag agg aaa ccc cca tcc ttc ttc ggg gcg tcc			1062
Ala Phe Arg Leu Val Lys Arg Lys Pro Pro Ser Phe Phe Gly Ala Ser			
330	335	340	
ttc ctc atg ggc tcc ctg ggt ggg atg ggc tac ttt gcc tac tgg tac			1110
Phe Leu Met Gly Ser Leu Gly Gly Met Gly Tyr Phe Ala Tyr Trp Tyr			
350	355	360	
ctc aag aaa aaa tac atc tagggccagg cctggggcctt ggtgtctgac			1158
Leu Lys Lys Lys Tyr Ile			
365			
aaaaaamaaa aaaaaaaaa			1176
<210> 163			
<211> 1084			
<212> DNA			
<213> Homo sapiens			
<220>			
<221> CDS			
<222> 135..194			
<400> 163			
aacgaaacgg taaccagccc tgggaagccc gcaagaggcc tcagcgggtgg ccgtccgagc			60
gccgagaggt gaggggtgccc ccgcctcacc tgcagagggg ccgttccggg ctccaacccg			120
gcaccttccg gaaa atg gcg gct gcc agg ccc agc ctg ggc cga gtc ctc			170
Met Ala Ala Ala Arg Pro Ser Leu Gly Arg Val Leu			
1	5	10	
cca gga tcc tct cct gtt cct gtg tgacatgcag gagaagttcc gccacaacat			224
Pro Gly Ser Ser Pro Val Pro Val			
15	20		
cgctacttcc ccacagatcg tctcagtggc tgcccgcgatg ctcaaggtgg cccggctgct			284
tgaggtgccg gtcagtctga cggagcagta cccacaaggc ctggggccca cggtgcccga			344
gctgggggact gagggccttc ggccgctggc caagacctgc ttcagcatgg tgcctgccct			404
gcagcaggag ctggacagtc ggccccagct gcgctctgtg ctgctctgtg gcattgaggc			464
acaggcctgc atcttgaaca cgaccctgga cctcctagac cgggggctgc aggtccatgt			524
ggtggtggac gctgtctct caccgcagcca ggtggaccgg ctggtggctc tggcccgcac			584
gagacagagt ggtgccttcc tctccaccag cgaagggtctc attctgcagc ttgtgggcga			644
tgccgtccac cccagttca aggagatcca gaaactcacc aaggagcccg cccagacag			704
cggactgctg ggcctcttcc aaggccagaa ctccctctcc cactgaactc caaccctgcc			764
ttgaggggaag accaccctcc tgtcaccggc acctcagtgg aagcccgctc ccccatccc			824
tggatcccaa gagtgggtgcg atccaccagg agtgccgccc ccttggggggg ggcaggggtgc			884
tgccttccca ttggacagct gctcccgga atgcaaata gactcctgga aactgggtgg			944
gaattggctg agccaagatg gaggcggggc tcggccccgg gccacttcac ggggcgggaa			1004
ggggagggga agaagagtct cagactgtgg gacacggact cgcagaataa acatatatgt			1064
ggcaaaaaaa aaaaaaaaa			1084

<210> 164  
 <211> 1793  
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 173..847

<400> 164

```

gsmggrggcc attacctaga acatcstaac cgaarratta tttgaaaaac cactggggttc      60
cgagttcatt actacaggaa aaactgttct cttctgtggc acagagaacc ctgcttcaaa      120
gcagaagtag cagttccgga gtccagctgg ctaaaactca tcccagagga ta atg gca      178
                                         Met Ala
                                         1
acc cat gcc tta gaa atc gct ggg ctg ttt ctt ggt ggt gtt gga atg      226
Thr His Ala Leu Glu Ile Ala Gly Leu Phe Leu Gly Gly Val Gly Met
      5      10      15
gtg ggc aca gtg gct gtc act gtc atg cct cag tgg aga gtg tcg gcc      274
Val Gly Thr Val Ala Val Thr Val Met Pro Gln Trp Arg Val Ser Ala
      20      25      30
ttc att gaa aac aac atc gtg gtt ttt gaa aac ttc tgg gaa gga ctg      322
Phe Ile Glu Asn Asn Ile Val Val Phe Glu Asn Phe Trp Glu Gly Leu
      35      40      45      50
tgg atg aat tgc gtg agg cag gct aac atc agg atg cag tgc aaa atc      370
Trp Met Asn Cys Val Arg Gln Ala Asn Ile Arg Met Gln Cys Lys Ile
      55      60      65
tat gat tcc ctg ctg gct ctt tct ccg gac cta cag gca gcc aga gga      418
Tyr Asp Ser Leu Leu Ala Leu Ser Pro Asp Leu Gln Ala Ala Arg Gly
      70      75      80
ctg atg tgt gct gct tcc gtg atg tcc ttc ttg gct ttc atg atg gcc      466
Leu Met Cys Ala Ala Ser Val Met Ser Phe Leu Ala Phe Met Met Ala
      85      90      95
atc ctt ggc atg aaa tgc acc agg tgc acg ggg gac aat gag aag gtg      514
Ile Leu Gly Met Lys Cys Thr Arg Cys Thr Gly Asp Asn Glu Lys Val
      100      105      110
aag gct cac att ctg ctg acg gct gga atc atc ttc atc atc acg ggc      562
Lys Ala His Ile Leu Leu Thr Ala Gly Ile Ile Phe Ile Ile Thr Gly
      115      120      125      130
atg gtg gtg ctc atc cct gtg agc tgg gtt gcc aat gcc atc atc aga      610
Met Val Val Leu Ile Pro Val Ser Trp Val Ala Asn Ala Ile Ile Arg
      135      140      145
gat ttc tat aac tca ata gtg aat gtt gcc caa aaa cgt gag ctt gga      658
Asp Phe Tyr Asn Ser Ile Val Asn Val Ala Gln Lys Arg Glu Leu Gly
      150      155      160
gaa gct ctc tac tta gga tgg acc acg gca ctg gtg ctg att gtt gga      706
Glu Ala Leu Tyr Leu Gly Trp Thr Thr Ala Leu Val Leu Ile Val Gly
      165      170      175
gga gct ctg ttc tgc tgc gtt ttt tgt tgc aac gaa aag agc agt agc      754
Gly Ala Leu Phe Cys Cys Val Phe Cys Cys Asn Glu Lys Ser Ser Ser
      180      185      190
tac aga tac tcg ata cct tcc cat cgc aca acc caa aaa agt tat cac      802
Tyr Arg Tyr Ser Ile Pro Ser His Arg Thr Thr Gln Lys Ser Tyr His
      195      200      205      210
acc gga aag aag tca ccg agc gtc tac tcc aga agt cag tat gtg      847
Thr Gly Lys Lys Ser Pro Ser Val Tyr Ser Arg Ser Gln Tyr Val
      215      220      225
tagttgtgta tgttttttta actttactat aaagccatgc aaatgacaaa aatctatatt      907
actttctcaa aatggacccc aaagaaactt tgattttactg ttcttaactg cctaacttta      967
attacaggaa ctgtgcatca gctatttatg attctataag ctatttcagc agaatgagat      1027
attaaaccca atgctttgat tgttctagaa agtattgttaa tttgttttct aaggtgggttc      1087

```

```

aagcatctac tctttttatc atttacttca aaatgacatt gctaaagact gcattattct 1147
actactgtaa tttctccacg acatagcatt atgtacatag atgagtgtaa catttatatc 1207
tcacatagag acatgcttat atgggtttat ttaaaatgaa atgccagtc attacactga 1267
ataaatagaa ctcaactatt gcttttcagg gaaatcatgg atagggttga agaagggttac 1327
tattaattgt ttaaaaaacag cttatggatt aatgtcctcc atttataatg aagattaaaa 1387
tgaaggcttt aatcagcatt gtaaaggaaa ttgaatggct ttctgatatg ctgtttttta 1447
gcctaggagt tagaaatcct aacttcttta tctctctctc ccagaggctt tttttttctt 1507
gtgtattaaa ttaacatttt taaaaagcag atattttgtc aaggggcttt gcattcaaac 1567
tgcttttcca gggctatact cagaagaaag ataaaagtgt gatctaagaa aaagtgatgg 1627
ttttaggaaa gtgaaaatat ttttgTTTTT gtatttgaag aagaatgatg cattttgaca 1687
agaaatcata tatgtatgta tatattttta taagtatttg agtacagact ttgagggtttc 1747
atcaatataa ataaaagagc agaaaagtaa aaaaaaaaaa aaaaaa 1793

```

```

<210> 165
<211> 1849
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 8..1141

```

```

<220>
<221> misc_feature
<222> 1707
<223> n=a, g, c or t

```

```

<400> 165
cgttgcc atg gat cct ggg gac gac tgg ctg gtg gaa tcc ttg cgc ttg      49
      Met Asp Pro Gly Asp Asp Trp Leu Val Glu Ser Leu Arg Leu
      1                    5                    10
tac cag gat ttc tat gca ttc gac ctg tca gga gcc act cga gtc ctt      97
Tyr Gln Asp Phe Tyr Ala Phe Asp Leu Ser Gly Ala Thr Arg Val Leu
15                    20                    25                    30
gaa tgg att gat gac aaa gga gtc ttt gtt gct ggc tat gaa agc ctg      145
Glu Trp Ile Asp Asp Lys Gly Val Phe Val Ala Gly Tyr Glu Ser Leu
35                    40                    45
aaa aag aat gaa att ctt cat ctg aaa tta cct ctc aga ctt tct gta      193
Lys Lys Asn Glu Ile Leu His Leu Lys Leu Pro Leu Arg Leu Ser Val
50                    55                    60
aag gaa aac aag ggc tta ttc cca gaa aga gat ttc aaa gtg cgc cat      241
Lys Glu Asn Lys Gly Leu Phe Pro Glu Arg Asp Phe Lys Val Arg His
65                    70                    75
gga gga ttt tca gac agg tct atc ttt gat cta aag cat gtg cca cat      289
Gly Gly Phe Ser Asp Arg Ser Ile Phe Asp Leu Lys His Val Pro His
80                    85                    90
acc aga ttg ctg gtt acc agt ggc ctt cca ggt tgt tat ctg cag gtg      337
Thr Arg Leu Leu Val Thr Ser Gly Leu Pro Gly Cys Tyr Leu Gln Val
95                    100                    105                    110
tgg cag gtt gca gag gac agt gat gtc att aaa gct gtc agc acc att      385
Trp Gln Val Ala Glu Asp Ser Asp Val Ile Lys Ala Val Ser Thr Ile
115                    120                    125
gct gtg cat gag aaa gag gag agt ctc tgg cct agg gtg gcc gtc ttc      433
Ala Val His Glu Lys Glu Glu Ser Leu Trp Pro Arg Val Ala Val Phe
130                    135                    140
tcc aca ttg gca ccc gga gtc ctc cat ggg gcg agg ctc cga agt ctg      481
Ser Thr Leu Ala Pro Gly Val Leu His Gly Ala Arg Leu Arg Ser Leu
145                    150                    155

```

cag gtc gtt gat ctg gag tcc cgg aag acc acg tac acc tca gat gtc	529
Gln Val Val Asp Leu Glu Ser Arg Lys Thr Thr Tyr Thr Ser Asp Val	
160 165 170	
agt gac agt gag gag ctg agt agc ctg cag gtc cta gat gcg gac acc	577
Ser Asp Ser Glu Glu Leu Ser Ser Leu Gln Val Leu Asp Ala Asp Thr	
175 180 185 190	
ttt gcc ttc tgc tgt gct tcg ggc cgg ctg ggg ctt gtt gac acc cgg	625
Phe Ala Phe Cys Cys Ala Ser Gly Arg Leu Gly Leu Val Asp Thr Arg	
195 200 205	
cag aag tgg gca ccg ttg gag aat cgc agc cct ggc cct ggg tct ggt	673
Gln Lys Trp Ala Pro Leu Glu Asn Arg Ser Pro Gly Pro Gly Ser Gly	
210 215 220	
gga gag aga tgg tgt gct gaa gtt ggg agc tgg ggc cag ggc cct ggg	721
Gly Glu Arg Trp Cys Ala Glu Val Gly Ser Trp Gly Gln Gly Pro Gly	
225 230 235	
ccc agc att gcc agc ctt agc tca gat ggg cgt ctt tgt ctt ctt gac	769
Pro Ser Ile Ala Ser Leu Ser Ser Asp Gly Arg Leu Cys Leu Leu Asp	
240 245 250	
ccc cgg gat ctc tgc cat cct gtg agc tca gtc cag tgc cca gta tcc	817
Pro Arg Asp Leu Cys His Pro Val Ser Ser Val Gln Cys Pro Val Ser	
255 260 265 270	
gta cct agc cct gac cca gag ctg ctg cga gtg act tgg gcc cca ggc	865
Val Pro Ser Pro Asp Pro Glu Leu Leu Arg Val Thr Trp Ala Pro Gly	
275 280 285	
ctg aag aat tgc ttg gcc atc tca ggt ttt gat ggt aca gtc cag gtc	913
Leu Lys Asn Cys Leu Ala Ile Ser Gly Phe Asp Gly Thr Val Gln Val	
290 295 300	
tat gat gcc aca tct tgg gat gga aca cgg agc caa gat gga aca cgg	961
Tyr Asp Ala Thr Ser Trp Asp Gly Thr Arg Ser Gln Asp Gly Thr Arg	
305 310 315	
agc caa gta gaa cct ctc ttc act cac aga ggt cac atc ttc cta gat	1009
Ser Gln Val Glu Pro Leu Phe Thr His Arg Gly His Ile Phe Leu Asp	
320 325 330	
gga aat ggg atg gac cct gct cct ttg gtc acc acc cac acc tgg cat	1057
Gly Asn Gly Met Asp Pro Ala Pro Leu Val Thr Thr His Thr Trp His	
335 340 345 350	
ccc tgc aga cca agg act ttg tta tca gca aca aat gat gcc tct ctg	1105
Pro Cys Arg Pro Arg Thr Leu Leu Ser Ala Thr Asn Asp Ala Ser Leu	
355 360 365	
cat gtg tgg gac tgg gtg gac ctt tgt gcc ccc cgc tgacaccagc	1151
His Val Trp Asp Trp Val Asp Leu Cys Ala Pro Arg	
370 375	
atctttccat ctaggcctct agaaagggga ggagctgctg tagtagcaag ggtgctgatg	1211
taggactcaa gtgactacca gtccctgtta ccagctgtgt ggccttgggc aagtctgcca	1271
gcgtcactta gcctcagttt ccttatctgt aaaatgagga tagtaagaac tacctcgtag	1331
tgatattgcg aagggttagaa gaaacgcctg gcataattac ttggtagcta ttgttagatc	1391
tgggagtgtg aaatggtagc gttttgtccc tgtcttcaca ctatcatagg gagaatcaaa	1451
agagctaaca aatataaaca tgctttgtga atttttttaa agaaaaaaat gtagggggggc	1511
caataaacat gaaaaaatcc cagccctagt agcaattaag gaaatagcaa aacaggattt	1571
ctgctcctct tgaggggggtc tcatgggaac acaggtgcac tttccacac ttgtccccc	1631
aggtgactag gttcaagaga catttgcttt tgggtggcccc acaaacattt ccttttgagg	1691
gcccatagtg aatatntaaa gtgtgctgga catggtggct catgcctgta atcccagcac	1751
tttcagaggc tgaggtgggc agattgcttg agctgaggag tttgagacca gcctgggcaa	1811
catagcaaga tcccttcccc aaaaaaaaaa aaaaaaaa	1849

<210> 166  
 <211> 1748  
 <212> DNA



<213> Homo sapiens

<220>

<221> CDS

<222> 136..264

<400> 166

```

attattttgaa aaaccactgg gttccgagtt cattactaca ggaaaaaactt tctcttctgt      60
ggcacagaga accctgcttc aaagcagaag tagcagttcc ggagtccagc tggctaaaac      120
tcatcccaga ggata atg gca acc cat gcc tta gaa atc gct ggg ctg ttt      171
          Met Ala Thr His Ala Leu Glu Ile Ala Gly Leu Phe
          1          5          10
ctt ggt ggt gtt gga atg gtg ggc aca gtg gct gtc act gtc atg cct      219
Leu Gly Gly Val Gly Met Val Gly Thr Val Ala Val Thr Val Met Pro
          15          20          25
cag tgg aga gtg tcg gcc ttc att gaa aac aac atc gtg gtt ttt      264
Gln Trp Arg Val Ser Ala Phe Ile Glu Asn Asn Ile Val Val Phe
          30          35          40
taaaaacttct gggaaggact gtggatgaat tgcgtgaggc aggctaacat caggatgcag      324
tgcaaaaatct atgattccct gctggctctt tctccggacc tacaggcagc cagaggactg      384
atgtgtgctg cttccgtgat gtccttcttg gctttcatga tggccatcct tggcatgaaa      444
tgcaccaggt gcacggggga caatgagaag gtgaaggctc acattctgct gacggctgga      504
atcatcttca tcatcacggg catggtggtg ctcacccctg tgagctgggt tgccaatgcc      564
atcatcagag atttctataa ctcaatagtg aatgttgccc aaaaacgtga gcttggagaa      624
gctctctact taggatggac cacggcactg gtgctgattg ttggaggagc tctgttctgc      684
tgcgtttttt gttgcaacga aaagagcagt agctacagat actcgatacc ttcccatcgc      744
acaacccaaa aaagttatca caccggaaag aagtcaccga gcgtctactc cagaagtcag      804
tatgtgtagt tgtgtatggt tttttaactt tactataaag ccatgcaaat gacaaaaatc      864
tatattactt tctcaaaatg gaccccaaag aaactttgat ttactgttct taactgcta      924
atcttaatta caggaactgt gcatcagcta tttatgattc tataagctat ttcagcagaa      984
tgagatatta aaccgaatgc tttgattggt ctagaagta tagtaatttg ttttctaagg      1044
tggktcaagc atctactctt tttatcattt acttcaaaat gacattgcta aagactgcat      1104
tattttacta ctgtaatttc tccacgacat agcattatct acatagatga gtgtaacatt      1164
tatatctcac atagagacat gcttatatgg ttkcatttaa aatgaaatgc cagtccatta      1224
cactgaataa atagaactca actattgctt ttcagggaat tcatggatag ggttgaagaa      1284
ggttactatt aattgtttta aaacagctta gggattaatg tcctccattt ataatgaaga      1344
ttaaaatgaa ggctttaatc agcattgtaa aggaaattga atggctttct gatatgctgt      1404
tttttagcct aggagttaga aatcctaact tctttatcct cttctcccag aggctttttt      1464
tttcttgtgt attaaattaa cattttttaa aagcagatat tttgtcaagg ggctttgcat      1524
tcaaaactgct ttccagggc tatactcaga agaaagataa aagtgtgatc taagaaaaag      1584
tgatgggtttt aggaaagtga aaatatTTTT gtttttgtat ttgaagaaga atgatgcatt      1644
ttgacaagaa atcatatatg tatggatata ttttaataag tatttgagta cagactttga      1704
ggtttcatca atataaataa aagagcaaaa aaaaaaaaaa aaaa      1748

```

<210> 167

<211> 1275

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 14..1048

<400> 167

```

agagggttggg aag atg gcg tgg cga ggc tgg gcg cag aga ggc tgg ggc      49
          Met Ala Trp Arg Gly Trp Ala Gln Arg Gly Trp Gly
          1          5          10
tgc ggc cag gcg tgg ggt gcg tcg gtg ggc ggc cgc agc tgc gag gag      97

```

Cys	Gly	Gln	Ala	Trp	Gly	Ala	Ser	Val	Gly	Gly	Arg	Ser	Cys	Glu	Glu	
		15					20					25				
ctc	act	gcg	gtc	cta	acc	ccg	ccg	cag	ctc	ctc	gga	cgc	agg	ttt	aac	145
Leu	Thr	Ala	Val	Leu	Thr	Pro	Pro	Gln	Leu	Leu	Gly	Arg	Arg	Phe	Asn	
	30					35					40					
ttc	ttt	att	caa	caa	aaa	tgc	gga	ttc	aga	aaa	gca	ccc	agg	aag	gtt	193
Phe	Phe	Ile	Gln	Gln	Lys	Cys	Gly	Phe	Arg	Lys	Ala	Pro	Arg	Lys	Val	
45					50					55					60	
gaa	cct	cga	aga	tca	gac	cca	ggg	aca	agt	ggg	gaa	gca	tac	aag	aga	241
Glu	Pro	Arg	Arg	Ser	Asp	Pro	Gly	Thr	Ser	Gly	Glu	Ala	Tyr	Lys	Arg	
				65					70					75		
agt	gct	ttg	att	cct	cct	gtg	gaa	gaa	aca	gtc	ttt	tat	cct	tct	ccc	289
Ser	Ala	Leu	Ile	Pro	Pro	Val	Glu	Glu	Thr	Val	Phe	Tyr	Pro	Ser	Pro	
			80						85				90			
tat	cct	ata	agg	agt	ctc	ata	aaa	cct	tta	ttt	ttt	act	gtt	ggg	ttt	337
Tyr	Pro	Ile	Arg	Ser	Leu	Ile	Lys	Pro	Leu	Phe	Phe	Thr	Val	Gly	Phe	
	95						100					105				
aca	ggc	tgt	gca	ttt	gga	tca	gct	gct	att	tgg	caa	tat	gaa	tca	ctg	385
Thr	Gly	Cys	Ala	Phe	Gly	Ser	Ala	Ala	Ile	Trp	Gln	Tyr	Glu	Ser	Leu	
	110					115					120					
aaa	tcc	agg	gtc	cag	agt	tat	ttt	gat	ggg	ata	aaa	gct	gat	tgg	ttg	433
Lys	Ser	Arg	Val	Gln	Ser	Tyr	Phe	Asp	Gly	Ile	Lys	Ala	Asp	Trp	Leu	
125					130					135					140	
gat	agc	ata	aga	cca	caa	aaa	gaa	gga	gac	ttc	aga	aag	gag	att	aac	481
Asp	Ser	Ile	Arg	Pro	Gln	Lys	Glu	Gly	Asp	Phe	Arg	Lys	Glu	Ile	Asn	
				145					150					155		
aag	tgg	tgg	aat	aac	cta	agt	gat	ggc	cag	cgg	act	gtg	aca	ggg	att	529
Lys	Trp	Trp	Asn	Asn	Leu	Ser	Asp	Gly	Gln	Arg	Thr	Val	Thr	Gly	Ile	
			160					165					170			
ata	gct	gca	aat	gtc	ctt	gta	ttc	tgt	tta	tgg	aga	gta	cct	tct	ctg	577
Ile	Ala	Ala	Asn	Val	Leu	Val	Phe	Cys	Leu	Trp	Arg	Val	Pro	Ser	Leu	
			175				180					185				
cag	cgg	aca	atg	atc	aga	tat	ttc	aca	tcg	aat	cca	gcc	tca	aag	gtc	625
Gln	Arg	Thr	Met	Ile	Arg	Tyr	Phe	Thr	Ser	Asn	Pro	Ala	Ser	Lys	Val	
	190					195				200						
ctt	tgt	tct	cca	atg	ttg	ctg	tca	aca	ttc	agt	cat	ttc	tcc	tta	ttt	673
Leu	Cys	Ser	Pro	Met	Leu	Leu	Ser	Thr	Phe	Ser	His	Phe	Ser	Leu	Phe	
205					210					215					220	
cac	atg	gca	gca	aat	atg	tat	gtt	ttg	tgg	agc	ttc	tct	tcc	agc	ata	721
His	Met	Ala	Ala	Asn	Met	Tyr	Val	Leu	Trp	Ser	Phe	Ser	Ser	Ser	Ile	
				225					230					235		
gtg	aac	att	ctg	ggg	caa	gag	cag	ttc	atg	gca	gtg	tac	cta	tct	gca	769
Val	Asn	Ile	Leu	Gly	Gln	Glu	Gln	Phe	Met	Ala	Val	Tyr	Leu	Ser	Ala	
			240					245					250			
ggg	gtt	att	tcc	aat	ttt	gtc	agt	tac	gtg	ggg	aaa	gtt	gcc	aca	gga	817
Gly	Val	Ile	Ser	Asn	Phe	Val	Ser	Tyr	Val	Gly	Lys	Val	Ala	Thr	Gly	
		255				260						265				
aga	tat	gga	cca	tca	ctt	ggg	gca	gcc	ctg	aaa	gcc	att	atc	gcc	atg	865
Arg	Tyr	Gly	Pro	Ser	Leu	Gly	Ala	Ala	Leu	Lys	Ala	Ile	Ile	Ala	Met	
	270					275					280					
gat	aca	gca	gga	atg	atc	ctg	gga	tgg	aaa	ttt	ttt	gat	cat	gcg	gca	913
Asp	Thr	Ala	Gly	Met	Ile	Leu	Gly	Trp	Lys	Phe	Phe	Asp	His	Ala	Ala	
285					290					295					300	
cat	ctt	ggg	gga	gct	ctt	ttt	gga	ata	tgg	tat	gtt	act	tac	ggg	cat	961
His	Leu	Gly	Gly	Ala	Leu	Phe	Gly	Ile	Trp	Tyr	Val	Thr	Tyr	Gly	His	
				305					310					315		
gaa	ctg	att	tgg	aag	aac	agg	gag	ccg	cta	gtg	aaa	atc	tgg	cat	gaa	1009
Glu	Leu	Ile	Trp	Lys	Asn	Arg	Glu	Pro	Leu	Val	Lys	Ile	Trp	His	Glu	



```

195      200      205
gcc ctc acc tac ata gtg gct ctc cta tac gaa gag ccc ttc acc gct 735
Ala Leu Thr Tyr Ile Val Ala Leu Leu Tyr Glu Glu Pro Phe Thr Ala
      210      215      220
gag atc tac cgg cag aaa gcc tcc ggg tcc cac aag agg agc 777
Glu Ile Tyr Arg Gln Lys Ala Ser Gly Ser His Lys Arg Ser
      225      230      235
tgattgagct gcaacagctt tgctgaaggc ctggccagcc tcttgacctg cccaagtgg 837
caggccctgc gcagggcgag aatggtgcct gctgctcagg gctcgcccc ggctgtgggt 897
gccccagtgc cttggaacct gctgccttgg ggaccctgga cgtgccgaca tatggccatt 957
gagctccaac ccacacattc ccattcacca ataaaggcac cctgacctca aaaaaaaaaa 1017
aaaaaa 1023

<210> 169
<211> 1085
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 38..400

<400> 169
aacaattcat gaagttgaag aaaagacact gtcagaa atg aac aca gaa gcg gag 55
Met Asn Thr Glu Ala Glu
      1      5
caa cag ctt ctc cat cac gcc aga aat ggc aat gct gaa gaa gta aga 103
Gln Gln Leu Leu His His Ala Arg Asn Gly Asn Ala Glu Glu Val Arg
      10      15      20
caa cta tta gag acc atg gcg agt aat gaa gtg att gct gac att aat 151
Gln Leu Leu Glu Thr Met Ala Ser Asn Glu Val Ile Ala Asp Ile Asn
      25      30      35
tgc aaa gga aga agt aag tct aac ttg ggc tgg aca ccc cta cat ctg 199
Cys Lys Gly Arg Ser Lys Ser Asn Leu Gly Trp Thr Pro Leu His Leu
      40      45      50
gca tgc tat ttt gga cac aga caa gtg gtc cag gat ctg ttg aag gct 247
Ala Cys Tyr Phe Gly His Arg Gln Val Val Gln Asp Leu Leu Lys Ala
      55      60      65      70
ggg gca gaa gtg aat gtg ttg aat gac atg gga gac acg ccg ctt cat 295
Gly Ala Glu Val Asn Val Leu Asn Asp Met Gly Asp Thr Pro Leu His
      75      80      85
cga gct gcc ttt aca gga cga aag gtg aaa atc att cta tgt tca atg 343
Arg Ala Ala Phe Thr Gly Arg Lys Val Lys Ile Ile Leu Cys Ser Met
      90      95      100
ttt gta agt gag gta ttt gga gga gta gtt acc att gtt ttc tct gtt 391
Phe Val Ser Glu Val Phe Gly Gly Val Val Thr Ile Val Phe Ser Val
      105      110      115
ata acc atc tgaccagcaa ccgaagaaag ccacacaaaa aaatgtatac 440
Ile Thr Ile
      120
accagcactt tgggtcaaaa ggccacagga tcttttgagt ctgacagtga ggtccagtac 500
taagggtcatg gagaccccc ctctgtagca tccctgtgag gagatcattc cgtttctgct 560
tgtgtactcc agcaatgggg aactcctgat tattcttttt ttttaaaaaa aaatagcttc 620
attgaggtat aacttacatt gcataaactt cacctgtgat attgtgaaat atatatttgg 680
tctttgacct tgtacactaa agatgtacaa aaagatgact ggcaaccctt ggcttcagga 740
tgggggctgg tcaccagaaa gaccaaggca ggactagggg gttgggactt tcagccgaac 800
tttgcaacct ccagggaggg tagaggggct gaaggggaaa tggctcgcta atggccagtg 860
gtttcatcaa tcatgcctat ttaatggaac ctccataaaa acctgaaagg acagggttct 920

```

aggagctcct gggtagctga acacgtggag gttcttgaat gatcacaccc agggagggca 980  
 tgggtgctct gtgcccttcc tccatgcctt gctttatgta tctcttcac tgtatccttt 1040  
 gtaataaagc agtaaacatg ttttctgaa aaaaaaaaaa aaaaa 1085

<210> 170  
 <211> 776  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 63..572

<400> 170  
 atatgtcatc aggccccccg cctgggaggt gtgctgccag agattttgcc tcttcaaggt 60  
 ga atg cgg ctt caa ggg gct atc ttt gtg ctc ctg ccc cac ctg ggg 107  
 Met Arg Leu Gln Gly Ala Ile Phe Val Leu Leu Pro His Leu Gly  
 1 5 10 15  
 ccc atc ctg gtc tgg ctg ttc act cgt gat cac atg tct ggt tgg tgt 155  
 Pro Ile Leu Val Trp Leu Phe Thr Arg Asp His Met Ser Gly Trp Cys  
 20 25 30  
 gag ggc ccg agg atg ctg tcc tgg tgc cca ttc tac aaa gtc tta ttg 203  
 Glu Gly Pro Arg Met Leu Ser Trp Cys Pro Phe Tyr Lys Val Leu Leu  
 35 40 45  
 ctt gta cag aca gcc atc tac tct gtc gtg ggc tat gcc tcc tac ctg 251  
 Leu Val Gln Thr Ala Ile Tyr Ser Val Val Gly Tyr Ala Ser Tyr Leu  
 50 55 60  
 gtg tgg aag gac ctg gga ggg ggc ttg ggg tgg ccc ctg gcc ctg cct 299  
 Val Trp Lys Asp Leu Gly Gly Gly Leu Gly Trp Pro Leu Ala Leu Pro  
 65 70 75  
 ctt ggc ctc tat gct gtt cag ctc acc atc agc tgg act gtc ctg gtt 347  
 Leu Gly Leu Tyr Ala Val Gln Leu Thr Ile Ser Trp Thr Val Leu Val  
 80 85 90 95  
 ctc ttt ttc aca gtc cac aac cct ggt ctg gcc ctg ctg cac ctg ctg 395  
 Leu Phe Phe Thr Val His Asn Pro Gly Leu Ala Leu Leu His Leu Leu  
 100 105 110  
 ctg ctg tat ggg ctg gtg gtg agc aca gca ctg atc tgg cat ccc atc 443  
 Leu Leu Tyr Gly Leu Val Val Ser Thr Ala Leu Ile Trp His Pro Ile  
 115 120 125  
 aac aaa ctg gct gcc ctg tta ctg ctg ccc tac cta gcc tgg ctc acc 491  
 Asn Lys Leu Ala Ala Leu Leu Leu Leu Pro Tyr Leu Ala Trp Leu Thr  
 130 135 140  
 gtg act tca gcc ctc acc tac cac ctg tgg agg gac agc ctt tgt cca 539  
 Val Thr Ser Ala Leu Thr Tyr His Leu Trp Arg Asp Ser Leu Cys Pro  
 145 150 155  
 gtg cac cag cct cag ccc acg gag aag agt gac tgaggcccta gggcatggga 592  
 Val His Gln Pro Gln Pro Thr Glu Lys Ser Asp  
 160 165 170  
 gaggagggac gccaggggtg gggaggaaga gtctgcaagc agggctgtgg agttaggggtt 652  
 caccccaatg ggaccaccct cctgggtccc ctggtgccgt ttttccttag aaatcagaga 712  
 aatgggaaag ggggggaaac tgattttaca cttaaataat aaaatcctat tagcaaaaaa 772  
 aaaa 776

<210> 171  
 <211> 1219  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 160..867

<400> 171

```

gtagtttagga gtctggagtc gtgagccgga gtcagaactg cgtctcgcga cccagggcgcg      60
ggtttccgga ggacagccaa caagcgatgc tgccgccgcc gtttcctgat tggttgtggg      120
tggctacctc ttcgttctga ttggccgcta gtgagcaag atg ctg agc aag ggt      174
                               Met Leu Ser Lys Gly
                               1       5
ctg aag cgg aaa cgg gag gag gag gag gag aag gaa cct ctg gca gtc      222
Leu Lys Arg Lys Arg Glu Glu Glu Glu Glu Glu Lys Glu Pro Leu Ala Val
                               10      15      20
gac tcc tgg tgg cta gat cct ggc cac aca gcg gtg gca cag gca ccc      270
Asp Ser Trp Trp Leu Asp Pro Gly His Thr Ala Val Ala Gln Ala Pro
                               25      30      35
ccg gcc gtg gcc tct agc tcc ctc ttt gac ctc tca gtg ctc aag ctc      318
Pro Ala Val Ala Ser Ser Ser Leu Phe Asp Leu Ser Val Leu Lys Leu
                               40      45      50
cac cac agc ctg cag cag agt gag ccg gac ctg cgg cac ctg gtg ctg      366
His His Ser Leu Gln Gln Ser Glu Pro Asp Leu Arg His Leu Val Leu
                               55      60      65
gtc gtg aac act ctg cgg cgc atc cag gcg tcc atg gca ccc gcg gct      414
Val Val Asn Thr Leu Arg Arg Ile Gln Ala Ser Met Ala Pro Ala Ala
                               70      75      80      85
gcc ctg cca cct gtg cct agc cca cct gca gcc ccc agt gtg gct gac      462
Ala Leu Pro Pro Val Pro Ser Pro Pro Ala Ala Pro Ser Val Ala Asp
                               90      95      100
aac tta ctg gca agc tcg gac gct gcc ctt tca gcc tcc atg gcc agc      510
Asn Leu Leu Ala Ser Ser Asp Ala Ala Leu Ser Ala Ser Met Ala Ser
                               105     110     115
ctc ctg gag gac ctc agc cac att gag ggc ctg agt cag gct ccc caa      558
Leu Leu Glu Asp Leu Ser His Ile Glu Gly Leu Ser Gln Ala Pro Gln
                               120     125     130
ccc ttg gca gac gag ggg cca cca ggc cgt agc atc ggg gga gca gcg      606
Pro Leu Ala Asp Glu Gly Pro Pro Gly Arg Ser Ile Gly Gly Ala Ala
                               135     140     145
ccc agc ctg ggt gcc ttg gac ctg ctg ggc cca gcc act ggc tgt cta      654
Pro Ser Leu Gly Ala Leu Asp Leu Leu Gly Pro Ala Thr Gly Cys Leu
                               150     155     160     165
ctg gac gat ggg ctt gag ggc ctg ttt gag gat att gac acc tct atg      702
Leu Asp Asp Gly Leu Glu Gly Leu Phe Glu Asp Ile Asp Thr Ser Met
                               170     175     180
tat gac aat gaa ctt tgg gca cca gcc tct gag ggc ctc aaa cca ggc      750
Tyr Asp Asn Glu Leu Trp Ala Pro Ala Ser Glu Gly Leu Lys Pro Gly
                               185     190     195
cct gag gat ggg ccg ggc aag gag gaa gct ccg gag ctg gac gag gcc      798
Pro Glu Asp Gly Pro Gly Lys Glu Glu Ala Pro Glu Leu Asp Glu Ala
                               200     205     210
gaa ttg gac tac ctc atg gat gtg ctg gtg ggc aca cag gca ctg gag      846
Glu Leu Asp Tyr Leu Met Asp Val Leu Val Gly Thr Gln Ala Leu Glu
                               215     220     225
cga ccg ccg ggg cca ggg cgc tgagccctcg tgctggaatg gttgtctggt      897
Arg Pro Pro Gly Pro Gly Arg
                               230     235
atctgaactg agcctgctgg ctggaccaac tgtcctcgaa aagacacagc tggtttccct      957
agtacagaga acagggcttg ggccactttg gagagacaga atctagtcct gggcaacttc      1017
acatccgtcc tctgtctca gggctggcag ggggagcctg gaattacccc ctagtgatgg      1077

```

aatgacaggg tctggtgggg acttaattcc ctggccctgg ggtcatagct tgggctgttc 1137  
 cttctctgat acgggaagag accccaatca gatttttcaa attaaagcca gtccctgggaa 1197  
 atctcaaaaa aaaaaaaaaa aa 1219

<210> 172  
 <211> 1487  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 68..640

<400> 172  
 gacgaaggac tggaagggtgg cggtggtgaa ggtgcaggcc gttggggcgg ctcagaggca 60  
 ggtgact atg aaa ggc tta tat ttc caa cag agt tcc aca gat gaa gaa 109  
     Met Lys Gly Leu Tyr Phe Gln Gln Ser Ser Thr Asp Glu Glu  
     1                    5                    10  
 ata aca ttt gta ttt caa gaa aag gaa gat ctt cct gtt aca gag gat 157  
 Ile Thr Phe Val Phe Gln Glu Lys Glu Asp Leu Pro Val Thr Glu Asp  
 15                    20                    25                    30  
 aac ttt gtg aaa ctt caa gtt aaa gct tgt gct ctg agc cag ata aat 205  
 Asn Phe Val Lys Leu Gln Val Lys Ala Cys Ala Leu Ser Gln Ile Asn  
                     35                    40                    45  
 aca aag ctt ctg gca gaa atg aag atg aaa aag gat tta ttt cct gtt 253  
 Thr Lys Leu Leu Ala Glu Met Lys Met Lys Lys Asp Leu Phe Pro Val  
                     50                    55                    60  
 ggg aga gaa att gct gga att gta tta gat gtt gga agc aag gta tca 301  
 Gly Arg Glu Ile Ala Gly Ile Val Leu Asp Val Gly Ser Lys Val Ser  
                     65                    70                    75  
 ttc ttt caa cca gat gat gaa gta gtt gga att ttg ccc ctg gac tct 349  
 Phe Phe Gln Pro Asp Asp Glu Val Val Gly Ile Leu Pro Leu Asp Ser  
                     80                    85                    90  
 gaa gac cct gga ctt tgt gaa gtt gtt aga gta cat gag cat tac ttg 397  
 Glu Asp Pro Gly Leu Cys Glu Val Val Arg Val His Glu His Tyr Leu  
                     95                    100                    105                    110  
 gtt cat aaa cca gaa aag gtc aca tgg acg gaa gca gca gga agc att 445  
 Val His Lys Pro Glu Lys Val Thr Trp Thr Glu Ala Ala Gly Ser Ile  
                     115                    120                    125  
 cgg gat gga gtg cgt gcc tat aca gct ctg cat tat ctt tct cat ctc 493  
 Arg Asp Gly Val Arg Ala Tyr Thr Ala Leu His Tyr Leu Ser His Leu  
                     130                    135                    140  
 tct cct gga aaa tca gtg ctg ata atg gat gga gca agt gca ttt ggt 541  
 Ser Pro Gly Lys Ser Val Leu Ile Met Asp Gly Ala Ser Ala Phe Gly  
                     145                    150                    155  
 aca ata gct att cag tta gca cat cat aga gga gcc aaa gta ttt caa 589  
 Thr Ile Ala Ile Gln Leu Ala His His Arg Gly Ala Lys Val Phe Gln  
                     160                    165                    170  
 cag cat gca gcc ttg aag ata agc agt gcc ttg aaa gat tca gac ctc 637  
 Gln His Ala Ala Leu Lys Ile Ser Ser Ala Leu Lys Asp Ser Asp Leu  
                     175                    180                    185                    190  
 cca tagcccgagt gattgatgta tctaattggga aagttcatgt tgctgaaagc 690  
 Pro  
 tgtttggaag aaacagggtgg cctgggagta gatattgtcc tagatgctgg agtgagatta 750  
 tatagtaaag atgatgaacc agctgtaaaa ctacaactac taccacataa acatgatatac 810  
 atcacattc ttggtgttgg aggccactgg gtaacaacag aagaaaacct tcagttggat 870  
 cctccagata gccactgcct ttctctcaag ggagcaacgt tagctttcct gaatgatgaa 930  
 gtttggaatt tgtcaaatgt acaacaggga aaatatcttt gtatcttaaa ggatgtgatg 990





ttc tac aca tca cac tgc gtc agc gcc agc tgc cgg cac gaa tac ccg	746
Phe Tyr Thr Ser His Cys Val Ser Ala Ser Cys Arg His Glu Tyr Pro	
190 195 200 205	
cta agc tgg atg aaa gag aag atc ttc tct gag gtg acg ccc aag tgt	794
Leu Ser Trp Met Lys Glu Lys Ile Phe Ser Glu Val Thr Pro Lys Cys	
210 215 220	
gaa gac tgt cag agc ctg gtg aag cct gat atc gtc ttt ttt ggt gag	842
Glu Asp Cys Gln Ser Leu Val Lys Pro Asp Ile Val Phe Phe Gly Glu	
225 230 235	
agc ctc cca gcg cgt ttc ttc tcc tgt atg cag tca gac ttc ctg aag	890
Ser Leu Pro Ala Arg Phe Phe Ser Cys Met Gln Ser Asp Phe Leu Lys	
240 245 250	
gtg gac ctc ctc ctg gtc atg ggt acc tcc ttg cag gtg cag ccc ttt	938
Val Asp Leu Leu Leu Val Met Gly Thr Ser Leu Gln Val Gln Pro Phe	
255 260 265	
gcc tcc ctc atc agc aag gca ccc ctc tcc acc cct cgc ctg ctc atc	986
Ala Ser Leu Ile Ser Lys Ala Pro Leu Ser Thr Pro Arg Leu Leu Ile	
270 275 280 285	
aac aag gag aaa gct ggc cag tcg gac cct ttc ctg ggg atg att atg	1034
Asn Lys Glu Lys Ala Gly Gln Ser Asp Pro Phe Leu Gly Met Ile Met	
290 295 300	
ggc ctc gga gga ggc atg gac ttt gac tcc aag aag gcc tac agg gag	1082
Gly Leu Gly Gly Met Asp Phe Asp Ser Lys Lys Ala Tyr Arg Asp	
305 310 315	
gtg gcc tgg ctg ggt gaa tgc gac cag ggc tgc ctg gcc ctt gct gag	1130
Val Ala Trp Leu Gly Glu Cys Asp Gln Gly Cys Leu Ala Leu Ala Glu	
320 325 330	
ctc ctt gga tgg aag aag gag ctg gag gac ctt gtc cgg agg gag cac	1178
Leu Leu Gly Trp Lys Lys Glu Leu Glu Asp Leu Val Arg Arg Glu His	
335 340 345	
gcc agc ata gat gcc cag tcg ggg gcg ggg gtc ccc aac ccc agc act	1226
Ala Ser Ile Asp Ala Gln Ser Gly Ala Gly Val Pro Asn Pro Ser Thr	
350 355 360 365	
tca gct tcc ccc aag aag tcc ccg cca cct gcc aag gac gag gcc agg	1274
Ser Ala Ser Pro Lys Lys Ser Pro Pro Pro Ala Lys Asp Glu Ala Arg	
370 375 380	
aca aca gag agg gag aaa ccc cag tgacagctgc atctcccagg cgggatgccg	1328
Thr Thr Glu Arg Glu Lys Pro Gln	
385	
agctcctcag ggacagctga gcccacccg ggccctggccc cctctttaacc agcagttctt	1388
gtctggggag ctcagaacat cccccaatct cttacagctc cctccccaaa actgggggtcc	1448
cagcaaccct ggcccccaac cccagcaaat ctctaaccac tcctagaggc caaggcttaa	1508
acaggcatct ctaccagccc cactgtctct aaccactcct gggctaagga gtaacctccc	1568
tcatctctaa ctgccccccac gggggccaggg ctaccccaga actttttaact cttccaggac	1628
agggagcttc gggccccccac tctgtctcct gccccgggg gcctgtgggt aagtaaacca	1688
tacctaacct accccagtgt ggggtgtgggc ctctgaatct aaccacaccc cagcgtaggg	1748
ggagtctgag ccgggagggc tcccagatct ctgccttcag ctcccaaagt ggggtggggg	1808
cccccttcac gtgggaccca cttcccatgc tggatgggca gaagacattg cttattggag	1868
acaaattaaa aacaaaaaca actaacaag aaaaaaaaa aaaaaaa	1915

<210> 174

<211> 1990

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 259..1701

```

<400> 174
ttagaacatc ytaatcaaaa aatttttggtg cgagagaaac aataggacgg aaacgccgag      60
gaacccgggt gaggcggcag cttcctaggt gacagacagg tacactgtat gctagccctg      120
tatctgtctg agcagtggaa tgtgccagga aagaaggagc aaccactgac tgatgaacct      180
ttgccagtct cccttccaag agggatgccg gagccttctg taagctcctc agatgtcact      240
ggatcttagg caacagggg atg agc ctg aac ctc cct gag gcc agc tta ctt      291
                Met Ser Leu Asn Leu Pro Glu Ala Ser Leu Leu
                1          5          10

agc aga gca tcc tgg cca gaa caa gcc aag gag cca aga cga gag gga      339
Ser Arg Ala Ser Trp Pro Glu Gln Ala Lys Glu Pro Arg Arg Glu Gly
                15          20          25

cac acg gac aaa caa cag aca gaa gac gta ctg gcc gct gga ctc cgc      387
His Thr Asp Lys Gln Gln Thr Glu Asp Val Leu Ala Ala Gly Leu Arg
                30          35          40

tgc ctc ccc cat ctc ccc gcc atc tgc gcc cgg agg atg agc cca gcc      435
Cys Leu Pro His Leu Pro Ala Ile Cys Ala Arg Arg Met Ser Pro Ala
                45          50          55

ttc agg gcc atg gat gtg gag ccc cgc gca aaa ggc gtc ctt ctg gag      483
Phe Arg Ala Met Asp Val Glu Pro Arg Ala Lys Gly Val Leu Leu Glu
        60          65          70          75

ccc ttt gtc cac cag gtc ggg ggg cac tca tgc gtg ctc cgc ttc aat      531
Pro Phe Val His Gln Val Gly Gly His Ser Cys Val Leu Arg Phe Asn
                80          85          90

gag aca acc ctg tgc aag ccc ctg gtc cca agg gaa cat cag ttc tac      579
Glu Thr Thr Leu Cys Lys Pro Leu Val Pro Arg Glu His Gln Phe Tyr
                95          100          105

gag acc ctc cct gct gag atg cgc aaa ttc act ccc cag tac aaa ggt      627
Glu Thr Leu Pro Ala Glu Met Arg Lys Phe Thr Pro Gln Tyr Lys Gly
                110          115          120

gtg gta tct gtg cgc ttt gaa gaa gat gaa gac agg aac ttg tgt cta      675
Val Val Ser Val Arg Phe Glu Glu Asp Glu Asp Arg Asn Leu Cys Leu
                125          130          135

ata gca tat cca ttg aaa ggg gac cat gga att gtg gac att gta gat      723
Ile Ala Tyr Pro Leu Lys Gly Asp His Gly Ile Val Asp Ile Val Asp
        140          145          150          155

aat tca gac tgt gaa cca aaa agt aag ctc cta agg tgg aca aca aac      771
Asn Ser Asp Cys Glu Pro Lys Ser Lys Leu Leu Arg Trp Thr Thr Asn
                160          165          170

aaa aaa cat cat gtc tta gaa aca gaa aag acc cct aag gac tgg gtg      819
Lys Lys His His Val Leu Glu Thr Glu Lys Thr Pro Lys Asp Trp Val
                175          180          185

cgt cag cac cgt aaa gag gag aaa atg aag agc cat aag tta gaa gaa      867
Arg Gln His Arg Lys Glu Glu Lys Met Lys Ser His Lys Leu Glu Glu
                190          195          200

gaa ttt gag tgg cta aag aaa tct gaa gtc ttg tac tac act gta gag      915
Glu Phe Glu Trp Leu Lys Lys Ser Glu Val Leu Tyr Tyr Thr Val Glu
        205          210          215

aag aag ggg aat ata agt tcc cag ctt aaa cac tat aac cct tgg agc      963
Lys Lys Gly Asn Ile Ser Ser Gln Leu Lys His Tyr Asn Pro Trp Ser
        220          225          230          235

atg aaa tgt cac cag caa cag tta cag aga atg aag gag aat gca aag      1011
Met Lys Cys His Gln Gln Gln Leu Gln Arg Met Lys Glu Asn Ala Lys
                240          245          250

cat cgg aac cag tac aaa ttt atc tta ctg gaa aac ctg act tcc cgc      1059
His Arg Asn Gln Tyr Lys Phe Ile Leu Leu Glu Asn Leu Thr Ser Arg
                255          260          265

tat gag gtg cct tgt gtc ctt gac ctc aag atg ggc aca cga caa cat      1107

```

00876997.060801

Tyr	Glu	Val	Pro	Cys	Val	Leu	Asp	Leu	Lys	Met	Gly	Thr	Arg	Gln	His		
		270					275					280					
ggt	gat	gat	gct	tca	gag	gag	aag	gca	gcc	aac	cag	atc	cga	aaa	tgt	1155	
Gly	Asp	Asp	Ala	Ser	Glu	Glu	Lys	Ala	Ala	Asn	Gln	Ile	Arg	Lys	Cys		
	285					290					295						
cag	cag	agc	aca	tct	gca	gtc	att	ggt	gtg	cgt	gtg	tgt	ggc	atg	cag	1203	
Gln	Gln	Ser	Thr	Ser	Ala	Val	Ile	Gly	Val	Arg	Val	Cys	Gly	Met	Gln		
300					305					310					315		
gtg	tac	caa	gca	ggc	agt	ggg	cag	ctc	atg	ttc	atg	aac	aag	tac	cat	1251	
Val	Tyr	Gln	Ala	Gly	Ser	Gly	Gln	Leu	Met	Phe	Met	Asn	Lys	Tyr	His		
				320					325						330		
gga	cgg	aag	cta	tcg	gtg	cag	ggc	ttc	aag	gag	gca	ctt	ttc	cag	ttc	1299	
Gly	Arg	Lys	Leu	Ser	Val	Gln	Gly	Phe	Lys	Glu	Ala	Leu	Phe	Gln	Phe		
			335					340					345				
ttc	cac	aat	ggg	cgg	tac	ctg	cgc	cgt	gaa	ctc	ctg	ggc	cct	gtg	ctc	1347	
Phe	His	Asn	Gly	Arg	Tyr	Leu	Arg	Arg	Glu	Leu	Leu	Gly	Pro	Val	Leu		
			350				355						360				
aag	aag	ctg	act	gag	ctc	aag	gca	gtg	ttg	gag	cga	cag	gag	tcc	tac	1395	
Lys	Lys	Leu	Thr	Glu	Leu	Lys	Ala	Val	Leu	Glu	Arg	Gln	Glu	Ser	Tyr		
			365			370					375						
cgc	ttc	tac	tca	agc	tcc	ctg	ctg	gtc	att	tat	gat	ggc	aag	gag	cgg	1443	
Arg	Phe	Tyr	Ser	Ser	Ser	Leu	Leu	Val	Ile	Tyr	Asp	Gly	Lys	Glu	Arg		
380					385					390					395		
ccc	gaa	gtg	gtc	ctg	gac	tca	gat	gct	gag	gat	ttg	gag	gac	ctg	tca	1491	
Pro	Glu	Val	Val	Leu	Asp	Ser	Asp	Ala	Glu	Asp	Leu	Glu	Asp	Leu	Ser		
				400				405						410			
gag	gaa	tca	gct	gat	gag	tct	gct	ggt	gcc	tat	gcc	tac	aaa	ccc	atc	1539	
Glu	Glu	Ser	Ala	Asp	Glu	Ser	Ala	Gly	Ala	Tyr	Ala	Tyr	Lys	Pro	Ile		
			415					420					425				
ggc	gcc	agc	tct	gta	gat	gtg	cgc	atg	atc	gac	ttt	gca	cac	acc	acc	1587	
Gly	Ala	Ser	Ser	Val	Asp	Val	Arg	Met	Ile	Asp	Phe	Ala	His	Thr	Thr		
			430				435					440					
tgc	agg	ctg	tat	ggc	gag	gac	acc	gtg	gtg	cat	gag	ggc	cag	gat	gct	1635	
Cys	Arg	Leu	Tyr	Gly	Glu	Asp	Thr	Val	Val	His	Glu	Gly	Gln	Asp	Ala		
			445			450					455						
ggc	tat	atc	ttc	ggg	ctc	cag	agc	ctg	ata	gac	att	gtc	aca	gag	ata	1683	
Gly	Tyr	Ile	Phe	Gly	Leu	Gln	Ser	Leu	Ile	Asp	Ile	Val	Thr	Glu	Ile		
460					465				470						475		
agt	gag	gag	agt	ggg	gag	tgagcttgct	agctgctcca	gtacttgaga								1731	
Ser	Glu	Glu	Ser	Gly	Glu												
				480													
gcgactctgt	gtccccaggma	cagctgtgct	gcgtcaggga	ggaagccagt	atggccaggt											1791	
ggtggctcct	gcagcctgga	gctgatgtgc	agtggcctct	gtgagcccca	gcctgagcca											1851	
gtcccagctg	tgcttgaggt	ctttatttat	tttaactatt	tcttcaacat	tccacatttg											1911	
atgatgatac	ctctttcttc	cctgagtgtg	tatgttctaa	tacaaatctt	tttgtttatt											1971	
ataaaaaaaaa	aaaaaaaaaa															1990	

<210> 175

<211> 1971

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 213..1274

<400> 175

ttcagcccca gccagatccc gcgtcaacgg acgcggaacg gcggaccccg taccttgga

60

gcacgcggagc accggcgggt gaaggcaagg tccctggact ggtcatatac ctcttgtggc	120
cctggcagaa tcaagatgag gccctgtcat gccctcccag tgaggcctac agtctgagca	180
gacagcatgg cctgccactg gcagtgaaca cc atg tct gca gga ggt ggc cgg	233
Met Ser Ala Gly Gly Arg	
1 5	
gcc ttt gct tgg caa gtg ttc ccc ccc atg ccc act tgc cgg gtc tat	281
Ala Phe Ala Trp Gln Val Phe Pro Pro Met Pro Thr Cys Arg Val Tyr	
10 15 20	
ggc aca gtg gca cac caa gat ggg cac ctg ctg gtg ttg ggg ggt tgt	329
Gly Thr Val Ala His Gln Asp Gly His Leu Leu Val Leu Gly Gly Cys	
25 30 35	
ggc cgg gct gga ctg ccc ctg gac act gct gag aca ctg gac atg gcc	377
Gly Arg Ala Gly Leu Pro Leu Asp Thr Ala Glu Thr Leu Asp Met Ala	
40 45 50 55	
tcg cac aca tgg ctg gca ctg gca ccc ctg ccc act gcc cgg gct ggt	425
Ser His Thr Trp Leu Ala Leu Ala Pro Leu Pro Thr Ala Arg Ala Gly	
60 65 70	
gca gct gcg gta gtt ctg ggc aag cag gtg cta gtg gtg ggt ggt gtg	473
Ala Ala Ala Val Val Leu Gly Lys Gln Val Leu Val Val Gly Gly Val	
75 80 85	
gat gag gtc cag agc ccg gta gct gct gta gag gcc ttc ctg atg gat	521
Asp Glu Val Gln Ser Pro Val Ala Ala Val Glu Ala Phe Leu Met Asp	
90 95 100	
gag ggc cgc tgg gag cgt cgg gcc acc ctc cct caa gca gcc atg ggg	569
Glu Gly Arg Trp Glu Arg Arg Ala Thr Leu Pro Gln Ala Ala Met Gly	
105 110 115	
gtt gca act gtg gag aga gat ggt atg gtg tat gct ctg ggg gga atg	617
Val Ala Thr Val Glu Arg Asp Gly Met Val Tyr Ala Leu Gly Gly Met	
120 125 130 135	
ggc cct gac acg gcc ccc cag gcc cag gta cgt gtg tat gag ccc cgt	665
Gly Pro Asp Thr Ala Pro Gln Ala Gln Val Arg Val Tyr Glu Pro Arg	
140 145 150	
cgg gac tgc tgg ctt tcg cta ccc tcc atg ccc aca ccc tgc tat ggg	713
Arg Asp Cys Trp Leu Ser Leu Pro Ser Met Pro Thr Pro Cys Tyr Gly	
155 160 165	
gcc tcc acc ttc ctg cac ggg aac aag atc tat gtc ctg ggg ggc cgc	761
Ala Ser Thr Phe Leu His Gly Asn Lys Ile Tyr Val Leu Gly Gly Arg	
170 175 180	
cag ggc aag ctc ccg gtg act gct ttt gaa gcc ttt gat ctg gag gcc	809
Gln Gly Lys Leu Pro Val Thr Ala Phe Glu Ala Phe Asp Leu Glu Ala	
185 190 195	
cgt aca tgg acc cgg cat cca agc cta ccc agc cgt cgg gcc ttt gct	857
Arg Thr Trp Thr Arg His Pro Ser Leu Pro Ser Arg Arg Ala Phe Ala	
200 205 210 215	
ggc tgc gcc atg gct gaa ggc agc gtc ttt agc ctg ggt ggc ctg cag	905
Gly Cys Ala Met Ala Glu Gly Ser Val Phe Ser Leu Gly Gly Leu Gln	
220 225 230	
cag cct ggg ccc cac aac ttc tac tct cgc cca cac ttt gtc aac act	953
Gln Pro Gly Pro His Asn Phe Tyr Ser Arg Pro His Phe Val Asn Thr	
235 240 245	
gtg gag atg ttt gac ctg gag cat ggg tcc tgg acc aaa ttg ccc cgc	1001
Val Glu Met Phe Asp Leu Glu His Gly Ser Trp Thr Lys Leu Pro Arg	
250 255 260	
agc ctg cgc atg agg gat aag agg gca gac ttt gtg gtt ggg tcc ctt	1049
Ser Leu Arg Met Arg Asp Lys Arg Ala Asp Phe Val Val Gly Ser Leu	
265 270 275	
ggg ggc cac att gtg gcc att ggg ggc ctt gga aac cag cca tgt cct	1097
Gly Gly His Ile Val Ala Ile Gly Gly Leu Gly Asn Gln Pro Cys Pro	

280	285	290	295	
ttg ggc tct gtg gag agc ttt agc ctt gca cgg cgg cgc tgg gag gca				1145
Leu Gly Ser Val Glu Ser Phe Ser Leu Ala Arg Arg Arg Trp Glu Ala				
	300	305	310	
ttg cct gcc atg ccc act gcc cgc tgc tcc tgc tct agt ctg cag gct				1193
Leu Pro Ala Met Pro Thr Ala Arg Cys Ser Cys Ser Ser Leu Gln Ala				
	315	320	325	
ggg ccc cgg ctg ttt gtt att ggg ggt gtg gcc cag ggc ccc agt caa				1241
Gly Pro Arg Leu Phe Val Ile Gly Gly Val Ala Gln Gly Pro Ser Gln				
	330	335	340	
gcc gtg gag gca ctg tgt ctg cgt gat ggg gtc tgaaggcttg gtgggagctg				1294
Ala Val Glu Ala Leu Cys Leu Arg Asp Gly Val				
	345	350		
tccactggag cagctcattg ccagaggcag ctatttctat ggctcctttt gctgctgagg				1354
acactcactg tggctctgtg ggatgagaga ggcattggggg tgagcacttg aaacactgcc				1414
ttggggcctt gggttagggg agcctttgtc tttagtgcag gacacacata tgcttacacc				1474
tacctttatc accattcgtt catgaatcat gcctagctcc atccttgccc tgggacctac				1534
taggccttcc atccaactgg gaaatgggga gaagcaaagc tggcctcatg ctcttcaggg				1594
tcagttccta tctggagttg accaggccta cccagttgc cattcctgaa aaatctcagc				1654
tgccaggctg cctttagggg ccctgtagac ccaggagagt tgagaggggtg ggggacacag				1714
agagaataga gaggatgttg gaactgccag agggccggag cgcaggagtt caagtggagg				1774
aatgctggct ttgagccctc tacactgctg gttgtatgac cttggacaag tcacttcacc				1834
tctctgtgcc tcagcatcct catctataaa tggggatctc tgaaaccttc ctacctacc				1894
tacctcacag ggctgttggtg aggacccagg gagtttggat gtggaagtaa aagtgtgcc				1954
aaaaaaaaaa aaaaaaa				1971

<210> 176  
 <211> 1613  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 68..127

<400> 176

gacgaaggac tggaagggtg cggtggtgaa ggtgcaggcc gttggggcgg ctcagaggca	60
ggtgact atg aaa ggc tta tat ttc caa cag agt tcc aca gat gaa gaa	109
Met Lys Gly Leu Tyr Phe Gln Gln Ser Ser Thr Asp Glu Glu	
1 5 10	
ata aca ttt gta ttt caa taaaaggaag atcttctctgt tacagaggat	157
Ile Thr Phe Val Phe Gln	
15 20	
aactttgtga aacttcaagt taaagcttgt gctctgagcc agataaatac aaagcttctg	217
gcagaaatga agatgaaaaa ggatttattt cctgttgagg gagaaattgc tggaattgta	277
ttagatgttg gaagcaagg atcattcttt caaccagatg atgaagtagt tggaattttg	337
ccccggact ctgaagaccc tggactttgt gaagttgtta gactacatga gcattacttg	397
gttcataaac cagaaaaggc cacatggacg gaagcagcag gaagcattcg ggtggagtg	457
cgtgcctata cagctctgca ttatctttct catctctctc ctggaaaatc agtgctgata	517
atggatggag caagtgcatt tggtaacaata gctattcagt tagcacatca tagaggagcc	577
aaagtgattt caacagcatg cagccttgaa gataagcagt gccttgaaag attcagacct	637
cccatagccc gagtgattga tgtatcta atgggaaagt atgttgctga aagctgtttg	697
gaagaaacag gtggcctggg agtagatatt gtcctagatg ctggagtgag attatatagt	757
aaagatgatg aaccagctgt aaaactacaa ctactaccac ataaacatga tatcatcaca	817
cttcttggtg ttggaggcca ctgggtaaca acagaagaaa accttcagtt ggatcctcca	877
gatagccact gccttttctt caagggagca acgttagctt tcttgaatga tgaagtttgg	937
aatttgtcaa atgtacaaca gggaamaata tctttgtatc ttaaaggatg tgatggagaa	997
gttatcaact ggtgttttca gacctcagtt ggatgaaccc attccactgt atgaggcaaaa	1057



ata gcc cga gtg att gat gta tct aat ggg aaa gtt cat gtt gct gaa	685
Ile Ala Arg Val Ile Asp Val Ser Asn Gly Lys Val His Val Ala Glu	
195 200 205	
agc tgt ttg gaa gaa aca ggt ggc ctg gga gta gat att gtc cta gat	733
Ser Cys Leu Glu Glu Thr Gly Gly Leu Gly Val Asp Ile Val Leu Asp	
210 215 220	
gct gga gtg aga tta tat agt aaa gat gat gaa cca gct gta aaa cta	781
Ala Gly Val Arg Leu Tyr Ser Lys Asp Asp Glu Pro Ala Val Lys Leu	
225 230 235	
caa cta cta cca cat aaa cat gat atc atc aca ctt ctt ggt gtt gga	829
Gln Leu Leu Pro His Lys His Asp Ile Ile Thr Leu Leu Gly Val Gly	
240 245 250 255	
ggc cac tgg gta aca aca gaa gaa aac ctt cag ttg gat cct cca gat	877
Gly His Trp Val Thr Thr Glu Glu Asn Leu Gln Leu Asp Pro Pro Asp	
260 265 270	
agc cac tgc ctt ttc ctc aag gga gca acg tta gct ttc ctg aat gat	925
Ser His Cys Leu Phe Leu Lys Gly Ala Thr Leu Ala Phe Leu Asn Asp	
275 280 285	
gaa gtt tgg aat ttg tca aat gta caa cag gga aaa tat ctt tat ctt	973
Glu Val Trp Asn Leu Ser Asn Val Gln Gln Gly Lys Tyr Leu Tyr Leu	
290 295 300	
aaa gga tgt gat gga gaa gtt atc aac tgg tgt ttt cag acc tca gtc	1021
Lys Gly Cys Asp Gly Glu Val Ile Asn Trp Cys Phe Gln Thr Ser Val	
305 310 315	
gga tgaacatatt ccagttttg aagccagaat tttctttgga aattgttgag	1074
Gly	
320	
aaaaaccaag gaagataaaa caagttgcat ttttaagcac gtttctctgc taagacaaga	1134
tgctcagttg acacatttga aaagtgtttg aaaaattctg gcttctaate ctgcctctgt	1194
tcccttttct ctccttgaaa gtccagcaca ccattcttgt ccttccccag tttcctcgcc	1254
ctccaccct ccagcttcat gtcagtggt gtgcttaata aaatggacat atttttctct	1314
aaaaaaaaa aaaaaakaaa aaaaaaaaaat aaaaaaaaaa aaaaaaa	1361

<210> 178  
 <211> 1113  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 109..585

<400> 178	
gcgggaccgg acttccggct ggtctgtggg gtttcggggt cgggggtttcc tgggtgggcgt	60
caggggcagg caacagagtg gcggccgcta cgccctgga acggggcc atg gag aag	117
Met Glu Lys	
1	
ctg cgg cga gtc ctg agc ggc cag gac gac gag gag cag ggc ctg act	165
Leu Arg Arg Val Leu Ser Gly Gln Asp Asp Glu Glu Gln Gly Leu Thr	
5 10 15	
gcg cag gtc ctg gat gcc tca tcc ctt agt ttc aac acc aga ttg aaa	213
Ala Gln Val Leu Asp Ala Ser Ser Leu Ser Phe Asn Thr Arg Leu Lys	
20 25 30 35	
tgg ttt gcc atc tgc ttc gta tgt ggc gtt ttc ttt tct att ctt gga	261
Trp Phe Ala Ile Cys Phe Val Cys Gly Val Phe Phe Ser Ile Leu Gly	
40 45 50	
act gga ttg ctg tgg ctt ccg ggc ggc ata aag ctt ttt gca gtg ttt	309
Thr Gly Leu Leu Trp Leu Pro Gly Gly Ile Lys Leu Phe Ala Val Phe	

																55																	60																	65																																	
tat	acc	ctc	ggc	aat	ctt	gct	gcg	tta	gcc	agt	aca	tgc	ttt	tta	atg																	357																																																			
Tyr	Thr	Leu	Gly	Asn	Leu	Ala	Ala	Leu	Ala	Ser	Thr	Cys	Phe	Leu	Met																																																																				
																70																	75																	80																																	
gga	cct	gtg	aag	caa	ctg	aag	aaa	atg	ttt	gaa	gca	aca	aga	ttg	ctt																	405																																																			
Gly	Pro	Val	Lys	Gln	Leu	Lys	Lys	Met	Phe	Glu	Ala	Thr	Arg	Leu	Leu																																																																				
																85																	90																	95																																	
gca	aca	att	gtt	atg	ctt	ttg	tgt	ttc	ata	ttt	acc	ctg	tgt	gct	gct																	453																																																			
Ala	Thr	Ile	Val	Met	Leu	Leu	Cys	Phe	Ile	Phe	Thr	Leu	Cys	Ala	Ala																																																																				
																100																	105																	110																	115																
ctt	tgg	tgg	cat	aag	aag	gga	ctg	gct	gtg	tta	ttc	tgc	ata	ttg	cag																	501																																																			
Leu	Trp	Trp	His	Lys	Lys	Gly	Leu	Ala	Val	Leu	Phe	Cys	Ile	Leu	Gln																																																																				
																120																	125																	130																																	
ttc	ttg	tca	atg	acc	tgg	tat	agc	ctg	tcg	tac	atc	cca	tat	gca	agg																	549																																																			
Phe	Leu	Ser	Met	Thr	Trp	Tyr	Ser	Leu	Ser	Tyr	Ile	Pro	Tyr	Ala	Arg																																																																				
																135																	140																	145																																	
gat	gca	gtt	att	aaa	tgc	tgt	tct	tct	ctc	cta	agt	tgaaaatcag																	595																																																						
Asp	Ala	Val	Ile	Lys	Cys	Cys	Ser	Ser	Leu	Leu	Ser																																																																								
																150																	155																																																		
aaacattgtg						gaaaagagca					cttgaatgta					tggtactcta					tgtttggtga					agtttgcttt										655																																															
tccccataaa						acactccagg					aacaactgac					gtgacagttg					aagaccgttt					tgtactaagt										715																																															
ctcatttttgt						atactggtaa					aaactacatg					cttgattaaa					ccattaaatg					cttghtaactt										775																																															
taaattcatt						atgtgtcatt					aatatacttt					tccaaagata					agatttttta					tcactgccag										835																																															
ttgtaaatta						tttttagcca					atttttaaat					cttttcaaag					cagctttgaa					atgtgaatat										895																																															
ttaaaggtag						acctcgtgct					gcaagataat					taaacttttt					tgcttttaaa					aaatgtctgc										955																																															
atttttaaga						tttttttttc					tttaaatgtg					aaactttatt					taagctagaa					amattgctta										1015																																															
ttatatgtaa						taaaaaataat					atataaatct					ttacaactkt					tgaaataaac					ccatccttgg										1075																																															
aaaaataaaa						aaaaaaaaaa					aqaaaaaaaa					aaaaaaaa																				1113																																															

```
<210> 179
<211> 1960
<212> DNA
<213> Homo sapiens
```

```
<220>  
<221> CDS  
<222> 29..577
```

<400> 179																
atcggccaac ggacgcgagg cgcgcgcc atg gaa cag cgg tta gct gag ttt																52
Met Glu Gln Arg Leu Ala Glu Phe																
1 5																
cgg gcg gcg cgg aaa cgg gcg ggt ctg gcg gcc caa ccc cct gct gcc																100
Arg Ala Ala Arg Lys Arg Ala Gly Leu Ala Ala Gln Pro Pro Ala Ala																
10 15 20																
agt cag ggc gca caa acc cca gga gag aag gcg gaa gca gca gcg act																148
Ser Gln Gly Ala Gln Thr Pro Gly Glu Lys Ala Glu Ala Ala Ala Thr																
25 30 35 40																
cta aag gca gcc cca ggc tgg cta aag cgg ttc ctg gta tgg aaa cct																196
Leu Lys Ala Ala Pro Gly Trp Leu Lys Arg Phe Leu Val Trp Lys Pro																
45 50 55																
agg ccc gcg agt gcc cgg gcc cag ccc ggc cta gtt cag gaa gcg gct																244
Arg Pro Ala Ser Ala Arg Ala Gln Pro Gly Leu Val Gln Glu Ala Ala																
60 65 70																
cag ccc cag ggc agc aca tca gag aca cca tgg aac aca gcc att cct																292
Gln Pro Gln Gly Ser Thr Ser Glu Thr Pro Trp Asn Thr Ala Ile Pro																
75 80 85																
ctg ccg tcg tgc tgg qac caq tct ttc ctg acc aat atc acc ttc ttg																340



```

Leu Pro Ser Cys Trp Asp Gln Ser Phe Leu Thr Asn Ile Thr Phe Leu
 90          95          100
aag gtt ctt ctc tgg ttg gtc ctg ctg gga ctg ttt gtg gaa ctg gaa      388
Lys Val Leu Leu Trp Leu Val Leu Leu Gly Leu Phe Val Glu Leu Glu
105          110          115          120
ttt ggc ctg gca tat ttt gtc ctg tcc ttg ttc tat tgg atg tac gtc      436
Phe Gly Leu Ala Tyr Phe Val Leu Ser Leu Phe Tyr Trp Met Tyr Val
          125          130          135
ggg aca cga ggc cct gaa gag aag aaa gag gga gag aag agc gcc tac      484
Gly Thr Arg Gly Pro Glu Glu Lys Lys Glu Gly Glu Lys Ser Ala Tyr
          140          145          150
tct gtg ttc aat cca ggc tgt gaa gcc atc cag ggc acc ctg act gca      532
Ser Val Phe Asn Pro Gly Cys Glu Ala Ile Gln Gly Thr Leu Thr Ala
          155          160          165
gag cag ttg gag cgc gag tta cag ttg aga ccc ctg gca ggg aga      577
Glu Gln Leu Glu Arg Glu Leu Gln Leu Arg Pro Leu Ala Gly Arg
          170          175          180
taggacccag ctgtgctgtc atgcagctaa cctctgatgt ggtcttcctc accattggct      637
atggatttga tttcagggtg ataggactaa gggcagcttg cgggtagct ctgtgactgc      697
atagtttttc taccttcttt ccctgatctt ttgctgccat ttgatctttg atagtttttg      757
tgaaactctc taaaatacat tcactgtggg tccgacgcaa tttataaaaa ttatgtactc      817
aagaaggagg acctgtttgt ttcatttctc atctgttttg gagatgattt tagagacta      877
gaaaggcact ggggagattc tcagcttaaa acatccagca gtttgaagta tgattaggta      937
catcagggct gcattgtcaa tgttctcttt aagtctttta acatttatag caattttttt      997
tttcccgagg agtttaggtt gcaagttttg ggtttcttgt ttgtttttgt tttgcttcct      1057
gctttaattc tttaattttc agtcattact ggtattgaaa aataaaaatat ctttaaaaca      1117
tctcctcttc agaaatagggt ccctcttcat tgcccatcac catcttccac tctcctatta      1177
ttttgccact actcagtaaa ggaaggtagg aagagacaaa cgcctaagtg cagggtgtggg      1237
gagggatttc acaagtgggt attaacggcc agttcagcaa gaagtgttga gtgtgtacaa      1297
aggggagggc tggaagtgtt aactccagac ccgttggtcg cttgagttgt ttcttatatt      1357
ctaaagcagc agtccctaac ctttttgcca ccagggacca gttttgtgga acacagtttt      1417
tccatggacg ggggtggtggt ggaggatgaa acttccacct cagatcatca ggcattagag      1477
tctcataagg agcacgcaac ctagatccct cgcattgcga gttcacaata cggttctaag      1537
ggcttttagag taagcagctt tttcacctgt gggcctcttg tgagaaattc tgtaaattgt      1597
gataatcagg ctggatttta atgctgcttt tccagtacaa tgtttagagt tgggttcatt      1657
aaaattaggc aaactcccat tgggttaggg cttctctcat tccattttgt ggctaaccct      1717
actgtgtttc agcccttgct gaaaattctt ctgatattgt ttgcccttcc tcacagccct      1777
ttggccattg ggagtttggt tgtccctcag agccatccgg tcaagcagat ggtctgttct      1837
atctcacaga aaagtctttt cttccatgag actgtctga actgaacatg taaaaagtat      1897
gggaaacaga tgaatcccta ttaaacadga agttttgatt gtattcaaaa aaaaaaaaaa      1957
aaa

```

<210> 180  
 <211> 1443  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 23..451

```

<400> 180
accggcgggc ggggcgggta ag atg gcg gcc ccg cgg cga ggg aga gga tcc      52
          Met Ala Ala Pro Arg Arg Gly Arg Gly Ser
          1          5          10
tcc aca gtg ctc tct tca gtt ccc ctt caa atg ctg ttt tat ctc agc      100
Ser Thr Val Leu Ser Ser Val Pro Leu Gln Met Leu Phe Tyr Leu Ser
          15          20          25

```

```

gga acg tac tac gcc ctg tat ttc ctc gcc acg ctc ctg atg atc acg      148
Gly Thr Tyr Tyr Ala Leu Tyr Phe Leu Ala Thr Leu Leu Met Ile Thr
          30                      35                      40
tat aaa agt cag gtg ttc agc tat cct cac cgc tac ctg gtc ctc gat      196
Tyr Lys Ser Gln Val Phe Ser Tyr Pro His Arg Tyr Leu Val Leu Asp
          45                      50                      55
ctt gct ctg ctg ttt ctg atg ggg att cta gaa gca gtt cgg tta tac      244
Leu Ala Leu Leu Phe Leu Met Gly Ile Leu Glu Ala Val Arg Leu Tyr
          60                      65                      70
ctg ggc acc agg ggc aac ctg aca gag gct gag agg ccg ctg gcc gcc      292
Leu Gly Thr Arg Gly Asn Leu Thr Glu Ala Glu Arg Pro Leu Ala Ala
          75                      80                      85                      90
agc ctg gcc ctc acg gct ggc acc gcc ctc ctc tct gcc cac ttc ctg      340
Ser Leu Ala Leu Thr Ala Gly Thr Ala Leu Leu Ser Ala His Phe Leu
          95                      100                      105
ctt tgg cag gcc cta gtg ttg tgg gcg gac tgg gcc ctc agc gcc acg      388
Leu Trp Gln Ala Leu Val Leu Trp Ala Asp Trp Ala Leu Ser Ala Thr
          110                      115                      120
ctc ctg gcc ctt cac ggc ctg gag gcc gtc ctg cag gtg gtt gcc atc      436
Leu Leu Ala Leu His Gly Leu Glu Ala Val Leu Gln Val Val Ala Ile
          125                      130                      135
gcg gcc ttc acc agg tagctacgga caccgaggat accccacact ggggccctcc      491
Ala Ala Phe Thr Arg
          140
tcctgggcct gaccagtccc ccagctgtca cctccccatt cctggacagg aagggcactt      551
ttcctagtga ctggccatag atggtttttg atggttccat ctgttctggc aggagtggga      611
gcaggagcca gggcagaaca aactgctgga ggccctggtg ttgggaacag ctgcgggggag      671
ggtagggacc agacagaact gccttcaaga tgagtcccag gagegcacac tcagccctgt      731
cagtgggggc tggcttttagc agccaggcct ccacagaccc ccatggggccc ccaggggccga      791
gagggaggac agagcccttc agaacagagg cctcatctca ctgcatcccc catcaccccc      851
tagttccccca atggtcctaa tttgtgttct gagatcccag tttactctgt ggccaggccc      911
cacctgtgtt tccaagtcgg gctggagacg caggatgggg taggccttgt gctctgagca      971
accccagctc tgcctcacag gcaggcaggc ccggtgcaag agtggactct gggttcctaa      1031
agcaataaat gcaacaagc caacagctct gctgcctagc aatttccatc ttagccacac      1091
ttctcccttc aggggcttcg gaggagaggt cagggctaag gccgggggatg atactgcagg      1151
agagagagca gcggaggggcc acattcggag cctccgtcca ctccagtttt atcagctttt      1211
gcttttgcac ggagtgtctaa acaaattcta gctctgtgtt tttttcccat tcccagattt      1271
actatcagtt ctccctaaaa agtatctaag ctgttacagt agctttccct tcaacttgatt      1331
ctattgtgtg ttttctatgt ttggaataat tacacccaaa tatctagata ttttctcttc      1391
accgcatttt gtaaataaag agatgtgtat gcctcaaaaa aaaaaaaaaa aa      1443

<210> 181
<211> 605
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 232..450

<400> 181
caaatacaaa tgccccaaga agactgagga taggagaaag aatatctcta cctgtgaaac      60
attgttagac tgccctggcta ggagttcatt gttgttttct gaaggacgta accaaccact      120
ccaaaactta caggcttaaa acaacaacaa tgtatcattt cttatgattc tgtgggttgg      180
ctgggtggtt cttctagctg aggcaggatg gtctaggata gctacatcca c atg tct      237
                                     Met Ser
                                     1
ggg gtc cca gct gag atg act ggg gct gtt gag gcc ttt ctc cct gtg      285

```

Gly	Val	Pro	Ala	Glu	Met	Thr	Gly	Ala	Val	Glu	Ala	Phe	Leu	Pro	Val			
5																		
gtg	tca	tcc	tcc	aga	agg	ctg	ccc	aga	ttt	gtc	cat	atg	gta	gca	gga	333		
Val	Ser	Ser	Ser	Arg	Arg	Leu	Pro	Arg	Phe	Val	His	Met	Val	Ala	Gly			
20																		
25																		
gtt	tcc	tcg	aag	caa	gag	agg	gca	aga	tcc	aac	aca	gaa	gca	ctt	ttc	381		
Val	Ser	Ser	Lys	Gln	Glu	Arg	Ala	Arg	Ser	Asn	Thr	Glu	Ala	Leu	Phe			
35																		
40																		
45																		
50																		
aag	ctc	tgt	ttc	cat	cac	att	tgc	caa	tgt	ctc	act	gat	gaa	cac	aag	429		
Lys	Leu	Cys	Phe	His	His	Ile	Cys	Gln	Cys	Leu	Thr	Asp	Glu	His	Lys			
55																		
60																		
65																		
ttc	cat	ggc	caa	gtc	cag	ttt	taagaaatgg	agaaataggg	cttggctcag							480		
Phe	His	Gly	Gln	Val	Gln	Phe												
70																		
tggtctcatgt	ctgtaatccc	agcacttttgg	gaggccaagg	catgcggatc	atttgagggtc											540		
aggagttcca	gaccagcctg	gccaacatgg	tgaaaaccca	tctctaccaa	aaaaaaaaa											600		
aaaaa																605		
<210> 182																		
<211> 1724																		
<212> DNA																		
<213> Homo sapiens																		
<220>																		
<221> CDS																		
<222> 758..1183																		
<400> 182																		
aactaaagcc	gggagtcg	cggtgaac	ggggca	gaagcagg	gccatgcc	aagagc	agccccaag	ccacccccaa								60		
gatccccctg	aacctgcacc	tccatcac	gagccc	atccagg	agcctccagg	agcccagaca										120		
ccagcccccc	accatggtaa	gtccttca	agggtgat	ctt	ggaagagg	aaagaggga										180		
caccagccag	gtggaggtgt	cctaaaaat	gaccatcaga	aatgggggtga	ggggaggggc											240		
atggtggact	tctgtggggg	tggggtgtct	ctcagtg	cagctcag	ctcaggtgcc	tccagcatcc										300		
cttaccaggg	agcaagctcc	catctgtagg	tgggtgggat	gccagggtgg	tatccctgga											360		
tccaaggata	gggcaggacc	tgggaagac	agagtgccc	agggagaatc	acagagtctg											420		
cagggacaag	gacatagcct	cctttgcttg	caaattaagg	gagccctttc	ccagtcacgc											480		
ccagctcttc	gtctccctgt	gtagccttgg	gctagtcact	tcccctctct	tggccccggg											540		
tcccacagat	gtcatatttg	gaaatccg	tcatagtcga	agttgctctt	caggggtctt											600		
tcagttgcaa	cattctcaag	gtctgtgggt	tctgccacag	agtcctcggc	tgagatggga											660		
agctatgtct	aacaagcgat	ggggtggatt	gacgccctcc	ctgtgccggg	gacgggcggg											720		
atggctgcag	cagaggcagg	agaggctgaa	tacgtcc	atg	cca	ccc	ttt	ggg	ggg							775		
Met Pro Pro Phe Gly Gly																		
1																		
5																		
cat	ccc	tta	tcc	caa	gag	gag	gat	ggc	agc	cag	agg	tgt	tgc	tgc	ctg	823		
His	Pro	Leu	Ser	Gln	Glu	Glu	Asp	Gly	Ser	Gln	Arg	Cys	Cys	Cys	Leu			
10																		
15																		
20																		
tca	agt	ctg	agg	tct	gtc	gat	gat	agc	aac	ggg	gag	act	gtc	gtg	atc	871		
Ser	Ser	Leu	Arg	Ser	Val	Asp	Asp	Ser	Asn	Gly	Glu	Thr	Val	Val	Ile			
25																		
30																		
35																		
atg	gcg	cta	ttc	cta	gca	gta	tcg	tac	cac	cat	aag	acg	caa	agt	aag	919		
Met	Ala	Leu	Phe	Leu	Ala	Val	Ser	Tyr	His	His	Lys	Thr	Gln	Ser	Lys			
40																		
45																		
50																		
agg	tgg	cca	ggg	ctg	acc	cca	ccc	cac	agc	tct	ctg	ctg	tgt	aga	cca	967		
Arg	Trp	Pro	Gly	Leu	Thr	Pro	Pro	His	Ser	Ser	Leu	Leu	Cys	Arg	Pro			
55																		
60																		
65																		
70																		
ctt	cag	ctt	tca	ttt	ctc	gtc	att	cag	tca	gtg	agg	atg	aga	gca	tgt	1015		
Leu	Gln	Leu	Ser</															

```

ggc tgt gac agc ggc cac tgc agg att ctt ggc agg tac agc tta cta 1063
Gly Cys Asp Ser Gly His Cys Arg Ile Leu Gly Arg Tyr Ser Leu Leu
          90                      95                      100
ggg tgg agt cag gga cat agg gca aga ggc aga ggt ggt gtt agt ctg 1111
Gly Trp Ser Gln Gly His Arg Ala Arg Gly Arg Gly Gly Val Ser Leu
          105                      110                      115
aga gac aac acc ttc ttt cag gaa gcc agt gag ggc cag gga cag tgg 1159
Arg Asp Asn Thr Phe Phe Gln Glu Ala Ser Glu Gly Gln Gly Gln Trp
          120                      125                      130
ctc atg cct gta atc cca gca ttt taggaggctg agacaggtag atcacttgag 1213
Leu Met Pro Val Ile Pro Ala Phe
          135                      140
gtcagggtgtt cgagaccagc ctggccaacg tgggtgaaacc tcgtctcttac taaaaaatac 1273
aaaaaattaa ctgggcgtgg tggcacacgc ctgtaatccc agctacatat gaggctgagg 1333
caagagaata acttgaaccc aggaggcgga ggggtgcagtg agctgagatc ctgccgctgc 1393
actccagcct gggtgacaga gcacactccg tctcaaaaaa ggaaagctga tgagaaattg 1453
ggcatcccgg aattcacacc caaaccatca gctggagctc tgagactggt ggggtgggaa 1513
ttcttccaag atgagaagca agccagggag gctcagggtcc tgggatgggc agggctttga 1573
tcaaaagaac acaggaagtg atttgctact tgaaagaaag gcaacccctc cccaaggaag 1633
ccctctgaaa atgcttagtc aacagtcggc ttggcagaca aggtctggga ggggccaccc 1693
gtatcgcaga ggacaaaaaa aaaaaaaaaa a 1724

<210> 183
<211> 1686
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 486..932

<400> 183
cggctcactg cagcctcttc ctcccagttc caagtgattc tctgtctca gcctcctgag 60
tggctgggat tacagggtgtg caccactacc acttggtctaa tttttatact tttagtagag 120
atgggggttt accatgttgg ccaggctggc cttgaactcc tgacctcagg tgatccgccc 180
gcctcggcct cccaaagtgc tgggggttaca ggcattgagc accgcacccg gcccccttcc 240
ttcgtcttag tcaatcctat cccacctctt ctccaccag tccccacac tgatgggtccc 300
aacacttcac catccaccac ctccctggag gggtagcccg aggtgctccg ctgggggactc 360
tgctcattct ggggggtgcag ttgacggctg gtcgtgatct tccccgtaat ctgtcccctc 420
ttacggaacc tagtctccgt tctgtccatg gccttcttct ggacactgct aggatccaga 480
agagt atg tta tca att ctc aag cct agg aga agt cag gag tgg aga aca 530
Met Leu Ser Ile Leu Lys Pro Arg Arg Ser Gln Glu Trp Arg Thr
          1          5          10          15
gct ctg aga aga tac tgt tgt cca act gat ctc cag gca cca cgg agt 578
Ala Leu Arg Arg Tyr Cys Cys Pro Thr Asp Leu Gln Ala Pro Arg Ser
          20          25          30
ccg gtc cct cca atc agg aag gtc gga atc tct gat gtc atc gtt cat 626
Pro Val Pro Pro Ile Arg Lys Val Gly Ile Ser Asp Val Ile Val His
          35          40          45
gcc aac ctg gca acc agt ttg aaa aaa aac aca tgt aac tgc cag gct 674
Ala Asn Leu Ala Thr Ser Leu Lys Lys Asn Thr Cys Asn Cys Gln Ala
          50          55          60
gat ctc ttg tcc tgg aga tcc tgg gtg aat ggt atc tcc tgc cac tgt 722
Asp Leu Leu Ser Trp Arg Ser Trp Val Asn Gly Ile Ser Cys His Cys
          65          70          75
ccc aac ctc aga cca ttg tcc aaa agc atc ttc agg gac tcc aca tcc 770
Pro Asn Leu Arg Pro Leu Ser Lys Ser Ile Phe Arg Asp Ser Thr Ser
          80          85          90          95

```

```

ctc tgt tcc ctg tcc cag cag agg ctg tgt cct ctc cac tca aag cct      818
Leu Cys Ser Leu Ser Gln Gln Arg Leu Cys Pro Leu His Ser Lys Pro
      100      105      110
gaa gca tgt tgg ggt ctc ttt gtc tct gta cat gcc cat ttc aga gtc      866
Glu Ala Cys Trp Gly Leu Phe Val Ser Val His Ala His Phe Arg Val
      115      120      125
cag gct ggt ggg aga ggg aac aga gtg gga aag aaa act agg gta agc      914
Gln Ala Gly Gly Arg Gly Asn Arg Val Gly Lys Lys Thr Arg Val Ser
      130      135      140
aga aac gat gaa acc tta taagagtgag attatcatgt gcaagagtga      962
Arg Asn Asp Glu Thr Leu
      145
gattatcatg tacaagagat cccaggaaat actgactttg atgaaaaagt cacatcagag      1022
cactcagttt tggcagagct ttttctgccg aatgtttact cacattcact gtccgagatt      1082
ctatactggg ggtacacacg tcctctgccc taaggcaatt ttgagtccaa gagacatttt      1142
gaggcctaaa aatcatagga aactgcccct gagctcacac atatttccaa tgggtgtcccc      1202
aatttcaggg aatccatgga ttacctaagc cagcccctcc agttcggcta agaaactcta      1262
gtctatatgt caagttttgt atcatatgta ttgctctgaa ctcagaaaatt tcccttccat      1322
ttatggattc tatgaataaa atatcacatg tacaaaaaga ctaagtcaaa aaatttcagc      1382
tgtgcacagt ggctcatgct tgtaatccca gcactttggg tggccgaggg gggaggattg      1442
cctgaggcca gcagttcaag accagtatgg gcaacatggc aagagcccat ctctaaaaaa      1502
acaaaaccaa accaaattgg ccaggtgtgg tggctggcac ctgtgttcca actacttggg      1562
agactcatgt gacaggaaga tcacttgagc ccgggggtta gaggctgcag tgagctatga      1622
tcttgccact gcactccagc ctgggtgaca gagcgagaca ccgtcgcaaa aaaaaaaaaa      1682
aaaa      1686

<210> 184
<211> 463
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 80..304

<400> 184
cttttaacag ctgaggtctc tctttaattc tcttaaatac catttctccc tcaaaaaaga      60
ccattagatc atttcacaa atg tat ctg cca cca aac agg tca gag ctt tgc      112
      Met Tyr Leu Pro Pro Asn Arg Ser Glu Leu Cys
      1      5      10
aac ttt gct ttg tct ctt aac ctc tat ggc aaa ggg ttt ttt agc ctg      160
Asn Phe Ala Leu Ser Leu Asn Leu Tyr Gly Lys Gly Phe Phe Ser Leu
      15      20      25
gtg gaa aag cat aac agc agg gat tta gaa gat aga gct agt tct ggc      208
Val Glu Lys His Asn Ser Arg Asp Leu Glu Asp Arg Ala Ser Ser Gly
      30      35      40
cca tca ctt tca tct cca tca cac ccg gac tgg ggt tat ata gtt ctg      256
Pro Ser Leu Ser Ser Pro Ser His Pro Asp Trp Gly Tyr Ile Val Leu
      45      50      55
att tta gtg gca acc ctg ggg gaa ctt gat acc cag gta ggt ggt cac      304
Ile Leu Val Ala Thr Leu Gly Glu Leu Asp Thr Gln Val Gly Gly His
      60      65      70      75
tgatcagtag ttgggagagg taggaattgg tgagtacagg taattagagg aaagtcttgt      364
gtcctgtttc ccccttttta attttatccc ttgctagaat taagatacta tatgcctcac      424
ttatcaatta cagtctaaat ccaaaagaaa aaaaaaaaaa      463

<210> 185
<211> 773

```

<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 188..691

<400> 185  
agttgcgggt tgcaggagtt caggaaagga ggtgggacta gagtcaacct ggaatagctc 60  
tacagtaaca atggcagcct ttttgttgct gggacatcca tacaggcaac ttagctgggtg 120  
aaaggactct ggattggttg gcagtctgct tttttttttc caaggtgata actttactgt 180  
agaagaa atg agg tta aca gaa aag agt gag gga gaa caa caa ctc aag 229  
Met Arg Leu Thr Glu Lys Ser Glu Gly Glu Gln Gln Leu Lys  
1 5 10  
ccc aac aac tct aat gca ccc aat gaa gat caa gaa gaa gaa atc caa 277  
Pro Asn Asn Ser Asn Ala Pro Asn Glu Asp Gln Glu Glu Glu Ile Gln  
15 20 25 30  
cag tca gaa cag cat act cca gca agg cag cga aca caa aga gca gac 325  
Gln Ser Glu Gln His Thr Pro Ala Arg Gln Arg Thr Gln Arg Ala Asp  
35 40 45  
aca cag cca tcc aga tgt cga ttg cct tca cgt agg aca cct aca aca 373  
Thr Gln Pro Ser Arg Cys Arg Leu Pro Ser Arg Arg Thr Pro Thr Thr  
50 55 60  
tcc agc gac aga acg atc aac ctt ctt gaa gtc ctt ccg tgg cct act 421  
Ser Ser Asp Arg Thr Ile Asn Leu Leu Glu Val Leu Pro Trp Pro Thr  
65 70 75  
gag tgg att ttc aac ccc tat cga ttg cct gct ctt ttt gag ctt tat 469  
Glu Trp Ile Phe Asn Pro Tyr Arg Leu Pro Ala Leu Phe Glu Leu Tyr  
80 85 90  
cct gaa ttt ctt ctg gtg ttt aaa gaa gcc ttc cat gac ata tcc cat 517  
Pro Glu Phe Leu Leu Val Phe Lys Glu Ala Phe His Asp Ile Ser His  
95 100 105 110  
tgt ctg aaa gcc cag atg gaa aag atc gga ctg ccc atc ata ctc cac 565  
Cys Leu Lys Ala Gln Met Glu Lys Ile Gly Leu Pro Ile Ile Leu His  
115 120 125  
ctc ttc gca ctc tcc acc ctc tac ttc tac aag ttt ttc ctt cct aca 613  
Leu Phe Ala Leu Ser Thr Leu Tyr Phe Tyr Lys Phe Phe Leu Pro Thr  
130 135 140  
att ctt tcc ctt tct ttc ttt att ctt ctt gta ctt ctg ctt ctg ctt 661  
Ile Leu Ser Leu Ser Phe Phe Ile Leu Leu Val Leu Leu Leu Leu Leu  
145 150 155  
ttt att att gtc ttc att ctg atc ttc ttc tgattctttt gtttcaataa 711  
Phe Ile Ile Val Phe Ile Leu Ile Phe Phe  
160 165  
acagcaatga gcatgaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 771  
aa 773

<210> 186  
<211> 753  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 94..573

<400> 186  
acttttcagg ggacattcag aggcattcagc cctttctctc tcaccagctc ccagagttcc 60

```

catctccatc cccaatccta aagaaggaaa tcg atg cca cgg tcc tca agg agc      114
                                1      5
                                Met Pro Arg Ser Ser Arg Ser
cct ggg gac cca ggc gcc cta ctc gaa gat gtg gcc cac aat ccc aga      162
Pro Gly Asp Pro Gly Ala Leu Leu Glu Asp Val Ala His Asn Pro Arg
                                10      15      20
ccc cgg agg att gcc cag cga ggc cgg aac acc agc agg atg gca gag      210
Pro Arg Arg Ile Ala Gln Arg Gly Arg Asn Thr Ser Arg Met Ala Glu
                                25      30      35
gac acc tcc cca aac atg aat gac aac atc ctg ttg cct gtc cgc aac      258
Asp Thr Ser Pro Asn Met Asn Asp Asn Ile Leu Leu Pro Val Arg Asn
                                40      45      50      55
aat gac caa gcc cta ggc ctg act cag tgc atg ctg gga tgt gtg tcc      306
Asn Asp Gln Ala Leu Gly Leu Thr Gln Cys Met Leu Gly Cys Val Ser
                                60      65      70
tgg ttc acc tgt ttt gcc tgc tcc ctg aga act cag gcc cag cag gtt      354
Trp Phe Thr Cys Phe Ala Cys Ser Leu Arg Thr Gln Ala Gln Gln Val
                                75      80      85
ctg ttt aac acg tgc aga gac aga gtt tca cca tgt tgc cca ggc tgg      402
Leu Phe Asn Thr Cys Arg Asp Arg Val Ser Pro Cys Cys Pro Gly Trp
                                90      95      100
tct caa act cca gtg atc ctc cca cct cag cct tcc gaa gtg ctg gga      450
Ser Gln Thr Pro Val Ile Leu Pro Pro Gln Pro Ser Glu Val Leu Gly
                                105      110      115
tta cag atg caa gct gct gtg cca gaa gct cat gga gaa gac agg cat      498
Leu Gln Met Gln Ala Ala Val Pro Glu Ala His Gly Glu Asp Arg His
                                120      125      130      135
tct gct cct ctg tgc ttt cgg tgt gtc cca ggg ccc tgc cca gtc cca      546
Ser Ala Pro Leu Cys Phe Arg Cys Val Pro Gly Pro Cys Pro Val Pro
                                140      145      150
ggg gga ggt atc cct ggg ccc tgg cac tgattatagg acactgggca      593
Gly Gly Gly Ile Pro Gly Pro Trp His
                                155      160
agacactgca ctgccacgtg actcagtttc cccatctgcc tgatgggtgt tgctgtgaga      653
attatgaaat gaaatgatga ccatgaaaat attgtagaag ccaagaaatg cttcagaagt      713
tataaagctc tccccaaacc gtgttaaaaa aaaaaaaaaa      753

```

<210> 187  
 <211> 754  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 181..462

```

<400> 187
atcctatcaa aagttacggt gaagtcaggg tgggtggcga gtccctgcaa ggtcgccct      60
ctgtgccaac acagcctgat ggcttcttgt ttcaggaaac atccagaatt acaactggcc      120
attgagttat tacatatcaa ttgaacaagg tagtttttaa atgaaagaaa atcttgcaac      180
atg aat aaa gag ata gac tct ttg aat ctg gca tac agc ttt ccc ttc      228
Met Asn Lys Glu Ile Asp Ser Leu Asn Leu Ala Tyr Ser Phe Pro Phe
1      5      10      15
ctt ctt cct gct ttc ctg gac aca ccg tgg aca gac cca ttt ccc tct      276
Leu Leu Pro Ala Phe Leu Asp Thr Pro Trp Thr Asp Pro Phe Pro Ser
20      25      30
gga ttc atg gta agg tcc cga gtg ctt ctg ata cag ctg ctg agc aga      324
Gly Phe Met Val Arg Ser Arg Val Leu Leu Ile Gln Leu Leu Ser Arg

```

```

      35      40      45
ccc cgc tca tct cag gag tcc cga gga cac tcg ctt ccc tgc agc ccg      372
Pro Arg Ser Ser Gln Glu Ser Arg Gly His Ser Leu Pro Cys Ser Pro
      50      55      60
tcc gcc ctc cat aag cct ggg ggc atc tgc cct gca gca ctg ggg agg      420
Ser Ala Leu His Lys Pro Gly Gly Ile Cys Pro Ala Ala Leu Gly Arg
      65      70      75      80
agc cac ctc ctt gtc tgg gaa cag cca agc ctc cgt gac agc      462
Ser His Leu Leu Val Trp Glu Gln Pro Ser Leu Arg Asp Ser
      85      90
tgaggattct tgtggattgt tctttctgta actggacagc acatccggaa ttccttgcca      522
tagctctgtg ccttgctggg gtctgaggtt cacaggtcag atgctgctgt ctggtccttc      582
ccaattgctg cgtgaattcc ttcattctca ccagtagctt cttgctctcc ccaagggagg      642
cacgtgctta gtaggagag aggcctacca aggttgccat ctgccatggg ctcaattgtg      702
tccccaaccc ccctgcaaat tatatattga agtcccaaaa aaaaaaaaaa aa      754

<210> 188
<211> 998
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 6..290

<220>
<221> misc_feature
<222> 871
<223> n=a, g, c or t

<400> 188
gattc atg aag gcc tcg ggt cct gac ctc tct gat gga ctc cac tgc ccc      50
Met Lys Ala Ser Gly Pro Asp Leu Ser Asp Gly Leu His Cys Pro
      1      5      10      15
agt cta att aga cat tta aga acc ttc tct gca gct gct gcc tta gcc      98
Ser Leu Ile Arg His Leu Arg Thr Phe Ser Ala Ala Ala Leu Ala
      20      25      30
cca aga tac cca acc aga ctt ccc agt tca ctg ctt cta tgg cac ctc      146
Pro Arg Tyr Pro Thr Arg Leu Pro Ser Ser Leu Leu Leu Trp His Leu
      35      40      45
tgc cag tgc ctc cat ctc ctc tat gca gtt tct acc tca tgc aac agc      194
Cys Gln Cys Leu His Leu Leu Tyr Ala Val Ser Thr Ser Cys Asn Ser
      50      55      60
cat ggg aag aga tcg gct gcc tgg gca atg acc aga aca gaa gac aca      242
His Gly Lys Arg Ser Ala Ala Trp Ala Met Thr Arg Thr Glu Asp Thr
      65      70      75
gat gcg cta aca gat tcc ttc gat gac agt ttc atc agt tct gca gat      290
Asp Ala Leu Thr Asp Ser Phe Asp Asp Ser Phe Ile Ser Ser Ala Asp
      80      85      90      95
taaagacttt caccagaaaa aaaaattacc tgattttgcc ctgaggcagc cagggagggg      350
tttgtccttg acaatccac tgacttattt aacaggtagc tcaaaaccca acaaaaactg      410
gaggaggctg ctccactgca gggatggttt caattcggtg actggagtat tgtactctcc      470
ttgcaccctg gctcatcccc acaaaagacc tttcaaagaa aacacttaat tacctccttg      530
cacaagccct gtaagcccta aggtgaaaag aaactcagca gacaagggtcc acagagaagg      590
agaaggcaca attcagtagg gacctacgct cagcaccagg ataaagaaac tgtccattcc      650
tgccacctcc taggaagcta aaagaattaa ggggaggccg ggcacggtgg ctcacgctg      710
taatcccagc actttgggag gccgaggcgg gtggatcatg aggtcaggag atcgagacca      770
tcctggctaa catggtgaaa ccccatctct actaaaaata caaaaaatta gccgggcgtg      830

```



gtggcgggcg cccctgtagtc ccagctactc gggaggctga nggcaggaga atggtgtgaa 890  
 cctgggagggc ggagccttgca gtgagccgag attgcgcctt gctccactcc agcctgagcg 950  
 acagagcgag actccgtctc aaaaaaaaaa argaaaaaaaaa aaaaaaaaaa 998

<210> 189  
 <211> 605  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 115..411

<400> 189  
 aagaaagggg tgaggcctaa gggacaatca ggatgttttt cagagagaag tgtggatgct 60  
 ggacaggaag aaccacagat accagatacg ggtactgttg taactctgtt ctcc atg 117  
 Met  
 1  
 aaa aaa aag gaa gaa aca aca ctt tca gag atg gag cct gtt gag cca 165  
 Lys Lys Lys Glu Glu Thr Thr Leu Ser Glu Met Glu Pro Val Glu Pro  
 5 10 15  
 cag tac caa cta gtc aat gct gaa tcg act tct ccc ttt cta cat tgc 213  
 Gln Tyr Gln Leu Val Asn Ala Glu Ser Thr Ser Pro Phe Leu His Cys  
 20 25 30  
 ctg aga gaa gtc att ggg gaa tac tct gta cac gaa ttt tca ctg ttg 261  
 Leu Arg Glu Val Ile Gly Glu Tyr Ser Val His Glu Phe Ser Leu Leu  
 35 40 45  
 ggg aaa aca gag agt caa ggg att gga ttg tgg att gca ttg gtg gtt 309  
 Gly Lys Thr Glu Ser Gln Gly Ile Gly Leu Trp Ile Ala Leu Val Val  
 50 55 60 65  
 ttc ctc agt ttc ctc atc ttc tcc aca agt ttc tac ata tcg aat gca 357  
 Phe Leu Ser Phe Leu Ile Phe Ser Thr Ser Phe Tyr Ile Ser Asn Ala  
 70 75 80  
 gag cag ccc ttc ttc aaa gaa cct cct acg gaa gct gct aag gaa ctc 405  
 Glu Gln Pro Phe Phe Lys Glu Pro Pro Thr Glu Ala Ala Lys Glu Leu  
 85 90 95  
 agt ctg tagctctgcg tggagccatg tgtaaact gaactgagac ctgccacctc 461  
 Ser Leu  
 ctactaccta agggccatt ttcattctgat atcatccccc agaaacaaac tcatgatgac 521  
 ttccatgttt ttttttagatt agatacatgg agaattttcc tttcccttag aattaaaatc 581  
 ctgcattcta aaaaaaaaaa aaaa 605

<210> 190  
 <211> 526  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 3..368

<400> 190  
 ag atc cga gcg acc atg gtg gcc cgg gtg tgg tcg ctg atg agg ttc 47  
 Ile Arg Ala Thr Met Val Ala Arg Val Trp Ser Leu Met Arg Phe  
 1 5 10 15  
 ctc atc aag gga agt gtg gct ggg ggc gcc gtc tac ctg gtg tac gac 95  
 Leu Ile Lys Gly Ser Val Ala Gly Gly Ala Val Tyr Leu Val Tyr Asp  
 20 25 30

cag gag ctg ctg ggg ccc agc gac aag agc cag gca gcc cta cag aag	143
Gln Glu Leu Leu Gly Pro Ser Asp Lys Ser Gln Ala Ala Leu Gln Lys	
35 40 45	
gct ggg gag gtg gtc ccc ccc gcc atg tac cag ttc agc cag tac gtg	191
Ala Gly Glu Val Val Pro Pro Ala Met Tyr Gln Phe Ser Gln Tyr Val	
50 55 60	
tgt cag cag aca ggc ctg cag ata ccc cag ctc cca gcc cct cca aag	239
Cys Gln Gln Thr Gly Leu Gln Ile Pro Gln Leu Pro Ala Pro Pro Lys	
65 70 75	
att tac ttt ccc atc cgt gac tcc tgg aat gca ggc atc atg acg gtg	287
Ile Tyr Phe Pro Ile Arg Asp Ser Trp Asn Ala Gly Ile Met Thr Val	
80 85 90 95	
atg tca gct ctg tcg gtg gcc ccc tcc aag gcc cgc gag tac tcc aag	335
Met Ser Ala Leu Ser Val Ala Pro Ser Lys Ala Arg Glu Tyr Ser Lys	
100 105 110	
gag ggc tgg gag tat gtg aag gcg cgc acc aag tagcagagtcac gcaggggccc	388
Glu Gly Trp Glu Tyr Val Lys Ala Arg Thr Lys	
115 120	
cctgccccgg ccagaacggg cagggctgcc actgacctga agactccgga ctgggacccc	448
actccgaggg cagctccccg ccttgccggc ccaataaagg acttcagaag tgaaaaaaaa	508
ataaaaaaaaa aaaaaaaaa	526

<210> 191  
 <211> 910  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 174..527

<400> 191	
atttttctgt taggccaaga gagaagagga tccttctctca gagcctccag cctcccttga	60
tcccttgcct gtgggcatat gtgggtcata tttccctccc atcacctct gcacgccacc	120
cccatcaccg ccacagaccc ccagcccttc agttgccttg cacctccttg gtg atg	176
Met	
1	
cag ccg tcc ttg tta agg tca tac agg ttg aag gcc caa tta agc ctg	224
Gln Pro Ser Leu Leu Arg Ser Tyr Arg Leu Lys Ala Gln Leu Ser Leu	
5 10 15	
tca tct aca gtt ccc cga aga atc acg gac aaa cca gcc aca aag tcc	272
Ser Ser Thr Val Pro Arg Arg Ile Thr Asp Lys Pro Ala Thr Lys Ser	
20 25 30	
tgg gaa gga ggc agg agg gag ctg tgt cct cgg gta ctc ttc acc caa	320
Trp Glu Gly Gly Arg Arg Glu Leu Cys Pro Arg Val Leu Phe Thr Gln	
35 40 45	
ctc ctt ctc tgg gtt tgg cct gga gat cct ggc cct gaa ctc cag gaa	368
Leu Leu Leu Trp Val Trp Pro Gly Asp Pro Gly Pro Glu Leu Gln Glu	
50 55 60 65	
aca ggc ttc cct ggc cca cct cgc cca gct cac ctc aaa act gac cga	416
Thr Gly Phe Pro Gly Pro Pro Arg Pro Ala His Leu Lys Thr Asp Arg	
70 75 80	
gcc atc atg gtt ggt gtc aaa ggc att gaa gag aaa agt ggc ata ggt	464
Ala Ile Met Val Gly Val Lys Gly Ile Glu Glu Lys Ser Gly Ile Gly	
85 90 95	
gct gga gtc tgc agg gtg agt gtg gag aag ttg gct tcc aca cag gag	512
Ala Gly Val Cys Arg Val Ser Val Glu Lys Leu Ala Ser Thr Gln Glu	
100 105 110	

agg act tcc tcc ctc taaggagctc cccatacccc ccatcacctt ggcattccca 567  
Arg Thr Ser Ser Leu

115

gctcctccag aatccctccc tccctcagcc tagagaagga caactgcttc cccttggggc 627  
ttgtcccctc acctccttga ggaaagaact gggagtaaact ctgcttgaag ttctcctcat 687  
tgacaattcc gctgggacat tccctggaagg agagggcacc aggctgaggg cagagacaaa 747  
atcccccttcc gttcaccgcc cccaccctcc atggcccaag actcccaggg aggggggataa 807  
tcttcaagcc tccagaggac tcaccacgtg gctcatgtga tgggagggaa gacttctttc 867  
ccagtgcaca aataaaaaaac atggaacgaa aaaaaaaaaa aaa 910

<210> 192

<211> 668

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 57..203

<400> 192

tcctgtcgac gtgttcttcc ggtggcggag cggcggatta gccttcgcgg ggcaaa atg 59  
Met

1

gag ctc gag gcc atg agc aga tat acc agc cca gtg aac cca cct gtc 107  
Glu Leu Glu Ala Met Ser Arg Tyr Thr Ser Pro Val Asn Pro Pro Val  
5 10 15

ttc ccc cat ctg acc gtg gtg ctt ttg gcc att ggc atg ttc ttc acc 155  
Phe Pro His Leu Thr Val Val Leu Leu Ala Ile Gly Met Phe Phe Thr  
20 25 30

gcc tgg ttc ttc gtg tat cct ttc act gag cag cca gag gac cag cat 203  
Ala Trp Phe Phe Val Tyr Pro Phe Thr Glu Gln Pro Glu Asp Gln His  
35 40 45

tagtgatgtg ggaagctcag ggagaaacca cgctaggtac atggaccccg ccggttttgt 263  
acattggatt ggggctgaga gaagattgcc gtgggctggg ctctctgcac tccacagtcc 323  
acctcttcgc tttgccttaa ctgctgtgcc cagttacgag gtcacctcta ccaagtacac 383  
tcgtgatata tataaagagc tccatctctc attagtggcc tcactcttca tgggctttgg 443  
agtccctcttc ctgctgtctt gggttggcat ctacgtgtga gcacccaagg gtaacaacca 503  
gatggcttca ctgaaacctg cttttgtaaa ttactttttt ttactgttgc tgggaagtgtc 563  
ccacctgctg ctcataataa atgcagatgt atagcaaaaa aaaaaaaaaa aaaaaaaaaa 623  
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 668

<210> 193

<211> 637

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 68..334

<400> 193

agttatgaag ttctaaaagc aagtcttaat caggaagtgt ccttgatcac caacggctcg 60  
cccaggc atg ctg gct ctc ttc cac ttc cac ctt cca cca tgg gat gac 109  
Met Leu Ala Leu Phe His Phe His Leu Pro Pro Trp Asp Asp  
1 5 10

gca gta aga agg cca tca gta gat gcc agt ccc tca acc ttg aac ttt 157  
Ala Val Arg Arg Pro Ser Val Asp Ala Ser Pro Ser Thr Leu Asn Phe  
15 20 25 30

```

cca gac gca gaa ctt tat gcc tcc att ttc ctc tgc tgc atg gcc cca 205
Pro Asp Ala Glu Leu Tyr Ala Ser Ile Phe Leu Cys Cys Met Ala Pro
          35          40          45
gga gag att tta att agc ttt cta acc ttg gtc cag att gca cat gca 253
Gly Glu Ile Leu Ile Ser Phe Leu Thr Leu Val Gln Ile Ala His Ala
          50          55          60
aat ggt aga gga tgc aac acc ccc gct tgt gga gct gcc gct tgt gtc 301
Asn Gly Arg Gly Cys Asn Thr Pro Ala Cys Gly Ala Ala Ala Cys Val
          65          70          75
tgg cat gaa aat tca caa gaa gag agg aaa tac tgaggagaaa atggcagatt 354
Trp His Glu Asn Ser Gln Glu Glu Arg Lys Tyr
          80          85
gtgtttgctg aatttgattg acgaagaagt caccatgaaa atcacagtga accatttggg 414
aagcaaaactg ccaaaaaaat aatagttagt catgctctca ggctgggtgt tttggctggt 474
gtgggtttct tgcatttcca gatgattgca aagagctgtt tctcaatttc tgcaacaagt 534
gccagctgaa attttgggtac cagtttcatt aaatatgtat aacaaaakaa aaaaaaaaaa 594
aaaaaaaaaa aaaaaaaaaa aaaaaaagaa aaaaaaaaaa aaa 637

<210> 194
<211> 706
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 183..443

<400> 194
agaagttctc agagggtgag ggtcccatc ctctgcagg acaggcccta gctaccgagt 60
cacagaaacc cagggccgaa gcaaagtccc aatcccagag aggctggggc acacctacaa 120
ctgaaaggag gcttagaaat ccttcagaga ccaccctatc ggttctctc cacctggaca 180
gg atg agc cag caa cac aga agg aag agg cct tcc tcc gaa aga aaa 227
Met Ser Gln Gln His Arg Arg Lys Arg Pro Ser Ser Glu Arg Lys
1 5 10 15
agc aca aga aag atg gac aca tgg cag agt ctt aaa gtc aaa gaa gta 275
Ser Thr Arg Lys Met Asp Thr Trp Gln Ser Leu Lys Val Lys Glu Val
20 25 30
ttc tgt aag cat aat tct tcc tat gaa tgc ctt ctc tat aaa gag gtt 323
Phe Cys Lys His Asn Ser Ser Tyr Glu Cys Leu Leu Tyr Lys Glu Val
35 40 45
gaa gca aga cag gtt tct aag aca gcc acc gat ggg tcc tac ctc ctc 371
Glu Ala Arg Gln Val Ser Lys Thr Ala Thr Asp Gly Ser Tyr Leu Leu
50 55 60
gta ttc aca tcc tat gta atc tcc tcc cca gtg tgg act gga cct ggt 419
Val Phe Thr Ser Tyr Val Ile Ser Ser Pro Val Trp Thr Gly Pro Gly
65 70 75
gac ttg ctt cca gtg aat aga ata tagcaaaagt gattgatgtc acctccaaga 473
Asp Leu Leu Pro Val Asn Arg Ile
80 85
ttcagctata gaagactatg actatgactt tcctcttggc tagcattctc gctaaccctt 533
cctgcttgct tgtactgagc tgcctatga agaggcccat gtagggtggc ctgggtgggg 593
gtgatctgtg gccaacagcc agcaaggaac taaatcctgt ttacaaccac atgagcttgg 653
aaggagatcc ttccccagta aagccaggag atgaatacaa aaaaaaaaaa aaa 706

<210> 195
<211> 670
<212> DNA
<213> Homo sapiens

```

<220>  
<221> CDS  
<222> 94..228

<400> 195  
actttttcagg ggacattcag aggcattcagc ccccttccctcc tcaccagctc ccagagttcc 60  
catctccatc cccaatccta aagaaggaaa tgc atg cca cgg tcc tca agg agc 114  
Met Pro Arg Ser Ser Arg Ser  
1 5  
cct ggg gac cca ggc gcc cta ctc gaa gat ggc cca caa tcc cag acc 162  
Pro Gly Asp Pro Gly Ala Leu Leu Glu Asp Gly Pro Gln Ser Gln Thr  
10 15 20  
ccg gag gat tgc cca gcg agg ccg gaa cac cag cag gat ggc aga gga 210  
Pro Glu Asp Cys Pro Ala Arg Pro Glu His Gln Gln Asp Gly Arg Gly  
25 30 35  
cac ctc ccc aaa cat gaa tgacaacatc ctgttgccctg tccgcaacaa 258  
His Leu Pro Lys His Glu  
40 45  
tgaccaagcc ctaggcctga ctcaagtgcac gctgggatgt gtgtccctggt tcacctgttt 318  
tgccctgctcc ctgagaactc aggcccagca ggttctgttt aacacgtgca gatgcaagct 378  
gctgtgccag aagctcatgg agaagacagg cattctgctc ctctgtgctt tcggtgtgtc 438  
ccagggccct gccagtcctc aggtggaagg tatccctggg ccctggcact gattatagga 498  
cactgggcaa gacactgcac cgccacgtga ctcaagtttcc ccatctgcct gatgggtgtt 558  
gctgtgagaa ttatgaaatg aaatgatgac catgaaaata ttgtagaagc caagaaatgc 618  
ttcagaagtt ataaagctct ccccaaaccg tgttatgaaa aaaaaaaaaa aa 670

<210> 196  
<211> 510  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 133..327

<400> 196  
aacctcaagg agccctgttg tgctaccgac tgcagagctc atggacatcc atcaggaagc 60  
ctccaatacc caaaccaggg gtagttgcct aatccatata catgtggata gctctttact 120  
taggaaacct tg atg gct tat ttg gat gac aaa ggt tcc ctt ttg gcg ata 171  
Met Ala Tyr Leu Asp Asp Lys Gly Ser Leu Leu Ala Ile  
1 5 10  
cat agc cat gcg aga caa cat agc cat gaa aca aac caa gtc cac cag 219  
His Ser His Ala Arg Gln His Ser His Glu Thr Asn Gln Val His Gln  
15 20 25  
tgg ctt cct agg aac aca ttt gct ttc ctg ata aaa gag gac aga tgc 267  
Trp Leu Pro Arg Asn Thr Phe Ala Phe Leu Ile Lys Glu Asp Arg Cys  
30 35 40 45  
agt tgc aga agt acc tgt gcc tct ttt tct ttt tct tct tct ttt tct 315  
Ser Cys Arg Ser Thr Cys Ala Ser Phe Ser Phe Ser Ser Ser Phe Ser  
50 55 60  
ttt tta atc tct taaatgcaga tataagaact ggtactgaag cagccatctt 367  
Phe Leu Ile Ser  
65  
gtgaccataa ggaagaagcc aagaacatca gaaccagtgg cctagccatt gcacagtcac 427  
ctaaacacac ctctggactt gttattatgt aaaaaaaaaa aaacacctgc tcttggttatt 487  
tgcaatccaa aaaaaaaaaa aaa 510

[illegible]

<400> 197

```
<210> 198
<211> 667
<212> DNA
<213> Homo sapiens
```

<400> 198

218

50	55	60	
cag atc tct agc tac ctc tac tta aat act gct ctt gtg gac ttg cct			240
Gln Ile Ser Ser Tyr Leu Tyr Leu Asn Thr Ala Leu Val Asp Leu Pro			
65	70	75	
ggt gtg gcg gcc tcc cag gca tgt gac tct cag cag gtg act tgg ctt			288
Gly Val Ala Ala Ser Gln Ala Cys Asp Ser Gln Gln Val Thr Trp Leu			
80	85	90	95
ctc tac gtt gct aat ggt gcc tac tcg gca tgt aac agg cct gga			333
Leu Tyr Val Ala Asn Gly Ala Tyr Ser Ala Cys Asn Arg Pro Gly			
100	105	110	
tgaacggtag ctgctgcggt tacattatta gcttcagttt gcccgcaccag gctagatggt			393
taatcagatt tcacagactt cacagtgtga gttggggatg tgacttcgta tgaaagtga			453
ggaactcagg ctcagagagg gtgagacgta ggagcatggc cactgcgcga gctcggggct			513
ggctgtgggt ttctcccat tccctgccca tctgggaagt cgctgccacc ccctacgctt			573
gtctgtgac tcccagtcct cctaaccctc cagaatgtaa acagcagcag atgaacaaaa			633
ataaaaaatac aaaaggccga aaaaaaaaaa aaaa			667

<210> 199  
 <211> 514  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 1..363

<400> 199	
acg agt tct tcc ggg gcg gag gtc acc atg gca gct gcc ttg gct cgg	48
Thr Ser Ser Ser Gly Ala Glu Val Thr Met Ala Ala Ala Leu Ala Arg	
1	5
ctt ggt ctg cgg cct gtc aaa cag gtt cgg gtt cag ttc tgt ccc ttc	96
Leu Gly Leu Arg Pro Val Lys Gln Val Arg Val Gln Phe Cys Pro Phe	
20	25
gag aaa aac gtg gaa tcg acg agg acc ttc ctg cag acg gtg agc agt	144
Glu Lys Asn Val Glu Ser Thr Arg Thr Phe Leu Gln Thr Val Ser Ser	
35	40
gag aag gtc cgc tcc act aat ctc aac tgc tca gtg att gcg gac gtg	192
Glu Lys Val Arg Ser Thr Asn Leu Asn Cys Ser Val Ile Ala Asp Val	
50	55
agg cat gac ggc tcc gag ccc tgc gtg gac gtg ctg ttc gga gac ggg	240
Arg His Asp Gly Ser Glu Pro Cys Val Asp Val Leu Phe Gly Asp Gly	
65	70
cat cgc ctg att atg cgc ggc gct cat ctc acc gct ctg gaa atg ctc	288
His Arg Leu Ile Met Arg Gly Ala His Leu Thr Ala Leu Glu Met Leu	
85	90
acc gcc ttc gcc tcc cac atc cgg gcc agg gac gcg gcg ggc agc ggg	336
Thr Ala Phe Ala Ser His Ile Arg Ala Arg Asp Ala Ala Gly Ser Gly	
100	105
gac aag ccg ggc gct gat act ggt cgc tgacagcgcc aaagagacca	383
Asp Lys Pro Gly Ala Asp Thr Gly Arg	
115	120
acaagatgat ttgcgtggac taggacactt aacctaagaa gagtttctact taatcattca	443
aatcactatc tgaaggggtca cggagcgcaa aataaagttt aaaaccctgc taccaaaaaa	503
aaaaaaaaa a	514

<210> 200  
 <211> 462  
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 41..337

<400> 200

```
cttcaccacc aaaactctcc actccaccag cacagccaaa atg ctc gca cgt gct      55
                                   Met Leu Ala Arg Ala
                                   1      5
act ttc cgc gcc gcc tcg gcc cca act ctc gtc gcc cgc cgc ggc ttc      103
Thr Phe Arg Ala Ala Ser Ala Pro Thr Leu Val Ala Arg Arg Gly Phe
                                   10      15      20
cag tcg acc cgc gcg caa atg gcc agc cca tac cac tac ccc gag ggt      151
Gln Ser Thr Arg Ala Gln Met Ala Ser Pro Tyr His Tyr Pro Glu Gly
                                   25      30      35
cct cgc agc aac ttg cca ttc gac ccg ctg aag aag ggc ttt gct ttc      199
Pro Arg Ser Asn Leu Pro Phe Asp Pro Leu Lys Lys Gly Phe Ala Phe
                                   40      45      50
aag tac tgg ggc ttt atg ggc acc gga ttc gcc ctt ccc ttc ctc ctt      247
Lys Tyr Trp Gly Phe Met Gly Thr Gly Phe Ala Leu Pro Phe Leu Leu
                                   55      60      65
gct gtc tgg caa aca gaa caa gcc gta aat gcg ctg aga cac ggc gtg      295
Ala Val Trp Gln Thr Glu Gln Ala Val Asn Ala Leu Arg His Gly Val
                                   70      75      80      85
gac atg cgt atc ggg atc ccg ggg aac acg gca ttt gta gat      337
Asp Met Arg Ile Gly Ile Pro Gly Asn Thr Ala Phe Val Asp
                                   90      95
taggtggagg gcccgcatcac ggctatacta gacatcacag catcaatttc attgtctgtc      397
ccccaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa
aaaaaa      457
                                     462
```

<210> 201

<211> 551

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 1..549

<400> 201

```
aga gag gga gcc cga gcc agg cca tct cca acc atg tcc gac gag gcc      48
Arg Glu Gly Ala Arg Ala Arg Pro Ser Pro Thr Met Ser Asp Glu Ala
1      5      10      15
tcg gcc atc act tcc tac gag aag ttt cta acc ccc gag gag ccc ttc      96
Ser Ala Ile Thr Ser Tyr Glu Lys Phe Leu Thr Pro Glu Glu Pro Phe
                                   20      25      30
cca ctc ctg gga cct cct cgc ggg gtg ggc acc tgc ccg agc gag gag      144
Pro Leu Leu Gly Pro Pro Arg Gly Val Gly Thr Cys Pro Ser Glu Glu
                                   35      40      45
ccg ggc tgc ctg gac atc agc gac ttc ggc tgc cag ctg tcc tcc tgc      192
Pro Gly Cys Leu Asp Ile Ser Asp Phe Gly Cys Gln Leu Ser Ser Cys
                                   50      55      60
cat cgc acc gac ccg ctc cac cgc ttc cac acc aac agg tgg aac cta      240
His Arg Thr Asp Pro Leu His Arg Phe His Thr Asn Arg Trp Asn Leu
65      70      75      80
act tct tgt gga aca agt gtt gcc agc tca gaa ggc agt gag gag ctg      288
```





tagcacttac tgggattggt cagatagcga gtttgaatgg cagttaccag gcagtgcacat 465  
tgccagtggg agtgatgnta ctttctgatg tcatacccag tattccaagt tcaccttgcc 525  
tgcttcctaa aaaaaaaaaa aaaaa 550

<210> 203  
<211> 408  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 1..315

<400> 203  
atc ggg ccg cga gcg ccc tcc ccg tcc ttt tcc gtg aga gac gta gag 48  
Ile Gly Pro Arg Ala Pro Ser Pro Ser Phe Ser Val Arg Asp Val Glu  
1 5 10 15  
ctg agc gac cca gcc cgc gag cga ggt gag atg ccg gtg gcc gtg ggt 96  
Leu Ser Asp Pro Ala Arg Glu Arg Gly Glu Met Pro Val Ala Val Gly  
20 25 30  
ccc tac gga cag tcc cag cca agc tgc ttc gac cgt gtc aaa atg ggc 144  
Pro Tyr Gly Gln Ser Gln Pro Ser Cys Phe Asp Arg Val Lys Met Gly  
35 40 45  
ttc gtg atg ggt tgc gcc gtg ggc atg gcg gcc ggg gcg ctc ttc ggc 192  
Phe Val Met Gly Cys Ala Val Gly Met Ala Ala Gly Ala Leu Phe Gly  
50 55 60  
acc ttt tcc tgt ctc agg atc gga atg ccg ggt cga gag ctg atg ggc 240  
Thr Phe Ser Cys Leu Arg Ile Gly Met Arg Gly Arg Glu Leu Met Gly  
65 70 75 80  
ggc att ggg aaa acc atg atg cag agt ggc ggc acc ttt ggc aca ttc 288  
Gly Ile Gly Lys Thr Met Met Gln Ser Gly Gly Thr Phe Gly Thr Phe  
85 90 95  
atg gcc att ggg atg ggc atc cga tgc taaccatggt tgccaactac 335  
Met Ala Ile Gly Met Gly Ile Arg Cys  
100 105  
atctgtccct tcccatcaat cccagcccat gtactaataa aagaaagtct ttgagcaaaa 395  
aaaaaaaaaa aaa 408

<210> 204  
<211> 665  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 94..582

<400> 204  
acttttcagg ggacattcag aggcattcag cccttctctc tcaccagctc ccagagttcc 60  
catctccatc cccaatccta aagaaggaaa tcc atg cca ccg tcc tca agg agc 114  
Met Pro Arg Ser Ser Arg Ser  
1 5  
cct ggg gac cca ggc gcc cta ctc gaa gat gtg gcc cac aat ccc aga 162  
Pro Gly Asp Pro Gly Ala Leu Leu Glu Asp Val Ala His Asn Pro Arg  
10 15 20  
ccc ccg agg att gcc cag cga ggc ccg aac acc agc agg atg gca gag 210  
Pro Arg Arg Ile Ala Gln Arg Gly Arg Asn Thr Ser Arg Met Ala Glu  
25 30 35

```

gac acc tcc cca aac atg aat gac aac atc ctg ttg cct gtc cgc aac      258
Asp Thr Ser Pro Asn Met Asn Asp Asn Ile Leu Leu Pro Val Arg Asn
40                               45                               50                               55
aat gac caa gcc cta ggc ctg act cag tgc atg ctg gga tgt gtg tcc      306
Asn Asp Gln Ala Leu Gly Leu Thr Gln Cys Met Leu Gly Cys Val Ser
60                               65                               70
tgg ttc acc tgt ttt gcc tgc tcc ctg aga act cag gcc cag cag gtt      354
Trp Phe Thr Cys Phe Ala Cys Ser Leu Arg Thr Gln Ala Gln Gln Val
75                               80                               85
ctg ttt aac acg tgc aga tgc aag ctg ctg tgc cag aag ctc atg gag      402
Leu Phe Asn Thr Cys Arg Cys Lys Leu Leu Cys Gln Lys Leu Met Glu
90                               95                               100
aag aca ggc att ctg ctc ctc tgt gct ttc ggt gtg tcc cag ggc cct      450
Lys Thr Gly Ile Leu Leu Leu Cys Ala Phe Gly Val Ser Gln Gly Pro
105                               110                               115
gcc cag tcc cag gtg gag gta tcc ctg ggc cct ggc act gat tat agg      498
Ala Gln Ser Gln Val Glu Val Ser Leu Gly Pro Gly Thr Asp Tyr Arg
120                               125                               130                               135
aca ctg ggc aag aca ctg cac tgc cac gtg act cag ttt ccc cat ctg      546
Thr Leu Gly Lys Thr Leu His Cys His Val Thr Gln Phe Pro His Leu
140                               145                               150
cct gat ggg tgt tgc tgt gag aat tat gaa atg aaa tgatgacccat      592
Pro Asp Gly Cys Cys Cys Glu Asn Tyr Glu Met Lys
155                               160
gaaaatattg tagaagccaa gaaatgcttc agaagttata aagctctccc caaacccgcaa      652
aaaaaaaaaa aaa                                                    665

<210> 205
<211> 1008
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 540..923

<400> 205
atttaggtga gctgccacgt ccggaggagg gcagcaagaa tgaaagacct ctagttttcc      60
agactcccgg agccctgggtc tctacaccac atggacgtta tccacctcct ctgtgtcctc      120
ccaaggcagc atttcagaag gtgatccacg gcaaagccgt cccttcaaata ccgtctttgt      180
gcccactgcc atagtcaacc ccgtgagaag cacagccggc cctgggactt taggacaagg      240
gtctcttcgg aaagggcgga gcagcatgag aaagagtaag tgggtggcaga gagatggatc      300
cctgcagaga cccctccagt ccgggatccc cactctcgtg gtaggctccc tcagacgcag      360
ccccaccatg gtccttcggc ctacagcagtt ccaattctac cagccacagg ggatcacctc      420
ctccccctca gccgtggtgg tggagatggg gtccaagcct gccctcacgg gggagcccgc      480
cctcacgtgc atcagcaggg gcagtgaggc ggatccactc cgcggccagc tccctcatt      539
atg gaa gac aaa gaa atc ccc atc aag agt gag cct ctg cca aaa ccg      587
Met Glu Asp Lys Glu Ile Pro Ile Lys Ser Glu Pro Leu Pro Lys Pro
1                               5                               10                               15
ccc gca tct gcc cca cca tcc atc ctg gtg aaa cca gaa aac tca aga      635
Pro Ala Ser Ala Pro Pro Ser Ile Leu Val Lys Pro Glu Asn Ser Arg
20                               25                               30
aat gga atc gaa aag caa gtc aaa acc gtg aga ttt cag aat tac agc      683
Asn Gly Ile Glu Lys Gln Val Lys Thr Val Arg Phe Gln Asn Tyr Ser
35                               40                               45
cct cct ccc acc aaa cat tac acc tcc cat ccc acc tcc gga aag cct      731
Pro Pro Pro Thr Lys His Tyr Thr Ser His Pro Thr Ser Gly Lys Pro
50                               55                               60

```



```

<400> 207
cttttacgac ggcgggaaa gcaacggcaa gggccgcagc cagcaccggg cggagagggc 60
tacc atg ggg aaa atc gcg ctg caa ctc aaa gcc acg ctg gag aac atc 109
      Met Gly Lys Ile Ala Leu Gln Leu Lys Ala Thr Leu Glu Asn Ile
      1          5          10          15
acc aac ctc cgg ccc gtg ggc gag gac ttc cgg tgg tac ctg aag atg 157
Thr Asn Leu Arg Pro Val Gly Glu Asp Phe Arg Trp Tyr Leu Lys Met
      20          25          30
aaa tgt ggc aac tgt ggt gag att tcg gac aag tgg cag tac atc cgg 205
Lys Cys Gly Asn Cys Gly Glu Ile Ser Asp Lys Trp Gln Tyr Ile Arg
      35          40          45
ctg atg gac agt gtg gca ctg aag ggg ggc cgt ggc agt gct tcc atg 253
Leu Met Asp Ser Val Ala Leu Lys Gly Gly Arg Gly Ser Ala Ser Met
      50          55          60
gtc cag aag tgc aag ctg tgt gca aga gaa aat tcc atc gag att tta 301
Val Gln Lys Cys Lys Leu Cys Ala Arg Glu Asn Ser Ile Glu Ile Leu
      65          70          75
agc agc acc atc aag cct tac aat gct gaa gac aat gag aac ttc aag 349
Ser Ser Thr Ile Lys Pro Tyr Asn Ala Glu Asp Asn Glu Asn Phe Lys
      80          85          90          95
aca ata gtg gag ttt gag tgc cgg ggc ctt gaa cca gtt gat ttc cag 397
Thr Ile Val Glu Phe Glu Cys Arg Gly Leu Glu Pro Val Asp Phe Gln
      100          105          110
ccg cas gwg rtw ttg ctg ctg aag gtg tgg agt cag gga cag cct tca 445
Pro Xaa Xaa Xaa Leu Leu Leu Lys Val Trp Ser Gln Gly Gln Pro Ser
      115          120          125
gtg aca tta atc tgc agg aga agg act ggg act gac tat gat gaa aag 493
Val Thr Leu Ile Cys Arg Arg Arg Thr Gly Thr Asp Tyr Asp Glu Lys
      130          135          140
gcc cag gag tct gtg gga atc tat gag gtc acc cac cag ttt gtg aag 541
Ala Gln Glu Ser Val Gly Ile Tyr Glu Val Thr His Gln Phe Val Lys
      145          150          155
tgc tgatccctct tccttcccag ttgcccttaa gaactgagaa aggacaaagt 594
Cys
160
actctaagca gcagagccca cagaggctcg ttcctttgac ccttggtctcc tgggtggctat 654
acgaaacctt cacaatctgc atgctggact ttattacagc ttcccaagcc ccatcaataa 714
agccctgttt cagcgtacaa aaaaaaaaaa aaaaa 749

```

```

<210> 208
<211> 594
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 117..467

```

```

<400> 208
aaatgtagcc tgggtggtgtt cccaggagga aaagaacgag agactggtgg cagcacaccc 60
tggggccccc actccccgcc gcaagtccctg aggatggcca gcagagaaac aagaaa atg 119
      Met
      1
gac tcc ctg gct gct gga gag ttg aat gcc agc cac cag cca tgg gtg 167
Asp Ser Leu Ala Ala Gly Glu Leu Asn Ala Ser His Gln Pro Trp Val
      5          10          15
cca gag ttt gta gcc tat tgg agg aaa aca cac caa gat cac ctc tgc 215
Pro Glu Phe Val Ala Tyr Trp Arg Lys Thr His Gln Asp His Leu Cys

```

20	25	30	
agc ctg cac agc cgg gcc ttt gga ctc ctg gat gct aga gtg acc tgg			263
Ser Leu His Ser Arg Ala Phe Gly Leu Leu Asp Ala Arg Val Thr Trp			
35	40	45	
gcg ctg agg agg gcc ccc gag cca gta cca gga aag gat aga ctc ctg			311
Ala Leu Arg Arg Ala Pro Glu Pro Val Pro Gly Lys Asp Arg Leu Leu			
50	55	60	65
ctt gca gca ttc cca gca gag gca tcg cct gtg gac acc gcg tct gtg			359
Leu Ala Ala Phe Pro Ala Glu Ala Ser Pro Val Asp Thr Ala Ser Val			
70	75	80	
tct gta tat ggc aga gct ccc aga tat atg cac aag gga gtg aaa aaa			407
Ser Val Tyr Gly Arg Ala Pro Arg Tyr Met His Lys Gly Val Lys Lys			
85	90	95	
tgt gtt tgc acc cca gtc tct aaa aat tca aca gcc tgg tta ctt ctg			455
Cys Val Cys Thr Pro Val Ser Lys Asn Ser Thr Ala Trp Leu Leu Leu			
100	105	110	
ggg ggt ata tcg taggtggcct taatacgtgt tatttgctca tctgtatttc			507
Gly Gly Ile Ser			
115			
ttactctttg cacaattaaa ccatgttcct tttacttatg tacattttta ataaaagaaa			567
ggtgtaacg aaaaaaaaaa aaaaaaa			594

<210> 209  
 <211> 2098  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 893..1897

<400> 209			
accaggtcct ccgtggtgca cctgaaatgg tcaacagaag tcttgtgaca cgtggaatca	60		
tttcagagtc accccttctg cctcctgctc aagcaacaga cctgccgac acccccgctg	120		
ggcccgcggt tctcagggtc ttcctaatacc cctgggcttt ccggcttgct gtgtgcctgg	180		
agtcaggccg ccgtgcggca ggctgttaac ctacgctcgg ggagagtggg atggagccac	240		
cttctcatgg aacgatcctc gccttccttc atctccattg ttttatggct tcacacggac	300		
cgtggctttc tgcattggaag cttggtggcc aggggtgctgt cactttggga agcagccaga	360		
gaaccacagg atgcgtgaat cggctccttc gtcttcattg gcattctcgg ccagggtggt	420		
gtcttgtgct gtgattagtg ggtcactggc aagtgtctga atgaagtgga ggttccggtg	480		
gcaacagtga cggggaaggg ctatgggtcc gcctcaatgt catctgcccc atccctgggc	540		
ctccaggaat ccagggtctc agccctgctt ttagaaggaa gtctgacgg ccacgtgga	600		
tctggaggac gtccggagct acagggcgga gatttcatct cgaaacctgg cggccagcag	660		
ggcgagcccc taccacagag tgaagtgga ctttgccctc tcgtgccacg aggacttgct	720		
ggcaccctac tctgagccca tcgagtggaa ataccacagc cctgaggagg agataagcct	780		
tggacctgcc tgcctggctct gggatttttt aagacgaagt caacaggcag ggtttttgct	840		
gcccttgagt ggcggggtgg acagcgcagc caccgctgc ctcactact cc atg tgc	898		
	Met Cys		
	1		
tgc cag gtc tgc gag gcc gtg agg agt gga aat gag gaa gtg ctg gct	946		
Cys Gln Val Cys Glu Ala Val Arg Ser Gly Asn Glu Glu Val Leu Ala			
5	10	15	
gat gtc cgc acc atc gtg aac cag atc agc tac acc ccc cag gat ccc	994		
Asp Val Arg Thr Ile Val Asn Gln Ile Ser Tyr Thr Pro Gln Asp Pro			
20	25	30	
cga gac ctc tgt gga cgc ata ctg acc acc tgc tac atg gcc agc aag	1042		
Arg Asp Leu Cys Gly Arg Ile Leu Thr Thr Cys Tyr Met Ala Ser Lys			
35	40	45	50

aac	tcc	tcc	cag	gag	acg	tgc	acc	cgg	gcc	aga	gag	ttg	gcc	cag	cag	1090
Asn	Ser	Ser	Gln	Glu	Thr	Cys	Thr	Arg	Ala	Arg	Glu	Leu	Ala	Gln	Gln	
			55						60					65		
att	gga	agc	cac	cac	atc	agt	ctc	aac	atc	gat	cca	gcc	gtg	aag	gcc	1138
Ile	Gly	Ser	His	His	Ile	Ser	Leu	Asn	Ile	Asp	Pro	Ala	Val	Lys	Ala	
			70					75				80				
gtc	atg	ggc	atc	ttc	agc	ctg	gtg	acg	ggg	aag	agc	cct	ctg	ttt	gca	1186
Val	Met	Gly	Ile	Phe	Ser	Leu	Val	Thr	Gly	Lys	Ser	Pro	Leu	Phe	Ala	
		85					90				95					
gct	cat	gga	gga	agc	agc	agg	gaa	aac	ctg	gcg	ctg	caa	aat	gtg	cag	1234
Ala	His	Gly	Gly	Ser	Ser	Arg	Glu	Asn	Leu	Ala	Leu	Gln	Asn	Val	Gln	
	100					105					110					
gct	cga	ata	cgg	atg	gtc	ctc	gcc	tat	ctg	ttt	gct	cag	ttg	agc	ctc	1282
Ala	Arg	Ile	Arg	Met	Val	Leu	Ala	Tyr	Leu	Phe	Ala	Gln	Leu	Ser	Leu	
115					120					125					130	
tgg	tct	cgg	ggc	gtc	cac	ggc	ggg	ctc	ctc	gtg	ctg	gga	tcc	gcc	aac	1330
Trp	Ser	Arg	Gly	Val	His	Gly	Gly	Leu	Leu	Val	Leu	Gly	Ser	Ala	Asn	
			135					140						145		
gtg	gat	gag	agt	ctc	ctg	ggc	tac	ctg	acc	aag	tac	gac	tgc	tcc	agt	1378
Val	Asp	Glu	Ser	Leu	Leu	Gly	Tyr	Leu	Thr	Lys	Tyr	Asp	Cys	Ser	Ser	
			150					155					160			
gcg	gac	atc	aac	ccc	ata	ggc	ggg	atc	agc	aag	acg	gac	ctc	agg	gcc	1426
Ala	Asp	Ile	Asn	Pro	Ile	Gly	Gly	Ile	Ser	Lys	Thr	Asp	Leu	Arg	Ala	
		165					170					175				
ttc	gtc	cag	ttc	tgc	atc	cag	cgc	ttc	cag	ctt	cct	gcc	ctg	cag	agc	1474
Phe	Val	Gln	Phe	Cys	Ile	Gln	Arg	Phe	Gln	Leu	Pro	Ala	Leu	Gln	Ser	
		180				185					190					
atc	ctg	ttg	gcg	ccg	gcc	acc	gca	gag	ctg	gag	ccc	ttg	gct	gat	gga	1522
Ile	Leu	Leu	Ala	Pro	Ala	Thr	Ala	Glu	Leu	Glu	Pro	Leu	Ala	Asp	Gly	
195				200						205				210		
cag	gtg	tcc	cag	acc	gac	gag	gaa	gat	atg	ggg	atg	aca	tat	gcg	gag	1570
Gln	Val	Ser	Gln	Thr	Asp	Glu	Glu	Asp	Met	Gly	Met	Thr	Tyr	Ala	Glu	
			215						220					225		
ctc	tcg	gtc	tat	ggg	aaa	ctc	agg	aag	gtg	gcc	aag	atg	ggg	ccc	tac	1618
Leu	Ser	Val	Tyr	Gly	Lys	Leu	Arg	Lys	Val	Ala	Lys	Met	Gly	Pro	Tyr	
			230					235					240			
agc	atg	ttc	tgc	aaa	ctc	ctc	ggc	atg	tgg	aga	cac	atc	tgc	acc	ccg	1666
Ser	Met	Phe	Cys	Lys	Leu	Leu	Gly	Met	Trp	Arg	His	Ile	Cys	Thr	Pro	
		245					250					255				
aga	cag	gtc	gct	gac	aaa	gtg	aag									

<210> 210  
 <211> 428  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 85..342

<400> 210  
 acactggtac agtcacctag cccatcagtt ccttcgtcga cagcgccggg gacatccaga 60  
 ctacaattta cagttcctct atcc atg tgc tgg gtt ata aat cat gcc atc 111  
 Met Cys Trp Val Ile Asn His Ala Ile  
 1 5  
 ctc cct aga atg aga atg cac agc aag cgg cag aca atc acc cgg cat 159  
 Leu Pro Arg Met Arg Met His Ser Lys Arg Gln Thr Ile Thr Arg His  
 10 15 20 25  
 tcg gca tct ctt tct ttt cac gcg ctc cct cgc tcc gcc ttt ctc cag 207  
 Ser Ala Ser Leu Ser Phe His Ala Leu Pro Arg Ser Ala Phe Leu Gln  
 30 35 40  
 ctc tgc ctt ctc agg cag ata cat cag ata cct tgt tta tcc atc ttc 255  
 Leu Cys Leu Leu Arg Gln Ile His Gln Ile Pro Cys Leu Ser Ile Phe  
 45 50 55  
 agc tcc act ctg agg gcg cag acg cac gat tcc ggg atc ggg tgc acc 303  
 Ser Ser Thr Leu Arg Ala Gln Thr His Asp Ser Gly Ile Gly Cys Thr  
 60 65 70  
 acg gcg aas cca ggc ggg aga cgg cag gag cag ctc agg taaccagggg 352  
 Thr Ala Xaa Pro Gly Gly Arg Arg Gln Glu Gln Leu Arg  
 75 80 85  
 aagcttgctg gccacggag atgcagccgt ggagctgtga ggaaagacgg tctggcttca 412  
 aaaaaaaaaa aaaaaa 428

<210> 211  
 <211> 769  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 155..433

<400> 211  
 atttttcccc ccttgctcgg gatggtgcc aaggaggctg tgcgggcccc gctccgcttc 60  
 gaatggtgga tgctgtgggg caccacctcc ttgaggacca aggcactcca gctgccagga 120  
 atttggtctgc taacctcaca cagctgagcc ttcc atg aaa att gct ctc tgc caa 175  
 Met Lys Ile Ala Leu Cys Gln  
 1 5  
 aga gaa ctt cct agt cca agg tca tgt cta ctc tcc aga gat gtg act 223  
 Arg Glu Leu Pro Ser Pro Arg Ser Cys Leu Leu Ser Arg Asp Val Thr  
 10 15 20  
 gga gtg att tgc acc cgg atg cct aga ctc gcc atc tgc tca aag act 271  
 Gly Val Ile Cys Thr Arg Met Pro Arg Leu Ala Ile Cys Ser Lys Thr  
 25 30 35  
 gct cag aaa gcc ctc cca tgc att ccc ctg ctg cat acc agc cca ctc 319  
 Ala Gln Lys Ala Leu Pro Cys Ile Pro Leu Leu His Thr Ser Pro Leu  
 40 45 50 55  
 tgc ctg cag ctg ctg tct gca gga ctt cat atc tat gcc aca ctg tgt 367



Cys Leu Gln Leu Leu Ser Ala Gly Leu His Ile Tyr Ala Thr Leu Cys  
60 65 70  
aaa agc tgt gct tca aga aat cac aaa aac att ttc ctg cac cta cta 415  
Lys Ser Cys Ala Ser Arg Asn His Lys Asn Ile Phe Leu His Leu Leu  
75 80 85  
cac agc ctg agt gcg gca taagttgacc ttgcttgcta agaaatgggg 463  
His Ser Leu Ser Ala Ala  
90  
caagaaatgc ttttttgtat gtgtcatgtc tgtttgtttt tcaattaaga gaggaaagca 523  
ttaggcagat ggaatgtaca tgtgaggatg aggagacaga aaacaagtag ccctttccat 583  
caagatagag gggtttcttg gggtgctggc tattgaatgt cactcctgat ttctctttcc 643  
aaggcactgt accaccagcc tactgagatt gtgtgggagc tttcatgggg gttgtatttc 703  
actgatgaaa ataaattttt tgcataatgt gaaaaaaaaa aaaaaaaaga aaaaaaaaaa 763  
aaaaaa 769  
<210> 212  
<211> 914  
<212> DNA  
<213> Homo sapiens  
<220>  
<221> CDS  
<222> 63..386  
<400> 212  
cttttttaggg agtccaaggt acagtcgccg cgtgcggagc ttgttactgg ttacttggcc 60  
tc atg gcg gtc cga gct tcg ttc gag aac aac tgt gag atc ggc tgc 107  
Met Ala Val Arg Ala Ser Phe Glu Asn Asn Cys Glu Ile Gly Cys  
1 5 10 15  
ttt gcc aag ctc acc aac acc tac tgt ctg gta gcg atc gga ggc tca 155  
Phe Ala Lys Leu Thr Asn Thr Tyr Cys Leu Val Ala Ile Gly Gly Ser  
20 25 30  
gag aac ttc tac agt gtg ttc gag ggc gag ctc tcc gat acc atc ccc 203  
Glu Asn Phe Tyr Ser Val Phe Glu Gly Glu Leu Ser Asp Thr Ile Pro  
35 40 45  
gtg gtg cac gcg tct atc gcc ggc tgc cgc atc atc ggg cgc atg tgt 251  
Val Val His Ala Ser Ile Ala Gly Cys Arg Ile Ile Gly Arg Met Cys  
50 55 60  
gtg gga gac aga aga aat tct ggc aga tgt gct caa ggt gga agt ctt 299  
Val Gly Asp Arg Arg Asn Ser Gly Arg Cys Ala Gln Gly Gly Ser Leu  
65 70 75  
cag aca gac agt ggc cga cca ggt gct agt agg aag cta ctg tgt ctt 347  
Gln Thr Asp Ser Gly Arg Pro Gly Ala Ser Arg Lys Leu Leu Cys Leu  
80 85 90 95  
cag caa tca ggg agg gct ggt gca tcc caa gac ttc aat tgaagaccag 396  
Gln Gln Ser Gly Arg Ala Gly Ala Ser Gln Asp Phe Asn  
100 105  
gatgagctgt cctctcttct tcaagtcgcc cttgtggcgg ggactgtgaa ccgaggcagt 456  
gaggtgattg ctgctgggat ggtggtgaat gactggtgtg ccttctgtgg cctggacaca 516  
accagcacag agctgtcagt ggtggagagt gtcttcaagc tgaatgaagc ccagcctagc 576  
accattgccca ccagcatgcg ggattccctc attgacagcc tcacctgagt caccttccaa 636  
gttgttccat gggctcctgg ctctggactg tggccaacct tctccacatt ccgccaatc 696  
tgtacctgat gctggcaggg aggtggcaga gagctcactg ggactgaggg gctgggcacc 756  
caaccctttt ccacctgtgc ttatcgcttg gatctatcat tactgcaaaa acctgctctg 816  
ttgtgctggc tggcaggccc tgtggtgtgt ggctgagggt tctgctgtcc tgtgccaccc 876  
cattaaagtg cagttccctc caaaaaaaaaa aaaaaaaaaa 914  
<210> 213

<211> 1489  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 460..1290

<400> 213  
 cttctttccc tctccgtttt ggtgggctgg ttgaagatga aatccactga ggaggggaagt 60  
 ccagcaccct gtgtgccagt ccagaactgg cccatctgta gacccctga aaatcatatg 120  
 ggcttggatt tggatattct caacagaaaag ggtaaaggc tgatgggtacc taaagcctgg 180  
 tacttgaatt ttgatcaaga taagctgcct taagttctct tcattacaca aatgatccta 240  
 gataattgat agatcctgtg gttcaactgg atttctagat agaagctgga ttcattgtgat 300  
 gccagaggag taaaatttca agagactgaa accagatctg agtttcgctg ttccagtctg 360  
 gacctctttg gtgctgtaaa tcctggatat actgtagatg agtactgcgt ttttctttta 420  
 tggactctct tcagcttctg gagacctcac tatcctatt atg tct ttg tgt gaa 474  
 Met Ser Leu Cys Glu  
 1 5  
 gac atg ctg ctt tgt aat tat cga aag tgt cgc atc aaa ctc tct ggc 522  
 Asp Met Leu Leu Cys Asn Tyr Arg Lys Cys Arg Ile Lys Leu Ser Gly  
 10 15 20  
 tat gca tgg gtc act gcc tgc tct cac atc ttc tgt gat cag cat ggc 570  
 Tyr Ala Trp Val Thr Ala Cys Ser His Ile Phe Cys Asp Gln His Gly  
 25 30 35  
 agt ggt gag ttt agt cgc tca cca gct atc tgt cct gcc tgc aac agt 618  
 Ser Gly Glu Phe Ser Arg Ser Pro Ala Ile Cys Pro Ala Cys Asn Ser  
 40 45 50  
 acc ctt tct gga aag cta gat att gtc cgc aca gaa ctc agt cca tca 666  
 Thr Leu Ser Gly Lys Leu Asp Ile Val Arg Thr Glu Leu Ser Pro Ser  
 55 60 65  
 gag gaa tat aaa gct atg gta ttg gca gga ctg cga cca gag atc gtg 714  
 Glu Glu Tyr Lys Ala Met Val Leu Ala Gly Leu Arg Pro Glu Ile Val  
 70 75 80 85  
 ttg gac att agc tcc cga gcg ctg gcc ttc tgg aca tat cag gta cat 762  
 Leu Asp Ile Ser Ser Arg Ala Leu Ala Phe Trp Thr Tyr Gln Val His  
 90 95 100  
 cag gaa cgt ctc tat caa gaa tac aat ttc agc aag gct gag ggc cat 810  
 Gln Glu Arg Leu Tyr Gln Glu Tyr Asn Phe Ser Lys Ala Glu Gly His  
 105 110 115  
 ctg aaa cag atg gag aag ata tat act cag caa ata caa agc aag gat 858  
 Leu Lys Gln Met Glu Lys Ile Tyr Thr Gln Gln Ile Gln Ser Lys Asp  
 120 125 130  
 gta gaa ttg acc tct atg aaa ggg gag gtt acc tcc atg aag aaa gta 906  
 Val Glu Leu Thr Ser Met Lys Gly Glu Val Thr Ser Met Lys Lys Val  
 135 140 145  
 cta gaa gaa tac aag aaa aag ttc agt gac atc tct gag aaa ctt atg 954  
 Leu Glu Glu Tyr Lys Lys Phe Ser Asp Ile Ser Glu Lys Leu Met  
 150 155 160 165  
 gag cgc aat cgt cag tat caa aag ctc caa ggc ctc tat gat agc ctt 1002  
 Glu Arg Asn Arg Gln Tyr Gln Lys Leu Gln Gly Leu Tyr Asp Ser Leu  
 170 175 180  
 agg cta cga aac atc act att gct aac cat gaa ggc acc ctt gaa cca 1050  
 Arg Leu Arg Asn Ile Thr Ile Ala Asn His Glu Gly Thr Leu Glu Pro  
 185 190 195  
 tcc atg att gca cag tct ggt gtt ctt ggc ttc cca tta ggt aac aac 1098  
 Ser Met Ile Ala Gln Ser Gly Val Leu Gly Phe Pro Leu Gly Asn Asn  
 200 205 210

tcc aag ttt cct ttg gat aat aca cct gtt cga aat cgg ggc gat gga	1146
Ser Lys Phe Pro Leu Asp Asn Thr Pro Val Arg Asn Arg Gly Asp Gly	
215 220 225	
gat gga gat ttt cag ttc aga cca ttt ttt gcg ggt tct ccc aca gca	1194
Asp Gly Asp Phe Gln Phe Arg Pro Phe Phe Ala Gly Ser Pro Thr Ala	
230 235 240 245	
cct gaa ccc agc aac agc ttt ttt agt ttt gtc tct cca agt cgt gaa	1242
Pro Glu Pro Ser Asn Ser Phe Phe Ser Phe Val Ser Pro Ser Arg Glu	
250 255 260	
tta gag cag cag caa gtt tct agc agg gcc ttc aaa gta aaa aga att	1290
Leu Glu Gln Gln Gln Val Ser Ser Arg Ala Phe Lys Val Lys Arg Ile	
265 270 275	
tgagccacgc atagtgtcac gcacctgtga tcccagctac ttaggagggtt gaggctggga	1350
ggatcacttg agcccaggag tctgaggctt tagtgatcta agatcatgcc actgcactcc	1410
agcctgggca acagagtggag accctgtttc taaaaaaaaa taaagataat ttagctaact	1470
tcaaaaaaaaaa aaaaaaaaaa	1489
<210> 214	
<211> 776	
<212> DNA	
<213> Homo sapiens	
<220>	
<221> CDS	
<222> 21..539	
<400> 214	
caaatatattc catcacgggg atg ctt gtc atg tac ctg ctt gcc gcc ctc ttt	53
Met Leu Val Met Tyr Leu Leu Ala Ala Leu Phe	
1 5 10	
ggt tac cta acc ttc tat gga gaa gtt gaa gat gaa tta ctt cat gcc	101
Gly Tyr Leu Thr Phe Tyr Gly Glu Val Glu Asp Glu Leu Leu His Ala	
15 20 25	
tac agc aaa gtg tat aca tta gac atc cct ctt ctc atg gtt cgc ctg	149
Tyr Ser Lys Val Tyr Thr Leu Asp Ile Pro Leu Leu Met Val Arg Leu	
30 35 40	
gca gtc ctt gtg gca gta aca cta act gtg ccc att gtc ctc ttc cca	197
Ala Val Leu Val Ala Val Thr Leu Thr Val Pro Ile Val Leu Phe Pro	
45 50 55	
att cgt aca tca gtg atc aca ctg tta ttt ccc aaa cga ccc ttc agc	245
Ile Arg Thr Ser Val Ile Thr Leu Leu Phe Pro Lys Arg Pro Phe Ser	
60 65 70 75	
tgg ata cga cat ttc ctg att gca gct gtg ctt att gca ctt aat aat	293
Trp Ile Arg His Phe Leu Ile Ala Ala Val Leu Ile Ala Leu Asn Asn	
80 85 90	
gtt ctg gtc atc ctt gtg cca act ata aaa tac atc ttc gga ttc ata	341
Val Leu Val Ile Leu Val Pro Thr Ile Lys Tyr Ile Phe Gly Phe Ile	
95 100 105	
ggg gct tct tct gcc act atg ctg att ttt att ctt cca gca gtt ttt	389
Gly Ala Ser Ser Ala Thr Met Leu Ile Phe Ile Leu Pro Ala Val Phe	
110 115 120	
tat ctt aaa ctt gtc aag aaa gaa act ttt agg tca ccc caa aag gtc	437
Tyr Leu Lys Leu Val Lys Lys Glu Thr Phe Arg Ser Pro Gln Lys Val	
125 130 135	
ggg gct tta att ttc ctt gtg gtt gga ata ttc ttc atg att gga agc	485
Gly Ala Leu Ile Phe Leu Val Val Gly Ile Phe Phe Met Ile Gly Ser	
140 145 150 155	
atg gca ctc att ata att gac tgg att tat gat cct cca aat tcc aag	533

Met Ala Leu Ile Ile Ile Asp Trp Ile Tyr Asp Pro Pro Asn Ser Lys  
160 165 170  
cat cac taacacaagg aaaaatactt tcttttcta ttggaaatgg ttacaagtta 589  
His His  
tactccaaaa gatatttgaa ttatcttgat tggaatgtta ttcataggaa ataacaggaa 649  
gattccaaag acgtttacca gtmatatcac caggcacctg cagaagagga aaatcactgt 709  
ttttgtcaag gatggttgat tatgtgttta aaataaaacc tgtggtgcac aaaaaaaaaa 769  
aaaaaaa 776

<210> 215  
<211> 1412  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 34..1143

<400> 215  
atgcggtgaa gggcgagcgg cgcggcggct gcg atg agt gcc tct gcg gcc acc 54  
Met Ser Ala Ser Ala Ala Thr  
1 5  
ggg gtc ttc gtg ctg tcc ctc tgc gcc atc ccg gtc acc tat gtc ttc 102  
Gly Val Phe Val Leu Ser Leu Ser Ala Ile Pro Val Thr Tyr Val Phe  
10 15 20  
aac cac ctg gcg gcc cag cat gat tcc tgg act att gta ggg gtt gct 150  
Asn His Leu Ala Ala Gln His Asp Ser Trp Thr Ile Val Gly Val Ala  
25 30 35  
gcc ctc atc ctg ttc ctg gta gca ctg ctg gct cgt gtc ctc gtc aaa 198  
Ala Leu Ile Leu Phe Leu Val Ala Leu Leu Ala Arg Val Leu Val Lys  
40 45 50 55  
aga aaa cca ccc cgg gac cca ctg ttc tat gtg tat gca gtt ttt gga 246  
Arg Lys Pro Pro Arg Asp Pro Leu Phe Tyr Val Tyr Ala Val Phe Gly  
60 65 70  
ttt acc agc gtg gtg aac ctc atc ata gga ctg gag caa gat gga atc 294  
Phe Thr Ser Val Val Asn Leu Ile Ile Gly Leu Glu Gln Asp Gly Ile  
75 80 85  
att gac ggg ttc atg aca cac tac ttg aga gag ggt gaa ccg tat ctg 342  
Ile Asp Gly Phe Met Thr His Tyr Leu Arg Glu Gly Glu Pro Tyr Leu  
90 95 100  
aac acc gca tat ggg cac atg atc tgc tac tgg gat ggc tct gct cat 390  
Asn Thr Ala Tyr Gly His Met Ile Cys Tyr Trp Asp Gly Ser Ala His  
105 110 115  
tat ctg atg tac ctg gtg atg gtg gca gcc ata gca tgg gag gaa act 438  
Tyr Leu Met Tyr Leu Val Met Val Ala Ala Ile Ala Trp Glu Glu Thr  
120 125 130 135  
tat aga acc att ggc cta tat tgg gtt gga tct att att atg agt gtt 486  
Tyr Arg Thr Ile Gly Leu Tyr Trp Val Gly Ser Ile Ile Met Ser Val  
140 145 150  
gtt gtt ttt gtg cca gga aac att gta ggg aag tat gga aca cga att 534  
Val Val Phe Val Pro Gly Asn Ile Val Gly Lys Tyr Gly Thr Arg Ile  
155 160 165  
tgc cct gct ttt ttc tta agc ata cca tat act tgt ctt cct gtc tgg 582  
Cys Pro Ala Phe Phe Leu Ser Ile Pro Tyr Thr Cys Leu Pro Val Trp  
170 175 180  
gct ggt ttc aga atc tat aat cag cca tca gaa aat tat aat tac ccc 630  
Ala Gly Phe Arg Ile Tyr Asn Gln Pro Ser Glu Asn Tyr Asn Tyr Pro  
185 190 195

tca aag gtt att caa gaa gcc caa gcg aaa gac ctg ctg aga aga cca	678
Ser Lys Val Ile Gln Glu Ala Gln Ala Lys Asp Leu Leu Arg Arg Pro	
200 205 210 215	
ttt gat tta atg ttg gtt gtg tgt ctc ctc ctg gca act gga ttt tgc	726
Phe Asp Leu Met Leu Val Val Cys Leu Leu Ala Thr Gly Phe Cys	
220 225 230	
ctg ttc aga ggt ttg att gct ttg gat tgc cca tct gag ctc tgc cga	774
Leu Phe Arg Gly Leu Ile Ala Leu Asp Cys Pro Ser Glu Leu Cys Arg	
235 240 245	
tta tat acg caa ttt caa gag ccc tat cta aag gat cct gct gct tat	822
Leu Tyr Thr Gln Phe Gln Glu Pro Tyr Leu Lys Asp Pro Ala Ala Tyr	
250 255 260	
cct aaa att cag atg ctg gca tat atg ttc tat tct gtt cct tac ttt	870
Pro Lys Ile Gln Met Leu Ala Tyr Met Phe Tyr Ser Val Pro Tyr Phe	
265 270 275	
gtg act gca ctg tat ggc tta gtg gtt cct gga tgt tcc tgg atg cct	918
Val Thr Ala Leu Tyr Gly Leu Val Val Pro Gly Cys Ser Trp Met Pro	
280 285 290 295	
gac atc aca ttg ata cat gct gga ggt ctg gct cag gct cag ttt tct	966
Asp Ile Thr Leu Ile His Ala Gly Gly Leu Ala Gln Ala Gln Phe Ser	
300 305 310	
cac att ggt gca tct ctt cat gct aga act gct tat gtc tac aga gtc	1014
His Ile Gly Ala Ser Leu His Ala Arg Thr Ala Tyr Val Tyr Arg Val	
315 320 325	
cct gaa gaa gca aaa atc ctt ttt tta gca tta aac ata gca tat gga	1062
Pro Glu Glu Ala Lys Ile Leu Phe Leu Ala Leu Asn Ile Ala Tyr Gly	
330 335 340	
gtt ctt cct cag ctc ttg gcc tat cgt tgt atc tac aaa cca gag ttc	1110
Val Leu Pro Gln Leu Leu Ala Tyr Arg Cys Ile Tyr Lys Pro Glu Phe	
345 350 355	
ttc ata aaa aca aag gca gaa gaa aaa gtg gaa taaaaatatt acttcatgtt	1163
Phe Ile Lys Thr Lys Ala Glu Glu Lys Val Glu	
360 365 370	
cctcctttct aaattactaa cttttgttat actggtactg atattttgtc ccattttcact	1223
ctctttctcat acgtgagtac ttaagaatat gtacattctt gctctgcact gtatgtgtga	1283
gctatatggg attgtgtaaa ttttttttga aggaaaatgg aaattcttga gaaacagttt	1343
gtttaaagaa atatattcaa aatcatttgt gaataaactt gatcatccat ctcaaaaaaa	1403
aaaaaaaaaa	1412

<210> 216

<211> 1773

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 6..1184

<400> 216

ccaac atg acc tac agg tgg ggg aca ctg ctc atg aag aga aag ttt gag	50
Met Thr Tyr Arg Trp Gly Thr Leu Leu Met Lys Arg Lys Phe Glu	
1 5 10 15	
gag ccc cgg cca gga ttt cat ggt gtc ttg ggt atc aat tcc atc act	98
Glu Pro Arg Pro Gly Phe His Gly Val Leu Gly Ile Asn Ser Ile Thr	
20 25 30	
ggg aag gag gag cct ctg tac ccc agc tac aag aga cag ttg cgc att	146
Gly Lys Glu Glu Pro Leu Tyr Pro Ser Tyr Lys Arg Gln Leu Arg Ile	
35 40 45	

His	Ile	Gln	Met	Lys	Leu	Ala	Arg	Leu	Glu	Phe	Glu	Ser	Leu	Glu	Ala		
			355					360					365				
ctc	aag	cag	caa	atg	aag	ctc	gtg	acc	gag	aac	ctg	aag	gag	gaa		1154	
Leu	Lys	Gln	Gln	Gln	Met	Lys	Leu	Val	Thr	Glu	Asn	Leu	Lys	Glu	Glu		
		370					375					380					
cca	atg	gaa	agc	ggg	aag	gag	aag	gca	acc	tgagt	gcccc	gcgtg	ccccag			1204	
Pro	Met	Glu	Ser	Gly	Lys	Glu	Lys	Ala	Thr								
		385					390										
ctg	ccctgtt	ggcag	aggcc	tgtgt	ctgtg	ccacac	ctgc	cacgg	tggca	gggggg	gtac					1264	
cgggg	gcagc	atcgt	ggctc	ctga	accag	accca	atgct	tagcc	aaacg	aagt	ggctcc					1324	
cat	gtggcaa	gcacc	ttct	cagtt	tcgca	gtggc	tttggc	tcggg	atcct	tggc	cagttcc					1384	
cccag	cccca	ccctg	ttctg	tcctt	cccag	ttcct	ttccg	ggccc	acac	gctg	ctccag					1444	
ctg	ccaactt	tgctg	cagag	ccact	gccgc	ccttg	agcct	ctcacc	atga	gtgag	ccacc					1504	
agct	ctccac	gttccc	ctca	tagca	gtgc	actccc	aaacc	ccacc	atggc	ccagg	gaccc					1564	
gtgg	acaggt	tgggg	atggg	gtgtg	tgccc	actgt	gctca	tcacag	gagc	ctcagt	ttgag					1624	
agt	gagcggg	gtacag	taag	gcagt	gcttc	ccacac	tggga	cctct	tttct	ggtt	ctcttt					1684	
tgca	atacat	taacag	accc	tttat	caaca	taaaca	aatag	taact	gagct	attaa	aggca					1744	
aaaaaaaa		taaaaa	aaaaa	aaaaaa												1773	
<210> 217																	
<211> 1251																	
<212> DNA																	
<213> Homo sapiens																	
<220>																	
<221> CDS																	
<222> 29..376																	
<400> 217																	
tatcc	ggtcc	tcggc	tgccg	cgggc	cacc	atg	gtc	ggt	ggc	gag	gcg	gct	gcc			52	
						Met	Val	Gly	Gly	Glu	Ala	Ala	Ala				
						1				5							
gca	gtg	gag	gag	ctg	gtt	tcg	ggg	gtg	cgg	cag	gcg	gcc	gac	ttc	gcg	100	
Ala	Val	Glu	Glu	Leu	Val	Ser	Gly	Val	Arg	Gln	Ala	Ala	Asp	Phe	Ala		
	10					15				20							
gag	cag	ttc	cgc	tcc	tac	tca	gag	agc	gag	aag	caa	tgg	aag	gcc	cgc	148	
Glu	Gln	Phe	Arg	Ser	Tyr	Ser	Glu	Ser	Glu	Lys	Gln	Trp	Lys	Ala	Arg		
	25				30					35				40			
atg	gaa	ttc	atc	ctg	cgc	cac	ctg	ccc	gac	tac	cgc	gac	ccg	ccc	gac	196	
Met	Glu	Phe	Ile	Leu	Arg	His	Leu	Pro	Asp	Tyr	Arg	Asp	Pro	Pro	Asp		
			45				50					55					
ggc	agt	ggc	cgc	ctg	gac	cag	ctg	ctc	tcc	ctc	tcc	atg	gtc	tgg	gcc	244	
Gly	Ser	Gly	Arg	Leu	Asp	Gln	Leu	Leu	Ser	Leu	Ser	Met	Val	Trp	Ala		
			60				65					70					
aac	cat	ctc	ttc	cta	ggc	tgc	agt	tac	aat	aaa	gac	ctt	tta	gac	aag	292	
Asn	His	Leu	Phe	Leu	Gly	Cys	Ser	Tyr	Asn	Lys	Asp	Leu	Leu	Asp	Lys		
		75				80					85						
gtg	atg	gaa	atg	gcc	gat	ggg	att	gaa	gtg	gaa	gac	ctg	cca	caa	ttt	340	
Val	Met	Glu	Met	Ala	Asp	Gly	Ile	Glu	Val	Glu	Asp	Leu	Pro	Gln	Phe		
	90					95					100						
act	acc	aga	agt	gaa	tta	atg	aaa	aag	cat	caa	agc	taag	ccagaa			386	
Thr	Thr	Arg	Ser	Glu	Leu	Met	Lys	Lys	His	Gln	Ser						
	105				110					115							
gattt	atcac	atttt	catca	tcagc	tacag	gattag	aaaag	gaggc	tggga	tgaat	gtgac					446	
atagac	caca	gcagc	tctct	taagac	tctct	ggtatt	acca	acataa	agag	gcagg	tggaa					506	
tgaga	aggag	tctgt	ctaga	ttggc	ttttt	taacatt	ctc	atttt	cccag	gagtt	atcac					566	
tgtaa	aagta	tgc	atg	gata	tttat	gtatt	tataa	atcat	gcact	ctaag	atgagt	tcat				626	
caac	attgta	aaagc	ctct	tttct	gtttt	cagg	ttttt	ttttt	cttat	cgaca	aggtc					686	

tcactctgtc	gcccaggcag	aatcacaaag	gtgcattatt	ggctcattgc	agcctcgaac	746
tcctgggctc	atattttcag	ggttttttgt	tttttgtttt	gtttttttga	gacagagtct	806
tgctctgttg	cccaggcagt	agtgcmagtg	gcgcgatata	ttttcagttt	ttaaactgtca	866
gaatttttgt	ttaaaatgcc	tttttgggct	gggccacagt	ggccttatgc	ccataataat	926
cccagcactt	tgggaggccg	aggtgagcag	atcacctgag	gttaggagtt	tgagaccagc	986
ctggccaaca	cgatgaaacc	ccgtctctac	taaaaataca	aacaaaatta	gctgggcatg	1046
gtggcggaca	tctgtaatcc	cagctactca	ggaggctgaa	gcagaagaac	tgcttgaacc	1106
tgggaggtgg	aggttgcaat	gagccaagat	cgcaccattg	cactccatcc	tgggcgacaa	1166
aaatgaaaca	ccgtctcaaa	aaaaaaataa	aaataataaa	ataaaatgcc	tttttgttgt	1226
tgatgtgaaa	aaaaaaaaaa	aaaaa				1251

<210> 218  
 <211> 894  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 78..566

<400> 218												
gcgcgccatc	ttggctccgg	atcgtgcgtg	aggcggtctc	gtgggcagcg	agagtcacag	60						
acaagacagc	aagcagg	atg gag cac tac	cgg aaa gct ggc tct gta gag	110								
		Met Glu His Tyr Arg Lys Ala Gly Ser Val Glu										
		1	5	10								
ctc cca gcg cct tcc cca atg ccc cag cta cct cct gat acc ctt gag						158						
Leu Pro Ala Pro Ser Pro Met Pro Gln Leu Pro Pro Asp Thr Leu Glu												
		15	20	25								
atg cgg gtc cga gat ggc agc aaa att cgc aac ctg ctg ggg ttg gct						206						
Met Arg Val Arg Asp Gly Ser Lys Ile Arg Asn Leu Leu Gly Leu Ala												
		30	35	40								
ctg ggt cgg ttg gag ggc ggc agt gct cgg cat gta gtg ttc tca ggt						254						
Leu Gly Arg Leu Glu Gly Gly Ser Ala Arg His Val Val Phe Ser Gly												
		45	50	55								
tct ggc agg gct gca gga aag gct gtc agc tgc gct gag att gtc aag						302						
Ser Gly Arg Ala Ala Gly Lys Ala Val Ser Cys Ala Glu Ile Val Lys												
		60	65	70		75						
cgg cgg gtc cca ggc ctg cac cag ctc acc aag cta cgt ttc ctt cag						350						
Arg Arg Val Pro Gly Leu His Gln Leu Thr Lys Leu Arg Phe Leu Gln												
		80	85	90								
act gag gac agc tgg gtc cca gcc tca cct gac aca ggg cta gac ccc						398						
Thr Glu Asp Ser Trp Val Pro Ala Ser Pro Asp Thr Gly Leu Asp Pro												
		95	100	105								
ctc aca gtg cgc cgc cat gtg cct gca gtg tgg gtg ctg ctc agc cgg						446						
Leu Thr Val Arg Arg His Val Pro Ala Val Trp Val Leu Leu Ser Arg												
		110	115	120								
gac ccc ctg gac ccc aat gag tgt ggt tac caa ccc cca gga gca ccc						494						
Asp Pro Leu Asp Pro Asn Glu Cys Gly Tyr Gln Pro Pro Gly Ala Pro												
		125	130	135								
cct ggc ctg ggt tcc atg ccc agc tcc agc tgt ggc cct cgt tcc cga						542						
Pro Gly Leu Gly Ser Met Pro Ser Ser Ser Cys Gly Pro Arg Ser Arg												
		140	145	150		155						
aga agg gct cga gac acc cga tcg tgaagacctg ctgagccagc ctgttctccg						596						
Arg Arg Ala Arg Asp Thr Arg Ser												
		160										
ggcctgaatg tctgggtgctg ttgtgccttt tctgagaagc gttgtgactg ctcaacatcc						656						
ccatcaaggt ttgagtcac aaaagtggac ctccctatca tgcttccct tccctctagc						716						
atgtgggaag ggactgctgt gaagaatgac agatgtgggg cctctgccaa gttctgcatt						776						





tgctaactta gcaaaatgaa gtttctataa agaggactca ggcattgctg aaagagttaa 785  
aagtaactgt gaacaaataa tttgttctgt gccttttgcc tggatatag caaataactca 845  
aaaaatattc aataattcaa tcaataaata taagtttcat cttacaccaa aaaaaaaaaa 905  
aaaaa 910

<210> 220  
<211> 519  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 103..405

<400> 220  
acttccggtg cgaaccgcct cggccgttcc ctgcgggagc ttactgagcg cggccgcca 60  
gccagctcc gccgccgagc gcctgtgccg gcacgbhaca cc atg gag cgc ccg 114  
Met Glu Arg Pro  
1  
gat aag gcg gcg ctg aac gca ctg cag cct cct gag ttc aga aat gaa 162  
Asp Lys Ala Ala Leu Asn Ala Leu Gln Pro Pro Glu Phe Arg Asn Glu  
5 10 15 20  
agc tca tta gca tct aca ctg aag acg ctc ctg ttc ttc aca gct tta 210  
Ser Ser Leu Ala Ser Thr Leu Lys Thr Leu Leu Phe Phe Thr Ala Leu  
25 30 35  
atg atc act gtt cct att ggg tta tat ttc aca act aaa tct tac ata 258  
Met Ile Thr Val Pro Ile Gly Leu Tyr Phe Thr Thr Lys Ser Tyr Ile  
40 45 50  
ttt gaa ggc gcc ctt ggg atg tcc aat agg gac agc tat ttt tac gct 306  
Phe Glu Gly Ala Leu Gly Met Ser Asn Arg Asp Ser Tyr Phe Tyr Ala  
55 60 65  
gct att gtt gca gtg gtc gcc gtc cat gtg gtg ctg gcc ctc ttt gtg 354  
Ala Ile Val Ala Val Val Ala Val His Val Val Leu Ala Leu Phe Val  
70 75 80  
tat gtg gcc tgg aat gaa ggc tca cga cag tgb cgt gaa ggc aaa cag 402  
Tyr Val Ala Trp Asn Glu Gly Ser Arg Gln Xaa Arg Glu Gly Lys Gln  
85 90 95 100  
gat taaagtgaac atcacctttt tatagcatta aattcatttt ttaaaatgat 455  
Asp  
aatgctggag ggggccatct gatttgaata aagttgaaag aacatgtaaa aaaaaaaaaa 515  
aaaa 519

<210> 221  
<211> 632  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 72..350

<400> 221  
agtgagaccg cgcggcaaca gcttgccggt gcggtagtc cgtgggagc cgcctggctg 60  
tgcaggcggc c atg gat tcc ttg cgg aaa atg ctg atc tca gtc gca atg 110  
Met Asp Ser Leu Arg Lys Met Leu Ile Ser Val Ala Met  
1 5 10  
ctg ggc gca ggg gct ggc gtg ggc tac gcg ctc ctc gtt atc gtg acc 158  
Leu Gly Ala Gly Ala Gly Val Gly Tyr Ala Leu Leu Val Ile Val Thr

15	20	25	
ccg gga gag cgg cgg aag cag gaa atg cta aag gag atg cca ctg cag			206
Pro Gly Glu Arg Arg Lys Gln Glu Met Leu Lys Glu Met Pro Leu Gln			
30	35	40	45
gac cca agg agc aga gag gag gcg gcc agg acc cag cag cta ttg ctg			254
Asp Pro Arg Ser Arg Glu Glu Ala Ala Arg Thr Gln Gln Leu Leu Leu			
50	55	60	
gcc act ctg cag gag gca gcg acc acg cag gag aac gtg gcc tgg agg			302
Ala Thr Leu Gln Glu Ala Ala Thr Thr Gln Glu Asn Val Ala Trp Arg			
65	70	75	
aag aac tgg atg gtt ggc ggc gaa ggc ggc gcc ggc ggg agg tca ccg			350
Lys Asn Trp Met Val Gly Gly Gly Gly Ala Gly Gly Arg Ser Pro			
80	85	90	
tgagaccgga cttgcctccg tgggcgcggc accttggtt gggcgcagga atccgaggca			410
gcctttctcc ttcggtgggcc cagcggagag tccggaccga gataccatgc caggactctc			470
cggggtcctg tgagctgccg tcgggtgagc acgtttcccc caaaccttg actgactgct			530
ttaaggtccg caagggcggc cagggccgag acgcgagtcg gatgtggtga actgaaagaa			590
ccaataaaat catgttcctc cacccaaaaa aaaaaaaaaa aa			632
<210> 222			
<211> 652			
<212> DNA			
<213> Homo sapiens			
<220>			
<221> CDS			
<222> 38..436			
<400> 222			
actgctgtcc cccgagctgc tctacgcgt ggcgcgg atg ggg cac ggg gac gag			55
		Met Gly His Gly Asp Glu	
	1	5	
atc gtt ctt gcg gac ttg aac ttc ccg gcc tcc tcc atc tgc cag tgt			103
Ile Val Leu Ala Asp Leu Asn Phe Pro Ala Ser Ser Ile Cys Gln Cys			
10	15	20	
ggg ccc atg gag atc cgt gca gac ggc ctg ggc atc ccg cag ctc ctg			151
Gly Pro Met Glu Ile Arg Ala Asp Gly Leu Gly Ile Pro Gln Leu Leu			
25	30	35	
gag gcc gtg ctg aag ctg ctg ccc ctg gac acc tat gtg gag agt ccg			199
Glu Ala Val Leu Lys Leu Leu Pro Leu Asp Thr Tyr Val Glu Ser Pro			
40	45	50	
gct gca gtc atg gag ctg gtg ccc agc gac aag gag agg ggc ctg cag			247
Ala Ala Val Met Glu Leu Val Pro Ser Asp Lys Glu Arg Gly Leu Gln			
55	60	65	70
acc cca gtg tgg acg gag tac gag tcc atc cta cgc agg gcc ggc tgt			295
Thr Pro Val Trp Thr Glu Tyr Glu Ser Ile Leu Arg Arg Ala Gly Cys			
75	80	85	
gtg aga gcc ctg gca aag ata gag agg ttt gag ttt tat gaa cgg gct			343
Val Arg Ala Leu Ala Lys Ile Glu Arg Phe Glu Phe Tyr Glu Arg Ala			
90	95	100	
aag aag gct ttt gct gtt gtg gca acg ggg gag acg gcc ctc tac gga			391
Lys Lys Ala Phe Ala Val Val Ala Thr Gly Glu Thr Ala Leu Tyr Gly			
105	110	115	
aac ctc atc ctc agg aag ggg gtg ctt gcc ctc aac ccc ctg ctg			436
Asn Leu Ile Leu Arg Lys Gly Val Leu Ala Leu Asn Pro Leu Leu			
120	125	130	
taggcctggt gaagaccacc tgggcccggaa gaggaactgg gggcaccctg agctccagta			496
ccaccactca caacaggcct cccagtggca gctcccagac ctggggccctg gccagggctc			556



Ser	Arg	Tyr	Asn	Phe	Arg	Arg	Thr	Phe	Gly	Ile	Glu	Leu	Ser	Ser	Asn		
				15					20					25			
tct	tcc	tat	tgc	aaa	cga	gga	aat	ggc	tac	aga	agc	aga	gtg	ccc	aaa		327
Ser	Ser	Tyr	Cys	Lys	Arg	Gly	Asn	Gly	Tyr	Arg	Ser	Arg	Val	Pro	Lys		
			30					35					40				
gaa	tgc	gaa	tgc	aac	tgg	ctt	cat	ctt	gaa	agc	gac	act	ctg	aag	aaa		375
Glu	Cys	Glu	Cys	Asn	Trp	Leu	His	Leu	Glu	Ser	Asp	Thr	Leu	Lys	Lys		
			45					50					55				
tta	ccc	ata	att	tct	ccc	tct	tgg	aca	tgc	aga	att	atc	ctg	ttc	ttg		423
Leu	Pro	Ile	Ile	Ser	Pro	Ser	Trp	Thr	Cys	Arg	Ile	Ile	Leu	Phe	Leu		
	60					65					70						
tat	ttt	tct	ggc	cag	ctt	ctc	caa	ctt	tcc	ctt	tct	tgt	ttg	caa	cta		471
Tyr	Phe	Ser	Gly	Gln	Leu	Leu	Gln	Leu	Ser	Leu	Ser	Cys	Leu	Gln	Leu		
	75				80				85						90		
att	aaa	ctt	taaggataaa	aaaaaaaaaa	aa												502
Ile	Lys	Leu															
<210> 225																	
<211> 1739																	
<212> DNA																	
<213> Homo sapiens																	
<220>																	
<221> CDS																	
<222> 171..1670																	
<400> 225																	
actctggcct	tgctgcttct	ctccagctcc	tgaacttttc	tttcttccat	catgctctga												60
gcccattcct	tgaaaactaa	aaggctccctg	actcccagtc	tgcagccatc	ctgggcctgc												120
tgagctctga	ttcaagtgcc	tgcctctgcc	ccttggtggg	ctgaagcttc	atg gag												176
					Met Glu												
					1												
gta	tcc	acc	aac	ccc	tcc	tcc	aac	atc	gat	cca	ggc	aac	tat	gtt	gaa		224
Val	Ser	Thr	Asn	Pro	Ser	Ser	Asn	Ile	Asp	Pro	Gly	Asn	Tyr	Val	Glu		
			5					10					15				
atg	aat	gat	tca	atc	acc	cac	cta	ccc	tct	aaa	gtg	gtg	ata	caa	gat		272
Met	Asn	Asp	Ser	Ile	Thr	His	Leu	Pro	Ser	Lys	Val	Val	Ile	Gln	Asp		
	20					25					30						
att	act	atg	gag	cta	cac	tgc	cct	ctg	tgc	aat	gat	tgg	ttc	cga	gac		320
Ile	Thr	Met	Glu	Leu	His	Cys	Pro	Leu	Cys	Asn	Asp	Trp	Phe	Arg	Asp		
	35				40					45					50		
cca	ctg	atg	cta	agc	tgt	ggc	cac	aac	ttc	tgt	gaa	gcc	tgt	atc	caa		368
Pro	Leu	Met	Leu	Ser	Cys	Gly	His	Asn	Phe	Cys	Glu	Ala	Cys	Ile	Gln		
				55					60					65			
gac	ttt	tgg	agg	ctg	caa	gca	aag	gaa	aca	ttc	tgt	cct	gag	tgt	aag		416
Asp	Phe	Trp	Arg	Leu	Gln	Ala	Lys	Glu	Thr	Phe	Cys	Pro	Glu	Cys	Lys		
			70					75					80				
atg	cta	tgt	cag	tat	aac	aac	tgt	aca	ttc	aac	cct	gta	ctg	gac	aag		464
Met	Leu	Cys	Gln	Tyr	Asn	Asn	Cys	Thr	Phe	Asn	Pro	Val	Leu	Asp	Lys		
	85					90						95					
ttg	gta	gag	aag	att	aag	aag	tta	ccc	tta	ctc	aag	ggc	cat	cca	cag		512
Leu	Val	Glu	Lys	Ile	Lys	Lys	Leu	Pro	Leu	Leu	Lys	Gly	His	Pro	Gln		
	100					105					110						
tgc	cca	gag	cat	gga	gag	aac	ctg	aaa	ctg	ttc	agt	aaa	cca	gat	ggg		560
Cys	Pro	Glu	His	Gly	Glu	Asn	Leu	Lys	Leu	Phe	Ser	Lys	Pro	Asp	Gly		
	115				120				125						130		
aaa	ctg	atc	tgc	ttt	caa	tgc	aag	gat	gct	cgg	ttg	tct	gtg	ggg	cag		608
Lys	Leu	Ile	Cys	Phe	Gln	Cys	Lys	Asp	Ala	Arg	Leu	Ser	Val	Gly	Gln		

																656
tct	aag	gag	ttc	ctg	caa	atc	tct	gat	gct	gtc	cat	ttc	ttc	atg	gag	656
Ser	Lys	Glu	Phe	Leu	Gln	Ile	Ser	Asp	Ala	Val	His	Phe	Phe	Met	Glu	
150				155				160								
gag	ctt	gcc	atc	caa	cag	ggg	caa	ctg	gag	aca	act	ctg	aag	gag	ctt	704
Glu	Leu	Ala	Ile	Gln	Gln	Gly	Gln	Leu	Glu	Thr	Thr	Leu	Lys	Glu	Leu	
165				170				175								
cag	acc	ctg	agg	aac	atg	cag	aag	gaa	gct	att	gct	gct	cac	aag	gaa	752
Gln	Thr	Leu	Arg	Asn	Met	Gln	Lys	Glu	Ala	Ile	Ala	Ala	His	Lys	Glu	
180				185				190								
aac	aag	cta	cat	ctg	cag	caa	cat	gtg	tcc	atg	gag	ttt	cta	aag	ctg	800
Asn	Lys	Leu	His	Leu	Gln	Gln	His	Val	Ser	Met	Glu	Phe	Leu	Lys	Leu	
195				200				205				210				
cat	cag	ttc	ctg	cac	agc	aaa	gaa	aag	gac	att	tta	act	gag	ctc	cgg	848
His	Gln	Phe	Leu	His	Ser	Lys	Glu	Lys	Asp	Ile	Leu	Thr	Glu	Leu	Arg	
215				220				225								
gaa	gag	ggg	aaa	gcc	ttg	aat	gag	gag	atg	gag	ttg	aat	ctg	agc	cag	896
Glu	Glu	Gly	Lys	Ala	Leu	Asn	Glu	Glu	Met	Glu	Leu	Asn	Leu	Ser	Gln	
230				235				240								
ctt	cag	gag	caa	tgt	ctc	tta	gcc	aag	gat	atg	ttg	gtg	agc	att	cag	944
Leu	Gln	Glu	Gln	Cys	Leu	Leu	Ala	Lys	Asp	Met	Leu	Val	Ser	Ile	Gln	
245				250				255								
gca	aag	acg	gaa	caa	cag	aac	tcc	ttc	gac	ttt	ctc	aaa	gac	atc	aca	992
Ala	Lys	Thr	Glu	Gln	Gln	Asn	Ser	Phe	Asp	Phe	Leu	Lys	Asp	Ile	Thr	
260				265				270								
act	ctc	tta	cat	agc	ttg	gag	caa	gga	atg	aag	gtg	ctg	gca	acc	aga	1040
Thr	Leu	Leu	His	Ser	Leu	Glu	Gln	Gly	Met	Lys	Val	Leu	Ala	Thr	Arg	
275				280				285				290				
gag	ctt	att	tcc	aga	aag	ctg	aac	ctg	ggc	cag	tac	aaa	ggg	cct	atc	1088
Glu	Leu	Ile	Ser	Arg	Lys	Leu	Asn	Leu	Gly	Gln	Tyr	Lys	Gly	Pro	Ile	
295				300				305								
cag	tac	atg	gta	tgg	agg	gaa	atg	cag	gac	act	ctc	tgc	cca	ggc	ctg	1136
Gln	Tyr	Met	Val	Trp	Arg	Glu	Met	Gln	Asp	Thr	Leu	Cys	Pro	Gly	Leu	
310				315				320								
tct	cca	cta	act	ctg	gac	cct	aaa	aca	gct	cac	cca	aat	ctg	gtg	ctc	1184
Ser	Pro	Leu	Thr	Leu	Asp	Pro	Lys	Thr	Ala	His	Pro	Asn	Leu	Val	Leu	
325				330				335								
tcc	aaa	agc	caa	acc	agc	gtc	cat	ggg	gac	att	aag	aag	ata	atg		1232
Ser	Lys	Ser	Gln	Thr	Ser	Val	Trp	His	Gly	Asp	Ile	Lys	Lys	Ile	Met	
340				345				350								
cct	gat	gat	cct	gag	agg	ttt	gac	tca	agt	gtg	gct	gta	ctg	ggc	tca	1280
Pro	Asp	Asp	Pro	Glu	Arg	Phe	Asp	Ser	Ser	Val	Ala	Val	Leu	Gly	Ser	
355				360				365				370				
aga	ggc	ttc	acc	tct	gga	aag	tgg	tac	tgg	gaa	gta	gaa	gta	gca	aag	1328
Arg	Gly	Phe	Thr	Ser	Gly	Lys	Trp	Tyr	Trp	Glu	Val	Glu	Val	Ala	Lys	
375				380				385								
aag	aca	aaa	tgg	aca	gtt	gga										

```

gga gga cag ttg tcc ttc tac aat gct aaa acc atg act cac att tac 1568
Gly Gly Gln Leu Ser Phe Tyr Asn Ala Lys Thr Met Thr His Ile Tyr
      455      460      465
acc ttc agt aac act ttc atg gag aaa ctt tat ccc tac ttc tgc ccc 1616
Thr Phe Ser Asn Thr Phe Met Glu Lys Leu Tyr Pro Tyr Phe Cys Pro
      470      475      480
tgc ctt aat gat ggt aga gag aat aaa gaa cca ttg cac atc tta cat 1664
Cys Leu Asn Asp Gly Arg Glu Asn Lys Glu Pro Leu His Ile Leu His
      485      490      495
cca cag taatgagtca taatattata caaattcaga gtgttatttaa agagggttttg 1720
Pro Gln
      500
aaataaaaaa aaaaaaaaaa 1739

<210> 226
<211> 657
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 199..618

<400> 226
aactggatag agtactgccc ctttcagccc atggagaaaag gcaaatgcct ctttcagagt 60
ctacctaatag ctttctcaga taaataagca tgaagaaaag tcaaagtcca ttctagctct 120
aaaataagga atgaaatgtt ttcctgatat gattttttgt tttcatctga taataatttt 180
atatatcaca gaaacagc atg gtt ctt act aaa cct ctt caa aga aat ggc 231
      Met Val Leu Thr Lys Pro Leu Gln Arg Asn Gly
      1      5      10
agc atg atg agc ttt gaa aat gtg aaa gaa aag agc aga gaa gga ggg 279
Ser Met Met Ser Phe Glu Asn Val Lys Glu Lys Ser Arg Glu Gly Gly
      15      20      25
ccc cat gca cac aca ccc gaa gaa gaa ttg tgt ttc gtg gta aca cac 327
Pro His Ala His Thr Pro Glu Glu Glu Leu Cys Phe Val Val Thr His
      30      35      40
tac cct cag gtt cag acc aca ctc aac ctg ttt ttc cat ata ttc aag 375
Tyr Pro Gln Val Gln Thr Thr Leu Asn Leu Phe Phe His Ile Phe Lys
      45      50      55
gtt ctt act caa cca ctt tcc ctt ctg tgg ggt tgt gat cag aag cct 423
Val Leu Thr Gln Pro Leu Ser Leu Leu Trp Gly Cys Asp Gln Lys Pro
      60      65      70      75
cgt act gtt cct acc ctt gga aac ggc gca tgg gat acc tgc caa caa 471
Arg Thr Val Pro Thr Leu Gly Asn Gly Ala Trp Asp Thr Cys Gln Gln
      80      85      90
cac ata cgc act tca tca tgg aca gca aac aca ctc gtc att caa aac 519
His Ile Arg Thr Ser Ser Trp Thr Ala Asn Thr Leu Val Ile Gln Asn
      95      100      105
cag cat tca cgg gaa agc act gtt tct gtt tgc ctt ttt atg tta atc 567
Gln His Ser Arg Glu Ser Thr Val Ser Val Cys Leu Phe Met Leu Ile
      110      115      120
cgc atg caa cat att ttg aaa aca gat aca ctt caa cag ttc aga ata 615
Arg Met Gln His Ile Leu Lys Thr Asp Thr Leu Gln Gln Phe Arg Ile
      125      130      135
tgc tagtactaat aaaaccaaca tggtaaaaaa aaaaaaaaaa 657
Cys
140

```

<210> 227  
<211> 888  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 182..481

<400> 227  
atcttgccctc tcagtggttca agcttgagcc cacgcattcca actcctgaga tcttactggg 60  
aagctgctga tcatcagttt caggaagtca gcatggatca gccttacgtt catggcctcc 120  
aggccctatt ctctgcctc acagggaccg gccaggatct ctatccttac agcacgttgg 180  
a atg tat atg ctc ctc tcc cca cat cgc ctt agg gag cag gca ggt gtc 229  
Met Tyr Met Leu Leu Ser Pro His Arg Leu Arg Glu Gln Ala Gly Val  
1 5 10 15  
agg ggc agc ata agg acg gcc aac agg aca gaa gac ggg ttg aag atc 277  
Arg Gly Ser Ile Arg Thr Ala Asn Arg Thr Glu Asp Gly Leu Lys Ile  
20 25 30  
cga gag gct gag tca ctt cca caa agt aac aca gct gat ttt aaa tgc 325  
Arg Glu Ala Glu Ser Leu Pro Gln Ser Asn Thr Ala Asp Phe Lys Cys  
35 40 45  
ctg cat tca gca tcc ctg cag cag gct cca ggt gga att cta atg gga 373  
Leu His Ser Ala Ser Leu Gln Gln Ala Pro Gly Gly Ile Leu Met Gly  
50 55 60  
cca gcc tcc agt ccc tgg acc tta gcc gtg gaa gga gag aag agg aca 421  
Pro Ala Ser Ser Pro Trp Thr Leu Ala Val Glu Gly Glu Lys Arg Thr  
65 70 75 80  
tct gca cct cct ctc aga gaa agc ctg atg cct act aaa gga ctt ggg 469  
Ser Ala Pro Pro Leu Arg Glu Ser Leu Met Pro Thr Lys Gly Leu Gly  
85 90 95  
tgg tgg acg cag tgaccctcag tctggagctt gttcactgaa cattggagac 521  
Trp Trp Thr Gln  
100  
tatcatttgc gcagatggtc ttgggcctct atgagcagca ggctgcaccc cacagtgacc 581  
tcctcattct actctgaggc atcttcatga aagcagatgt ccattgaaaa gcacccaagt 641  
gcagtctcag ctgatgaact tcagaggcga ttgagacaaa ggctctcggg cccctctgcc 701  
cttggatggg gcctctggta tgcacttggc ctctgtgtct ttatttagac tggtcacttc 761  
acaacccatc atgtcacccc acccctaacc gtgcccactc tgggtcctcc cctcaactgc 821  
ctgacttccc actttgagct cagcaaaggc aatagatggt ttgtctgctt cgaaaaaaaa 881  
aaaaaaaa 888

<210> 228  
<211> 716  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 161..517

<400> 228  
acctgtcatt atgcttacta acgttcggga cgtctcccgg gctgcttggg cgaggagagg 60  
caggggtgtg tgaccccggt gggtactgtg ctgcgctaga gcacctaggg cctgctgaag 120  
ccctccctcg cccgcgcctc tccttagtcc ttgagatgag atg gca agt tac agc 175  
Met Ala Ser Tyr Ser  
1 5  
ggc ttc tcc ggc ctg ctg gag att cgc tac ggg cca gga cac cgc agc 223

Gly	Phe	Ser	Gly	Leu	Leu	Glu	Ile	Arg	Tyr	Gly	Pro	Gly	His	Arg	Ser		
				10					15					20			
tgc	ctt	ccc	caa	ttc	gct	ttc	ttt	ccg	cag	ccg	ccg	ctg	ccc	cga	ccc		271
Cys	Leu	Pro	Gln	Phe	Ala	Phe	Phe	Pro	Gln	Pro	Pro	Leu	Pro	Arg	Pro		
				25				30					35				
cgg	atc	tgc	atg	tgg	gtg	ctg	gct	gag	ctg	ctg	gag	cta	ggg	tgt	cct		319
Arg	Ile	Cys	Met	Trp	Val	Leu	Ala	Glu	Leu	Leu	Glu	Leu	Gly	Cys	Pro		
				40				45				50					
gag	cag	agc	ctg	agg	gac	gcc	atc	acc	ctg	gac	ctc	ttc	tgc	cac	gcg		367
Glu	Gln	Ser	Leu	Arg	Asp	Ala	Ile	Thr	Leu	Asp	Leu	Phe	Cys	His	Ala		
				55			60				65						
ctc	att	ttc	tgc	cgc	cag	cag	ggc	ttc	tca	ctg	gag	cag	acg	tca	gcg		415
Leu	Ile	Phe	Cys	Arg	Gln	Gln	Gly	Phe	Ser	Leu	Glu	Gln	Thr	Ser	Ala		
				70			75				80				85		
gct	tgt	gcc	ctg	ctc	cag	gat	ctt	cac	aag	gct	tgt	att	ggg	gag	agg		463
Ala	Cys	Ala	Leu	Leu	Gln	Asp	Leu	His	Lys	Ala	Cys	Ile	Gly	Glu	Arg		
				90				95					100				
ggg	cag	cta	cca	ggg	ttg	agc	ccc	agg	gag	aag	agg	aac	cgg	gcc	tgg		511
Gly	Gln	Leu	Pro	Gly	Leu	Ser	Pro	Arg	Glu	Lys	Arg	Asn	Arg	Ala	Trp		
				105				110				115					
cac	aag	tgaccatggg	aagcagaagc	aggggatttc	tgccctggaat	atgtcattat											567
His	Lys																
tagtagcatc	atcatacaca	agccatcagc	tttccaatcc	actgcttcct	tatctagaaa												627
ttaaggatac	agcacacatt	ttacaggact	gttctgagaa	ataatatatg	caaatatatg												687
catagtgcac	aataaaaaaaaa	aaaaaaaaaa															716
<210> 229																	
<211> 654																	
<212> DNA																	
<213> Homo sapiens																	
<220>																	
<221> CDS																	
<222> 86..505																	
<400> 229																	
agttcgcggg	gtcagcctcc	gcctccgagc	ctcagttgtc	ttctctgtga	ggtgggaatg												60
ccggtgaatc	ctgccgctgg	cgtgg	atg	aga	agt	gaa	tgc	gtg	ctc	gga	gct						112
			Met	Arg	Ser	Glu	Cys	Val	Leu	Gly	Ala						
			1				5										
gcg	agt	gac	agc	ggg	cag	gag	gcg	ccc	agg	gac	act	tgg	ttt	ctc	cag		160
Ala	Ser	Asp	Ser	Gly	Gln	Glu	Ala	Pro	Arg	Asp	Thr	Trp	Phe	Leu	Gln		
				10			15			20				25			
ggc	tgg	aag	gct	tct	aga	agg	ttc	ctc	atc	aag	gga	agt	gtg	gct	ggg		208
Gly	Trp	Lys	Ala	Ser	Arg	Arg	Phe	Leu	Ile	Lys	Gly	Ser	Val	Ala	Gly		
				30				35						40			
ggc	gcc	gtc	tac	ctg	gtg	tac	gac	cag	gag	ctg	ctg	ggg	ccc	agc	gac		256
Gly	Ala	Val	Tyr	Leu	Val	Tyr	Asp	Gln	Glu	Leu	Leu	Gly	Pro	Ser	Asp		
				45				50				55					
aag	agc	cag	gca	gcc	cta	cag	aag	gct	ggg	gag	gtg	gtc	ccc	ccc	gcc		304
Lys	Ser	Gln	Ala	Ala	Leu	Gln	Lys	Ala	Gly	Glu	Val	Val	Pro	Pro	Ala		
				60			65				70						
atg	tac	cag	ttc	agc	cag	tac	gtg	tgt	cag	cag	aca	ggc	ctg	cag	ata		352
Met	Tyr	Gln	Phe	Ser	Gln	Tyr	Val	Cys	Gln	Gln	Thr	Gly	Leu	Gln	Ile		
				75			80				85						
ccc	cag	ctc	cca	gcc	cct	cca	aag	att	tac	ttt	ccc	atc	cgt	gac	tcc		400
Pro	Gln	Leu	Pro	Ala	Pro	Pro	Lys	Ile	Tyr	Phe	Pro	Ile	Arg	Asp	Ser		
				90			95				100				105		





<221> CDS  
<222> 56..355

<400> 231

```

aattcgggtg gagctgagcc ggagacaggc agttgtgaaa aacttcagga caaaa atg      58
                                         Met
                                         1
ttt cat tta agg act tgt gct gct aag ttg agg cca ttg acg gct tcc      106
Phe His Leu Arg Thr Cys Ala Ala Lys Leu Arg Pro Leu Thr Ala Ser
                    5                    10                    15
cag act gtt aag aca ttt tca caa aac aga cca gca gca gct agg aca      154
Gln Thr Val Lys Thr Phe Ser Gln Asn Arg Pro Ala Ala Ala Arg Thr
                    20                    25                    30
ttt caa cag att cgt gct att ctg cac ctg ttg ctg ctg agc cct ttc      202
Phe Gln Gln Ile Arg Ala Ile Leu His Leu Leu Leu Leu Ser Pro Phe
                    35                    40                    45
tca gtg gga cta gtt cga act atg tgg agg aga tgt act gtg ctt ggc      250
Ser Val Gly Leu Val Arg Thr Met Trp Arg Arg Cys Thr Val Leu Gly
50                    55                    60                    65
tgg aaa acc cca aaa gtg tac ata aga cag ggt ccc act gtt gtc cag      298
Trp Lys Thr Pro Lys Val Tyr Ile Arg Gln Gly Pro Thr Val Val Gln
                    70                    75                    80
gct gga gtg cag tgg cgg gat ctc ggc ttg ctg caa cct ccg act cct      346
Ala Gly Val Gln Trp Arg Asp Leu Gly Leu Leu Gln Pro Pro Thr Pro
                    85                    90                    95
ggg ttc aag tgattcttat gcctcagcct cccgagtaac tgggactaca      395
Gly Phe Lys
                    100
ggtgcacgtc accacgcctg actagttttt gtatttttag tagagatggg attttacttt      455
gttgggccagg ctgggtcttga acccctggcc tcaagtgatc caccacactt ggcctcccaa      515
agtgtctggga ttacaggtat gatcaaccac gcctggccat gtcatgcctt gtgacagaat      575
tcctttattc tgttttgagc caataaatat ttatagggtt cgaaaaaaaa aaaaaaaaaa      634

```

<210> 232  
<211> 583  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 76..498

<400> 232

```

aatatagcca gccgcggctg cccttgcgct tcccagactg gcgggggtccg tgggtcgggga      60
tcgagattgc gggct atg gcg cgg aag gtt ttt cgt cag tac tgg gat atc      111
                    Met Ala Pro Lys Val Phe Arg Gln Tyr Trp Asp Ile
                    1                    5                    10
ccc gat ggc acc gat tgc cac cgc aaa gcc tac agc acc acc agt att      159
Pro Asp Gly Thr Asp Cys His Arg Lys Ala Tyr Ser Thr Thr Ser Ile
                    15                    20                    25
gcc agc gtc gct ggc ctg acc gcc gct gcc tac aga gtc aca ctc aat      207
Ala Ser Val Ala Gly Leu Thr Ala Ala Ala Tyr Arg Val Thr Leu Asn
                    30                    35                    40
cct ccg ggc acc ttc ctt gaa gga gtg gct aag gtt gga caa tac acg      255
Pro Pro Gly Thr Phe Leu Glu Gly Val Ala Lys Val Gly Gln Tyr Thr
45                    50                    55                    60
ttc act gca gct gct gtc ggg gcc gtg ttt ggc ctc acc acc tgc atc      303
Phe Thr Ala Ala Ala Val Gly Ala Val Phe Gly Leu Thr Thr Cys Ile

```

09076997 060801

```

        65              70              75
agc gcc cat gtc cgc gag aag ccc gac gac ccc ctg aac tac ttc ctc      351
Ser Ala His Val Arg Glu Lys Pro Asp Asp Pro Leu Asn Tyr Phe Leu
        80              85              90
ggg ggc tgc gcc gga ggc ctg act ctg gga gca cgc acg cac aac tac      399
Gly Gly Cys Ala Gly Gly Leu Thr Leu Gly Ala Arg Thr His Asn Tyr
        95              100             105
ggg att ggc gcc gcc gcc tgc gtg tac ttt ggc ata gcg gcc tcc ctg      447
Gly Ile Gly Ala Ala Ala Cys Val Tyr Phe Gly Ile Ala Ala Ser Leu
        110             115             120
gtc aag atg ggc cgg ctg gag ggc tgg gag gtg ttt gca aaa ccc aag      495
Val Lys Met Gly Arg Leu Glu Gly Trp Glu Val Phe Ala Lys Pro Lys
        125             130             135             140
gtg tgagccctgt gcctgccggg acctccagcc tgcagaatgc gtccagaaat      548
Val
aaattctgtg tctgtgtgaa aaaaaaaaaa aaaaaa      583

<210> 233
<211> 753
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 199..600

<400> 233
attttttccga tgccaggcac cctcaaggca cagaggctgg ggctcatggt ggggggcactt      60
ggcctctcca ggctcgaag gcttctctgg gctgatgcga gctggggaac gggagggacg      120
gacgtgggag cgagaacgtc acactggagg cagctgggtg cacgatgggg gacagagtga      180
aagagccttc gtgtcacc atg gcc aca cac ccc gat ggc ttc cgg ctt gag      231
                Met Ala Thr His Pro Asp Gly Phe Arg Leu Glu
                1              5              10
gga ccc ctg gct gca gcc cac agc cct ggg cct tgc act gtg ctc tac      279
Gly Pro Leu Ala Ala Ala His Ser Pro Gly Pro Cys Thr Val Leu Tyr
                15              20              25
gaa ggc cct gtc cgt ggg ctc tgc ccy ttt gcc ccg cga aat tcc aac      327
Glu Gly Pro Val Arg Gly Leu Cys Pro Phe Ala Pro Arg Asn Ser Asn
                30              35              40
acc atg gcg gcg gct gcc ctg gct gcc ccc agc ctg ggc ttc gat ggg      375
Thr Met Ala Ala Ala Ala Leu Ala Ala Pro Ser Leu Gly Phe Asp Gly
                45              50              55
gtg att ggg gtg ctc gtg gct gat acc agc ctc acg gac atg cac gtg      423
Val Ile Gly Val Leu Val Ala Asp Thr Ser Leu Thr Asp Met His Val
        60              65              70              75
gtg gat gta gag ctg agc gga ccc cgg ggc ccc act ggc cga agc ttt      471
Val Asp Val Glu Leu Ser Gly Pro Arg Gly Pro Thr Gly Arg Ser Phe
                80              85              90
gct gtg cac acc cgc aga gag aac cct gcc gag cca ggc gcg gtc acc      519
Ala Val His Thr Arg Arg Glu Asn Pro Ala Glu Pro Gly Ala Val Thr
                95              100             105
ggc tcc gcc acc gtc acg gcc ttc tgg cgg agc ctc ctg gcc tgc tgc      567
Gly Ser Ala Thr Val Thr Ala Phe Trp Arg Ser Leu Leu Ala Cys Cys
                110             115             120
cag ctc ccc tcc agg ccg ggg atc cat ctc tgc tgagaagcct cctccctccc      620
Gln Leu Pro Ser Arg Pro Gly Ile His Leu Cys
                125             130
gagacaagat catctgctg gcctctcacc accaccatcc caccctgcc ctgccccact      680

```

tccccagggt ctcccttctg actcagtaaa gatcaccgct gcctcccccc gcaaataaaa 740  
 aaaaaaaaaaaa aaa 753

<210> 234  
 <211> 762  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 211..612

<400> 234  
 atttccgatg ccaggcaccc tcaaggcaca gaggctgggg ctcattgttg gggcacttgg 60  
 cctctccagg cctcgaaggc ttctcctggg ctgatgagag ctgggggaacg ggagggacgg 120  
 acgtgggagc gagaacgtca cactggaggc agctgggtggc acgatggggg acagagttaa 180  
 aggtagcaag tcaagagcct tcgtgtcacc atg gcc aca cac ccc gat ggc ttc 234  
 Met Ala Thr His Pro Asp Gly Phe  
 1 5  
 cgg ctt gag gga ccc ctg gct gca gcg cac agc cct ggg cct tgc act 282  
 Arg Leu Glu Gly Pro Leu Ala Ala His Ser Pro Gly Pro Cys Thr  
 10 15 20  
 gtg ctc tac gaa ggc cct gtc cgt ggg ctc tgc ccc ttt gcc ccg cga 330  
 Val Leu Tyr Glu Gly Pro Val Arg Gly Leu Cys Pro Phe Ala Pro Arg  
 25 30 35 40  
 aat tcc aac acc atg tcg gcg gct gcc ctg gct gcc ccc agc ctg ggc 378  
 Asn Ser Asn Thr Met Ser Ala Ala Ala Leu Ala Ala Pro Ser Leu Gly  
 45 50 55  
 ttc gat ggg gtg att ggg gtg ctc gtg gct gat acc agc ctc acg gac 426  
 Phe Asp Gly Val Ile Gly Val Leu Val Ala Asp Thr Ser Leu Thr Asp  
 60 65 70  
 atg cac gtg gtg gat gta gag ctg agc gga ccc cgg ggc ccc acg tgc 474  
 Met His Val Val Asp Val Glu Leu Ser Gly Pro Arg Gly Pro Thr Cys  
 75 80 85  
 cga agc ttt gct gtg cac acc cgc aga gag aac cct gcc gag cca ggc 522  
 Arg Ser Phe Ala Val His Thr Arg Arg Glu Asn Pro Ala Glu Pro Gly  
 90 95 100  
 gcg gtc acc ggc tcc gcc acc gtc acg gcc ttc tgg cgg agc ctc ctg 570  
 Ala Val Thr Gly Ser Ala Thr Val Thr Ala Phe Trp Arg Ser Leu Leu  
 105 110 115 120  
 gcc tgc tgc cag ctc ccc tcc agg ccg ggg atc cat ctc tgc 612  
 Ala Cys Cys Gln Leu Pro Ser Arg Pro Gly Ile His Leu Cys  
 125 130  
 tgagaagcct cctccctccc gagacaagat catctgcctg gcctctcacc accaccatcc 672  
 caccctgcc ctgccccact tccccagggt ctcccttctg actcagtaaa gatcaccgct 732  
 gcctcccccc gccaaaaaaaa aaaaaaaaaa 762

<210> 235  
 <211> 537  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 5..259

<400> 235  
 aaaa atg cta aag gta gaa gca act ggt agt ccc gag gaa ggg tgg gcg 49

Met	Leu	Lys	Val	Glu	Ala	Thr	Gly	Ser	Pro	Glu	Glu	Gly	Trp	Ala		
1				5				10					15			
ggt	gga	gag	ccc	cgg	act	gga	gct	cct	gcg	aac	tcc	cct	tcc	tgc	cct	97
Gly	Gly	Glu	Pro	Arg	Thr	Gly	Ala	Pro	Ala	Asn	Ser	Pro	Ser	Cys	Pro	
			20					25					30			
cag	gag	atg	cca	ctg	cag	gac	cca	agg	agc	agg	gag	gag	gcg	gcc	agg	145
Gln	Glu	Met	Pro	Leu	Gln	Asp	Pro	Arg	Ser	Arg	Glu	Glu	Ala	Ala	Arg	
			35					40					45			
acc	cag	cag	cta	ttg	ctg	gcc	act	ctg	cag	gag	gca	gcg	acc	acg	cag	193
Thr	Gln	Gln	Leu	Leu	Leu	Ala	Thr	Leu	Gln	Glu	Ala	Ala	Thr	Thr	Gln	
			50					55					60			
gag	aac	gtg	gcc	tgg	agg	aag	aac	tgg	atg	gtt	ggc	ggc	gaa	ggc	ggc	241
Glu	Asn	Val	Ala	Trp	Arg	Lys	Asn	Trp	Met	Val	Gly	Gly	Glu	Gly	Gly	
			65					70					75			
gcc	agc	ggg	agg	tca	ccg	tgagaccgga	cttgccctccg	tgggcgccgg								289
Ala	Ser	Gly	Arg	Ser	Pro											
80						85										
accttggtt	gggcgcagga	atccgaggca	gcctttctcc	ttcgtggggcc	cagcggagag											349
tccggaccga	gataccatgc	caggactctc	cgggggtcctg	tgagctgccg	tccgggtgagc											409
acgtttcccc	caaaccctgg	actgactgct	ttaaggtccg	caaggcgggc	cagggccgag											469
acgcgagtcg	gatgtggtga	actgaaagaa	ccaataaaat	catgttcctc	caaaaaaaaa											529
aaaaaaaa																537
<210>	236															
<211>	994															
<212>	DNA															
<213>	Homo sapiens															
<220>																
<221>	CDS															
<222>	23..370															
<400>	236															
gattgctggt	tgctgtaaag	tg	atg	ggg	agg	ccc	tgg	atg	gtg	atg	ata	ttg				52
			Met	Gly	Arg	Pro	Trp	Met	Val	Met	Ile	Leu				
			1				5				10					
gag	tca	aaa	tct	gaa	gaa	aag	atg	tgg	tat	ggt	gta	ttc	ctg	tgg	gca	100
Glu	Ser	Lys	Ser	Glu	Glu	Lys	Met	Trp	Tyr	Gly	Val	Phe	Leu	Trp	Ala	
			15					20				25				
ctg	gtg	tct	tct	ctc	ttc	ttt	cat	gtc	cct	gct	gga	tta	ctg	gcc	ctc	148
Leu	Val	Ser	Ser	Leu	Phe	Phe	His	Val	Pro	Ala	Gly	Leu	Leu	Ala	Leu	
			30					35				40				
ttc	acc	ctc	aga	cat	cac	aaa	tat	ggt	agg	ttc	atg	tct	gta	agc	atc	196
Phe	Thr	Leu	Arg	His	His	Lys	Tyr	Gly	Arg	Phe	Met	Ser	Val	Ser	Ile	
			45				50				55					
ctg	ttg	atg	ggc	atc	gtg	gga	cca	att	act	gct	gga	atc	ttg	aca	agt	244
Leu	Leu	Met	Gly	Ile	Val	Gly	Pro	Ile	Thr	Ala	Gly	Ile	Leu	Thr	Ser	
			60				65				70					
gca	gct	att	gct	gga	gtt	tac	cga	gca	gca	ggg	aag	gaa	atg	ata	cca	292
Ala	Ala	Ile	Ala	Gly	Val	Tyr	Arg	Ala	Ala	Gly	Lys	Glu	Met	Ile	Pro	
			75				80				85			90		
ttt	gaa	gcc	ctc	aca	ctg	ggc	act	gga	cag	aca	ttt	tgc	gtc	ttg	gtg	340
Phe	Glu	Ala	Leu	Thr	Leu	Gly	Thr	Gly	Gln	Thr	Phe	Cys	Val	Leu	Val	
			95				100				105					
gtc	tcc	ttt	tta	cgg	att	tta	gct	act	cta	tagcatacat	ccttatgctg					390
Val	Ser	Phe	Leu	Arg	Ile	Leu	Ala	Thr	Leu							
			110				115									
agatgttgaa	cttaaaacttt	atggaatcct	cctaaagaat	acattatgga	gtgtagtggt											450

```

ttcttagttc ttcaaaggga agcaacttgg atgaacagga acatgaagga caacacatct 510
cagccttttc ttcattttga agctcctaga attgaagact tatgtggact cctattgttc 570
tcaacccaaa caagtctttt ggctttcttt tttgtagata ttttaatttaa gcagttttca 630
tgtgtacctt tacccaagcc aagtcaacag tgtctctggg gtggcatcct ttgcactgaa 690
atttacagta ttctgtgaga tgtcgcatat tttgaagaaa ccgtggaaga tactggttta 750
tttcaaataa gcagagtatg ttgtattaaa atcttatcta atcttgatta aaatttggca 810
aactcttttc tttgctacat cttagtgcga ataaatgcc aatagggtttt gggtgagtat 870
agttttgaaa acaaatttgg tgaaataaag caggaaaaaa aattttaagta taactcaagt 930
agtggtcttg gttccactgt ttataaataa aaagtagata acaatggaaa aaaaaaaaaa 990
aaaa

```

<210> 237  
 <211> 662  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 41..352

```

<400> 237
tagctaaaaa ttgagggttc taaataactaa ggaagaaggg atg aat aga tat tgt 55
Met Asn Arg Tyr Cys
1 5
ggc aag ata ttt gtc tct gtc atg gtt aaa ttg caa aaa aat aaa ctt 103
Gly Lys Ile Phe Val Ser Val Met Val Lys Leu Gln Lys Asn Lys Leu
10 15 20
acc tcc ttc ccc agg cag cca ttg tta aca ttt ttt gaa tat cta gaa 151
Thr Ser Phe Pro Arg Gln Pro Leu Thr Phe Phe Glu Tyr Leu Glu
25 30 35
aaa gtc ctt tgt tca gga tta ttt tcc cac tct gcc aag agt cac cat 199
Lys Val Leu Cys Ser Gly Leu Phe Ser His Ser Ala Lys Ser His His
40 45 50
gac ctg ctc aca cgc cac cct tat gaa act gcc gcg cca ctt ctc agc 247
Asp Leu Leu Thr Arg His Pro Tyr Glu Thr Ala Ala Pro Leu Leu Ser
55 60 65
tcc cat ttg att ctc aca gaa gct cta cga aat ggg ttg ggc aaa tgt 295
Ser His Leu Ile Leu Thr Glu Ala Leu Arg Asn Gly Leu Gly Lys Cys
70 75 80 85
cat gat cct cat ttc aca ggg gaa gaa act gag gcc cag agg ggg aaa 343
His Asp Pro His Phe Thr Gly Glu Glu Thr Glu Ala Gln Arg Gly Lys
90 95 100
ctg act acc taaaattgcc atgtaggccg gcgcggtggc tcacgcctgt 392
Leu Thr Thr
aatcccagca ctgtgggagg ccaaggcggg tggatcgcca ggtcaggaga tcgagaccat 452
cctggctggc acttgaagcc ccgtctctac tagggataca aataattggc cgggtgtggt 512
ggcgggcgcc tgtgkwcca gctgttcggc aggctgagga gggcgaatgg tgtgagcctg 572
ggaggcggag cttgcggtgg gccgggattg cgccactgca ctccagcctg ggcgacagag 632
ccagattccg tccaaaaaaa aaaaaaaaaa 662

```

<210> 238  
 <211> 1829  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 3..1319

<400> 238

252

290	295	300	
ctc agg tcc gag gcg gtg gag cgg ctg agc gtg ctg cgg acc aag gcc			959
Leu Arg Ser Glu Ala Val Glu Arg Leu Ser Val Leu Arg Thr Lys Ala			
305	310	315	
atg cgg gag aag gag gag cag cgg ggg ctg cgc aag tac aac tac acg			1007
Met Arg Glu Lys Glu Glu Gln Arg Gly Leu Arg Lys Tyr Asn Tyr Thr			
320	325	330	335
ctg ctg cgc gtg cgc ctc ccc gat ggc tgc ctc ctg cag ggc act ttc			1055
Leu Leu Arg Val Arg Leu Pro Asp Gly Cys Leu Leu Gln Gly Thr Phe			
340	345	350	
tac gct cgg gag cgg ctg ggg gcg gtg tac ggg ttc gtc cgg gag gcc			1103
Tyr Ala Arg Glu Arg Leu Gly Ala Val Tyr Gly Phe Val Arg Glu Ala			
355	360	365	
ctg cag agc gac tgg ctg cct ttt gag ctg ctg gcc tgc gga ggg cag			1151
Leu Gln Ser Asp Trp Leu Pro Phe Glu Leu Leu Ala Ser Gly Gly Gln			
370	375	380	
aag ctg tcc gag gac gag aac ctg gcc ttg aac gag tgc ggg ctg gtg			1199
Lys Leu Ser Glu Asp Glu Asn Leu Ala Leu Asn Glu Cys Gly Leu Val			
385	390	395	
ccc tct gcc ctc ctg acc ttc tgc tgg gac atg gct gtg ctg gag gac			1247
Pro Ser Ala Leu Leu Thr Phe Ser Trp Asp Met Ala Val Leu Glu Asp			
400	405	410	415
atc aag gcc gcg ggg gcc gag ccg gac tcc atc ctg aaa ccc gag ctc			1295
Ile Lys Ala Ala Gly Ala Glu Pro Asp Ser Ile Leu Lys Pro Glu Leu			
420	425	430	
ctg tca gcc atc gag aag ctc ttg tgaaataaaa gcagggttgg cctcagccct			1349
Leu Ser Ala Ile Glu Lys Leu Leu			
435			
gtgggtctgt ctcatgctct cctgttctt ctccccgcc cccagggcc tccaagccac			1409
ctctggaat acttggtctt gccccatggg cacgggaggg gcgccagccg tggagctgtg			1469
gaattgggcc ccgtggcaga gccccatcc cttgggggct gtggggatgc gcccaagccc			1529
ccgaggggaga ggccctggga caccaacaaa tctaagccct ccttagctct tggtaactgt			1589
gtcatgaagc tgccggacag acacacgtgg catctccctg ggcaggagag caggcctgca			1649
gcatgggtcc cggtcccgtg tgccgtgggt ggcagtggct gcacctggca ctagggtgctg			1709
tctgtggatg tgggtgacaa cggcaggagg ggacgtggc cttcctgcac atagacctgc			1769
agttagtaaa tcataagccc aaataaacag gttgtttgaa tataaaaaaa aaaaaaaaaa			1829
<210>	239		
<211>	1083		
<212>	DNA		
<213>	Homo sapiens		
<220>			
<221>	CDS		
<222>	421..768		
<400>	239		
aaggatgtgc tctttcccaa ggagagggag ctctgttgcc tccttccac agaactcactc			60
tgtgcaaaacc tcttccctc cttggcccca gtctcccaa ttctaaaatc ggatactgga			120
taaaatgcc aaggaagaacc tagggatgca ccaggaacca cgcgcctgaa tgccacaggt			180
ttgatattgat tcatgacct catctggaca caagctctaa aatacttgag ccttggcaga			240
aatggctgat agagtccaca gaacacgctg tcctcatctc agagaggaga actctgaacc			300
cagaggggaa ggatttacct gcagttgtat ggcaagccag aggtaggcgc tgcactggaa			360
cgcagcctaa ccagcctaaa gaaaccatgg gaggagaggc tcttaccctc tcctttgcag			420
atg tgg gcc cgg ctg cct cac act cca gag cag atg ggc cac agg ctt			468
Met Trp Ala Arg Leu Pro His Thr Pro Glu Gln Met Gly His Arg Leu			
1	5	10	15
ata ggt ccc aag gaa gct tca ctt cat gtg gta ccc agc tgg cca gcc			516



Ile	Gly	Pro	Lys	Glu	Ala	Ser	Leu	His	Val	Val	Pro	Ser	Trp	Pro	Ala		
			20					25					30				
agg	aag	atg	gag	ggg	ctt	ctg	gct	ggc	ctc	tct	tcc	tct	cct	aga	aag		564
Arg	Lys	Met	Glu	Gly	Leu	Leu	Ala	Gly	Leu	Ser	Ser	Ser	Pro	Arg	Lys		
		35					40					45					
tca	tgc	tgg	ccc	ttt	tgg	gtc	cat	ggg	cca	aag	gtt	cat	gaa	ggg	ggc		612
Ser	Cys	Trp	Pro	Phe	Trp	Val	His	Gly	Pro	Lys	Val	His	Glu	Gly	Gly		
		50					55				60						
tct	gcc	tgt	gag	aca	tca	agc	tcc	tgg	gtt	gaa	gga	ctt	gga	tta	aga		660
Ser	Ala	Cys	Glu	Thr	Ser	Ser	Ser	Trp	Val	Glu	Gly	Leu	Gly	Leu	Arg		
		65				70				75					80		
aga	gtg	aca	tca	gtg	cac	agt	tta	tgc	caa	ggg	ctt	ggg	gcc	tca	gtc		708
Arg	Val	Thr	Ser	Val	His	Ser	Leu	Cys	Gln	Gly	Leu	Gly	Ala	Ser	Val		
					85				90						95		
cag	ctt	ctt	cct	gga	cca	cca	cca	aca	aca	acc	agt	gat	aaa	aat	aat		756
Gln	Leu	Leu	Pro	Gly	Pro	Pro	Pro	Thr	Thr	Thr	Ser	Asp	Lys	Asn	Asn		
			100					105					110				
tat	act	agt	ggc	tgacatttat	ggattcttcc	tacacactag	gctataccac										808
Tyr	Thr	Ser	Gly														
			115														
agcgagtgcc	tcgaaaggaa	atatagtata	gcactgtgcc	gtccaacatg	gcggccacta												868
gccacatgca	ctactgagca	cttgaaatgt	ggctagccca	cattgagatg	tgctgtaaat												928
aaagaataga	caccagatttt	ccaagactta	gtaccaaaaa	aagaatgtaa	aatttctcat												988
taacaatttt	ttttcttaca	tttattacat	gttaacatga	cgctattttgg	agtttaaata												1048
aatgcattat	taaaattcaa	aaaaaaaaaa	aaaaaa														1083

<210> 240  
 <211> 1831  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 78..590

<400> 240

aaggacttaa	gcgccccgga	gccggggaggc	gaacttgga	cccgcctggcc	tcgctcggtg												60
cgcgccctccc	tccccgc	atg	cag	ccc	gcc	gag	cgc	tcg	cgg	gtc	ccc	agg					110
		Met	Gln	Pro	Ala	Glu	Arg	Ser	Arg	Val	Pro	Arg					
		1				5				10							
atc	gac	ccg	tac	gga	ttc	gag	cgg	cct	gag	gac	ttc	gac	gac	gcc	gcc		158
Ile	Asp	Pro	Tyr	Gly	Phe	Glu	Arg	Pro	Glu	Asp	Phe	Asp	Asp	Ala	Ala		
			15					20					25				
tac	gag	aag	ttt	ttc	tcc	agc	tac	ctg	gtc	acg	ctc	acc	cgc	agg	gcg		206
Tyr	Glu	Lys	Phe	Phe	Ser	Ser	Tyr	Leu	Val	Thr	Leu	Thr	Arg	Arg	Ala		
		30					35					40					
atc	aaa	tgg	tcc	cgg	ctg	ctg	cag	ggc	ggg	ggc	gtc	ccc	agg	agc	cgg		254
Ile	Lys	Trp	Ser	Arg	Leu	Gln	Gly	Gly	Gly	Gly	Val	Pro	Arg	Ser	Arg		
		45				50					55						
aca	gtg	aag	cgc	tat	gtc	cgg	aaa	ggg	gtc	ccg	ctg	gag	cac	cgt	gcc		302
Thr	Val	Lys	Arg	Tyr	Val	Arg	Lys	Gly	Val	Pro	Leu	Glu	His	Arg	Ala		
		60				65				70					75		
cgc	gtc	tgg	atg	gtg	ctg	agt	ggg	gcc	cag	gcg	cag	atg	gac	cag	aat		350
Arg	Val	Trp	Met	Val	Leu	Ser	Gly	Ala	Gln	Ala	Gln	Met	Asp	Gln	Asn		
					80				85					90			
ccc	ggc	tac	tac	cac	cag	ctt	ctc	cag	gga	gag	aga	aac	ccc	agg	ctg		398
Pro	Gly	Tyr	Tyr	His	Gln	Leu	Leu	Gln	Gly	Glu	Arg	Asn	Pro	Arg	Leu		
				95				100						105			

```

gag gac gcc atc agg aca gac ctg aac cgg acc ttc ccc gac aac gtg      446
Glu Asp Ala Ile Arg Thr Asp Leu Asn Arg Thr Phe Pro Asp Asn Val
      110                      115                      120
aag ttc cgg aag acc acg gac ccc tgc tta cag agg acc ctg tac aat      494
Lys Phe Arg Lys Thr Thr Asp Pro Cys Leu Gln Arg Thr Leu Tyr Asn
      125                      130                      135
gtg ctg ctg gca tat ggg cac cat aac cag gga gtg ggc tac tgc cag      542
Val Leu Leu Ala Tyr Gly His His Asn Gln Gly Val Gly Tyr Cys Gln
      140                      145                      150                      155
gga atg aat ttt ata gca gga tat ctg att ctt ata aca aat aat gaa      590
Gly Met Asn Phe Ile Ala Gly Tyr Leu Ile Leu Ile Thr Asn Asn Glu
      160                      165                      170
taagaatctt tttggctgtt agatgctctt gttggaagaa tactaccaga ttactacagc      650
ccggccatgc tgggcctgaa gaccgaccag gaggtcctcg gggagctggt gcgggcgaag      710
ctgccggctg tgggggccct gatggagcgt ctcggtgtgc tgtggacgct gctggtgtcc      770
cgctggttca tctgcctgtt tgtggacatc ttgcccgctg agacagtgtc tcggatctgg      830
gactgtttgt ttaacgaagg ctggaagatt atcttccggt tggccctgac ctttaattaag      890
cagcaccagg agttgatttt ggaagccacc agcgttccag acatttgcga taagtttaag      950
cagataacca aagggagttt cgtgatggag tgtcacacgt ttatgcagggt gtgtggggct      1010
gcacgtggct cagtcccctc ccagggggcc ccgctcacc tgcagcccgg gggctgctct      1070
gaccaccggg aggatgcaca ggatgggcac cagtgggcat agggcacagg atgagcctcc      1130
agctctgtcc tgcattctgcc ccctgcgcct ggctccgag ggctttcctg tctatggcgg      1190
ccctgtcttc ttggccctgg cactgcggac gctgctcctg gtctaatagg ctgtactcat      1250
ctgctgtgtg tggtgccaga agtgtggctt cccgaggccc ggctcccca ctgggtcctg      1310
gacctggcgc aggccgtata gactcaggct ctgatgaggg cgttgtggga gctgtacctg      1370
acaggccttc tgaggaagcc aagacgccag gagaggctca ggccctgggag tcagtagttt      1430
cctaagaggg agtggaggct cggggccact ctgggtgcag catggcaaac gtgggcggta      1490
tttcagcagc tgggccttca tcaaagagaa gacctgttg gccgggcgcg gtggctcacg      1550
cctgcagtcc cagcactttg ggaggccaag gcgtgtggat cacctgaggt caggagtcca      1610
agaccagcct ggccaacacg gtgaaacccc gtctctacta aaaaatacaa aaattagcca      1670
gggtgtgggtg ctcacgctta tgtagtccca gttactcggg aggctgaggg acgagaatca      1730
cttgaacctg ggaggcggag gttgcagtga gccgagatcg cgccactgca ctccagcctg      1790
ggcaacagag tgagactctg tctcaaaaaa aaaaaaaaaa a      1831

```

<210> 241  
 <211> 1830  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 78..608

```

<400> 241
aaggacttaa gcgccccgga gccgggaggg gaacttgga cccgctggcc tcgctcggtg      60
cgcgctccc tcccgcg atg cag ccc gcc gag cgc tgc cgg gtc ccc agg      110
      Met Gln Pro Ala Glu Arg Ser Arg Val Pro Arg
      1                      5                      10
atc gac ccg tac gga ttc gag cgg cct gag gac ttc gac gac gcc gcc      158
Ile Asp Pro Tyr Gly Phe Glu Arg Pro Glu Asp Phe Asp Asp Ala Ala
      15                      20                      25
tac gag aag ttt ttc tcc agc tac ctg gtc acg ctc acc cgc agg gcg      206
Tyr Glu Lys Phe Phe Ser Ser Tyr Leu Val Thr Leu Thr Arg Arg Ala
      30                      35                      40
atc aaa tgg tcc cgg ctg ctg cag ggc ggg ggc gtc ccc agg agc cgg      254
Ile Lys Trp Ser Arg Leu Leu Gln Gly Gly Gly Val Pro Arg Ser Arg
      45                      50                      55
aca gtg aag cgc tat gtc cgg aaa ggg gtc ccg ctg gag cac cgt gcc      302

```

Thr	Val	Lys	Arg	Tyr	Val	Arg	Lys	Gly	Val	Pro	Leu	Glu	His	Arg	Ala		
60					65				70						75		
cgc	gtc	tgg	atg	gtg	ctg	agt	ggg	gcc	cag	gcg	cag	atg	gac	cag	aat		350
Arg	Val	Trp	Met	Val	Leu	Ser	Gly	Ala	Gln	Ala	Gln	Met	Asp	Gln	Asn		
				80				85						90			
ccc	ggc	tac	tac	cac	cag	ctt	ctc	cag	gga	gag	aga	aac	ccc	agg	ctg		398
Pro	Gly	Tyr	Tyr	His	Gln	Leu	Leu	Gln	Gly	Glu	Arg	Asn	Pro	Arg	Leu		
			95					100					105				
gag	gac	gcc	atc	agg	aca	gac	ctg	aac	cgg	acc	ttc	ccc	gac	aac	gtg		446
Glu	Asp	Ala	Ile	Arg	Thr	Asp	Leu	Asn	Arg	Thr	Phe	Pro	Asp	Asn	Val		
		110					115					120					
aag	ttc	cgg	aag	acc	acg	gac	ccc	tgc	tta	cag	agg	acc	ctg	tac	aat		494
Lys	Phe	Arg	Lys	Thr	Thr	Asp	Pro	Cys	Leu	Gln	Arg	Thr	Leu	Tyr	Asn		
	125					130					135						
gtg	ctg	ctg	gca	tat	ggg	cac	cat	aac	cag	gga	gtg	ggc	tac	tgc	cag		542
Val	Leu	Leu	Ala	Tyr	Gly	His	His	Asn	Gln	Gly	Val	Gly	Tyr	Cys	Gln		
	140				145				150						155		
gga	atg	aat	ttt	ata	gca	gga	tat	ctg	att	ctt	ata	aca	aat	aat	gat		590
Gly	Met	Asn	Phe	Ile	Ala	Gly	Tyr	Leu	Ile	Leu	Ile	Thr	Asn	Asn	Asp		
				160				165					170				
aag	aat	ctt	ttt	ggc	tgt	tagatgctct	tgttgaaga	atactaccag									638
Lys	Asn	Leu	Phe	Gly	Cys												
			175														
attactacag	cccggccatg	ctgggcctga	agaccgacca	ggaggtcctc	ggggagctgg												698
tgcgggcgaa	gctgccggct	gtggggggccc	tgatggagcg	tctcgggtgtg	ctgtggacgc												758
tgctgggtgtc	ccgctggttc	atctgcctgt	ttgtggacat	cttgcccgtg	gagacagtgc												818
ttcgggatctg	ggactgtttg	tttaacgaag	gctcgaagat	tatcttccgg	ttggccctga												878
ccttaattaa	gcagcaccag	gagttgattt	tggaagccac	cagcgttcca	gacatttgcg												938
ataagtttaa	gcagataacc	aaagggagtt	tcgtgatgga	gtgtcacacg	tttatgcagg												998
tgtgtggggc	tgacacgtggc	tcagtcacct	cccagggggc	cccgcctcac	ctgcagcccc												1058
ggggctgctc	tgaccacccg	gaggatgcac	aggatgggca	ccagtgggca	tagggcacag												1118
gatgagcctc	cagctctgtc	ctgcatctgc	cccctgcgcc	tggcctccga	gggctttcct												1178
gtctatggcg	gccctgtctt	cttggccctg	gcactgcgga	cgtgtctcct	ggtcctaattg												1238
gctgtactca	tctgtctgtg	gtgggtgccag	aagtgtggct	ttccgaggcc	cggcctcccc												1298
actgggtcct	ggacctggcg	caggccgtat	agactcaggt	cctgatgagg	gcgttgtggg												1358
agctgtacct	gacaggcctt	ctgaggaagc	caagacgcca	ggagaggctc	aggcctggga												1418
gtcagtagtt	tcctaagagg	gagtggaggc	tcggggccac	tctgggtgca	gcatggcaaaa												1478
cgtgggctcag	atttcagcag	ctgggccttc	atcaaagaga	agaccatgtt	ggccggggcgc												1538
gggtggctcac	gctgcagtc	ccagcacttt	gggagggcca	ggcgtgtgga	tcacctgagg												1598
tcaggagttc	aagaccagcc	tgcccaacac	ggtgaaaccc	cgtctctact	aaaaaataca												1658
aaaattagcc	aggtgtgggtg	gctcacgctt	atgtagtccc	agttactcgg	gaggctgagg												1718
cacgagaatc	acttgaacct	gggaggcgga	ggttgccagt	agccgagatc	gcgccactgc												1778
actccagcct	gggcaacaga	gtgagactct	gtctcaaaaa	aaaaaaaaaa	aa												1830

<210> 242  
 <211> 508  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -27...-1

<400> 242  
 Met Asp Pro Lys Leu Gly Arg Met Ala Ala Ser Leu Leu Ala Val Leu  
 -25 -20 -15  
 Leu Leu Leu Leu Leu Glu Arg Gly Met Phe Ser Ser Pro Ser Pro Pro  
 -10 -5 1 5

Pro	Ala	Leu	Leu	Glu	Lys	Val	Phe	Gln	Tyr	Ile	Asp	Leu	His	Gln	Asp
				10					15					20	
Glu	Phe	Val	Gln	Thr	Leu	Lys	Glu	Trp	Val	Ala	Ile	Glu	Ser	Asp	Ser
			25					30					35		
Val	Gln	Pro	Val	Pro	Arg	Phe	Arg	Gln	Glu	Leu	Phe	Arg	Met	Met	Ala
		40				45					50				
Val	Ala	Ala	Asp	Thr	Leu	Gln	Arg	Leu	Gly	Ala	Arg	Val	Ala	Ser	Val
	55					60				65					
Asp	Met	Gly	Pro	Gln	Gln	Leu	Pro	Asp	Gly	Gln	Ser	Leu	Pro	Ile	Pro
70					75					80				85	
Pro	Val	Ile	Leu	Ala	Glu	Leu	Gly	Ser	Asp	Pro	Thr	Lys	Gly	Thr	Val
				90					95					100	
Cys	Phe	Tyr	Gly	His	Leu	Asp	Val	Gln	Pro	Ala	Asp	Arg	Gly	Asp	Gly
			105					110					115		
Trp	Leu	Thr	Asp	Pro	Tyr	Val	Leu	Thr	Glu	Val	Asp	Gly	Lys	Leu	Tyr
		120				125						130			
Gly	Arg	Gly	Ala	Thr	Asp	Asn	Lys	Gly	Pro	Val	Leu	Ala	Trp	Ile	Asn
	135					140				145					
Ala	Val	Ser	Ala	Phe	Arg	Ala	Leu	Glu	Gln	Asp	Leu	Pro	Val	Asn	Ile
	150				155					160					165
Lys	Phe	Ile	Ile	Glu	Gly	Met	Glu	Glu	Ala	Gly	Ser	Val	Ala	Leu	Glu
				170					175					180	
Glu	Leu	Val	Glu	Lys	Glu	Lys	Asp	Arg	Phe	Phe	Ser	Gly	Val	Asp	Tyr
			185					190					195		
Ile	Val	Ile	Ser	Asp	Asn	Leu	Trp	Ile	Ser	Gln	Arg	Lys	Pro	Ala	Ile
		200				205						210			
Thr	Tyr	Gly	Thr	Arg	Gly	Asn	Ser	Tyr	Phe	Met	Val	Glu	Val	Lys	Cys
	215					220					225				
Arg	Asp	Gln	Asp	Phe	His	Ser	Gly	Thr	Phe	Gly	Gly	Ile	Leu	His	Glu
	230				235					240					245
Pro	Met	Ala	Asp	Leu	Val	Ala	Leu	Leu	Gly	Ser	Leu	Val	Asp	Ser	Ser
				250					255					260	
Gly	His	Ile	Leu	Val	Pro	Gly	Ile	Tyr	Asp	Glu	Val	Val	Pro	Leu	Thr
			265					270					275		
Glu	Glu	Glu	Ile	Asn	Thr	Tyr	Lys	Ala	Ile	His	Leu	Asp	Leu	Glu	Glu
		280					285					290			
Tyr	Arg	Asn	Ser	Ser	Arg	Val	Glu	Lys	Phe	Leu	Phe	Asp	Thr	Lys	Glu
	295					300					305				
Glu	Ile	Leu	Met	His	Leu	Trp	Arg	Tyr	Pro	Ser	Leu	Ser	Ile	His	Gly
	310				315					320					325
Ile	Glu	Gly	Ala	Phe	Asp	Glu	Pro	Gly	Thr	Lys	Thr	Val	Ile	Pro	Gly
				330					335					340	
Arg	Val	Ile	Gly	Lys	Phe	Ser	Ile	Arg	Leu	Val	Pro	His	Met	Asn	Val
			345					350					355		
Ser	Ala	Val	Glu	Lys	Gln	Val	Thr	Arg	His	Leu	Glu	Asp	Val	Phe	Ser
		360					365					370			
Lys	Arg	Asn	Ser	Ser	Asn	Lys	Met	Val	Val	Ser	Met	Thr	Leu	Gly	Leu
		375				380					385				
His	Pro	Trp	Ile	Ala	Asn	Ile	Asp	Asp	Thr	Gln	Tyr	Leu	Ala	Ala	Lys
					395					400					405
Arg	Ala	Ile	Arg	Thr	Val	Phe	Gly	Thr	Glu	Pro	Asp	Met	Ile	Arg	Asp
				410					415					420	
Gly	Ser	Thr	Ile	Pro	Ile	Ala	Lys	Met	Phe	Gln	Glu	Ile	Val	His	Lys
			425					430					435		
Ser	Val	Val	Leu	Ile	Pro	Leu	Gly	Ala	Val	Asp	Asp	Gly	Glu	His	Ser
		440					445					450			
Gln	Asn	Glu	Lys	Ile	Asn	Arg	Trp	Asn	Tyr	Ile	Glu	Gly	Thr	Lys	Leu
	455					460					465				

Phe Ala Ala Phe Phe Leu Glu Met Ala Gln Leu His  
 470 475 480

<210> 243  
 <211> 331  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -31...-1

<400> 243  
 Met Trp Leu Trp Glu Asp Gln Gly Gly Leu Leu Gly Pro Phe Ser Phe  
 -30 -25 -20  
 Leu Leu Leu Val Leu Leu Leu Val Thr Arg Ser Pro Val Asn Ala Cys  
 -15 -10 -5 1  
 Leu Leu Thr Gly Ser Leu Phe Val Leu Leu Arg Val Phe Ser Phe Glu  
 5 10 15  
 Pro Val Pro Ser Cys Arg Ala Leu Gln Val Leu Lys Pro Arg Asp Arg  
 20 25 30  
 Ile Ser Ala Ile Ala His Arg Gly Gly Ser His Asp Ala Pro Glu Asn  
 35 40 45  
 Thr Leu Ala Ala Ile Arg Gln Ala Ala Lys Asn Gly Ala Thr Gly Val  
 50 55 60 65  
 Glu Leu Asp Ile Glu Phe Thr Ser Asp Gly Ile Pro Val Leu Met His  
 70 75 80  
 Asp Asn Thr Val Asp Arg Thr Thr Asp Gly Thr Gly Arg Leu Cys Asp  
 85 90 95  
 Leu Thr Phe Glu Gln Ile Arg Lys Leu Asn Pro Ala Ala Asn His Arg  
 100 105 110  
 Leu Arg Asn Asp Phe Pro Asp Glu Lys Ile Pro Thr Leu Met Glu Ala  
 115 120 125  
 Val Ala Glu Cys Leu Asn His Asn Leu Thr Ile Phe Phe Asp Val Lys  
 130 135 140 145  
 Gly His Ala His Lys Ala Thr Glu Ala Leu Lys Lys Met Tyr Met Glu  
 150 155 160  
 Phe Pro Gln Leu Tyr Asn Asn Ser Val Val Cys Ser Phe Leu Pro Glu  
 165 170 175  
 Val Ile Tyr Lys Met Arg Gln Thr Asp Arg Asp Val Ile Thr Ala Leu  
 180 185 190  
 Thr His Arg Pro Trp Ser Leu Ser His Thr Gly Asp Gly Lys Pro Arg  
 195 200 205  
 Tyr Asp Thr Phe Trp Lys His Phe Ile Phe Val Met Met Asp Ile Leu  
 210 215 220 225  
 Leu Asp Trp Ser Met His Asn Ile Leu Trp Tyr Leu Cys Gly Ile Ser  
 230 235 240  
 Ala Phe Leu Met Gln Lys Asp Phe Val Ser Pro Ala Tyr Leu Lys Lys  
 245 250 255  
 Trp Ser Ala Lys Gly Ile Gln Val Val Gly Trp Thr Val Asn Thr Phe  
 260 265 270  
 Asp Glu Lys Ser Tyr Tyr Glu Ser His Leu Gly Ser Ser Tyr Ile Thr  
 275 280 285  
 Asp Ser Met Val Glu Asp Cys Glu Pro His Phe  
 290 295 300

<210> 244  
 <211> 274

<212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -17...-1

<400> 244  
 Met Asp Arg Pro Gly Phe Val Ala Ala Leu Val Ala Gly Gly Val Ala  
           -15                  -10                  -5  
 Gly Val Ser Val Asp Leu Ile Leu Phe Pro Leu Asp Thr Ile Lys Thr  
   1                  5                  10                  15  
 Arg Leu Gln Ser Pro Gln Gly Phe Ser Lys Ala Gly Gly Phe His Gly  
                   20                  25                  30  
 Ile Tyr Ala Gly Val Pro Ser Ala Ala Ile Gly Ser Phe Pro Asn Ala  
                   35                  40                  45  
 Ala Ala Phe Phe Ile Thr Tyr Glu Tyr Val Lys Trp Phe Leu His Ala  
           50                  55                  60  
 Asp Ser Ser Ser Tyr Leu Thr Pro Met Lys His Met Leu Ala Ala Ser  
   65                  70                  75  
 Ala Gly Glu Val Val Ala Cys Leu Ile Arg Val Pro Ser Glu Val Val  
 80                  85                  90                  95  
 Lys Gln Arg Ala Gln Val Ser Ala Ser Thr Arg Thr Phe Gln Ile Phe  
                   100                  105                  110  
 Ser Asn Ile Leu Tyr Glu Glu Gly Ile Gln Gly Leu Tyr Arg Gly Tyr  
                   115                  120                  125  
 Lys Ser Thr Val Leu Arg Glu Ile Pro Phe Ser Leu Val Gln Phe Pro  
           130                  135                  140  
 Leu Trp Glu Ser Leu Lys Ala Leu Trp Ser Trp Arg Gln Asp His Val  
   145                  150                  155  
 Val Asp Ser Trp Gln Ser Ala Val Cys Gly Ala Phe Ala Gly Gly Phe  
 160                  165                  170                  175  
 Ala Ala Ala Val Thr Thr Pro Leu Asp Val Ala Lys Thr Arg Ile Met  
                   180                  185                  190  
 Leu Ala Lys Ala Gly Ser Ser Thr Ala Asp Gly Asn Val Leu Ser Val  
                   195                  200                  205  
 Leu His Gly Val Trp Arg Ser Gln Gly Leu Ala Gly Leu Phe Ala Gly  
           210                  215                  220  
 Val Phe Pro Arg Met Ala Ala Ile Ser Leu Gly Gly Phe Ile Phe Leu  
   225                  230                  235  
 Gly Ala Tyr Asp Arg Thr His Ser Leu Leu Leu Glu Val Gly Arg Lys  
 240                  245                  250                  255  
 Ser Pro

<210> 245  
 <211> 406  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -35...-1

<400> 245  
 Met Arg Gly Ser Val Glu Cys Thr Trp Gly Trp Gly His Cys Ala Pro  
   -35                  -30                  -25                  -20  
 Ser Pro Leu Leu Leu Trp Thr Leu Leu Leu Phe Ala Ala Pro Phe Gly  
                   -15                  -10                  -5

```

Leu Leu Gly Glu Lys Thr Arg Gln Val Ser Leu Glu Val Ile Pro Asn
      1                                5                                10
Trp Leu Gly Pro Leu Gln Asn Leu Leu His Ile Arg Ala Val Gly Thr
      15                                20                                25
Asn Ser Thr Leu His Tyr Val Trp Ser Ser Leu Gly Pro Leu Ala Val
      30                                35                                40                                45
Val Met Val Ala Thr Asn Thr Pro His Ser Thr Leu Ser Val Asn Trp
      50                                55                                60
Ser Leu Leu Leu Ser Pro Glu Pro Asp Gly Gly Leu Met Val Leu Pro
      65                                70                                75
Lys Asp Ser Ile Gln Phe Ser Ser Ala Leu Val Phe Thr Arg Leu Leu
      80                                85                                90
Glu Phe Asp Ser Thr Asn Val Ser Asp Thr Ala Ala Lys Pro Leu Gly
      95                                100                                105
Arg Pro Tyr Pro Pro Tyr Ser Leu Ala Asp Phe Ser Trp Asn Asn Ile
      110                                115                                120                                125
Thr Asp Ser Leu Asp Pro Ala Thr Leu Ser Ala Thr Phe Gln Gly His
      130                                135                                140
Pro Met Asn Asp Pro Thr Arg Thr Phe Ala Asn Gly Ser Leu Ala Phe
      145                                150                                155
Arg Val Gln Ala Phe Ser Arg Ser Ser Arg Pro Ala Gln Pro Pro Arg
      160                                165                                170
Leu Leu His Thr Ala Asp Thr Cys Gln Leu Glu Val Ala Leu Ile Gly
      175                                180                                185
Ala Ser Pro Arg Gly Asn Arg Ser Leu Phe Gly Leu Glu Val Ala Thr
      190                                195                                200                                205
Leu Gly Gln Gly Pro Asp Cys Pro Ser Met Gln Glu Gln His Ser Ile
      210                                215                                220
Asp Asp Glu Tyr Ala Pro Ala Val Phe Gln Leu Asp Gln Leu Leu Trp
      225                                230                                235
Gly Ser Leu Pro Ser Gly Phe Ala Gln Trp Arg Pro Val Ala Tyr Ser
      240                                245                                250
Gln Lys Pro Gly Gly Arg Glu Ser Ala Leu Pro Cys Gln Ala Ser Pro
      255                                260                                265
Leu His Pro Ala Leu Ala Tyr Ser Leu Pro Gln Ser Pro Ile Val Arg
      270                                275                                280                                285
Ala Phe Phe Gly Ser Gln Asn Asn Phe Cys Ala Phe Asn Leu Thr Phe
      290                                295                                300
Gly Ala Ser Thr Gly Pro Gly Tyr Trp Asp Gln His Tyr Leu Ser Trp
      305                                310                                315
Ser Met Leu Leu Gly Val Gly Phe Pro Pro Val Asp Gly Leu Ser Pro
      320                                325                                330
Leu Val Leu Gly Ile Met Ala Val Ala Leu Gly Ala Pro Gly Leu Met
      335                                340                                345
Leu Leu Gly Gly Gly Leu Val Leu Leu Leu His His Lys Lys Tyr Ser
      350                                355                                360                                365
Glu Tyr Gln Ser Ile Asn
      370

```

<210> 246

<211> 24

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -16...-1

<400> 246  
 Met Ala Pro Leu Gly Met Leu Leu Gly Leu Leu Met Ala Ala Cys Thr  
           -15                              -10                              -5  
 Pro Ser Ala Ser Val Ile Arg Thr  
 1  5

<210> 247  
 <211> 348  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -29...-1

<400> 247  
 Met Ala Pro Gln Ser Leu Pro Ser Ser Arg Met Ala Pro Leu Gly Met  
                               -25                              -20                              -15  
 Leu Leu Gly Pro Leu Met Ala Ala Cys Phe Thr Phe Cys Leu Ser His  
                               -10                              -5                              1  
 Gln Asn Leu Lys Glu Phe Ala Leu Thr Asn Pro Glu Lys Ser Ser Thr  
           5                              10                              15  
 Lys Glu Thr Glu Arg Lys Glu Thr Lys Ala Glu Glu Glu Leu Asp Ala  
 20                              25                              30                              35  
 Glu Val Leu Glu Val Phe His Pro Thr His Glu Trp Gln Ala Leu Gln  
                               40                              45                              50  
 Pro Gly Gln Ala Val Pro Ala Gly Ser His Val Arg Leu Asn Leu Gln  
                               55                              60                              65  
 Thr Gly Glu Arg Glu Ala Lys Leu Gln Tyr Glu Asp Lys Phe Arg Asn  
           70                              75                              80  
 Asn Leu Lys Gly Lys Arg Leu Asp Ile Asn Thr Asn Thr Tyr Thr Ser  
           85                              90                              95  
 Gln Asp Leu Lys Ser Ala Leu Ala Lys Phe Lys Glu Gly Ala Glu Met  
 100                              105                              110                              115  
 Glu Ser Ser Lys Glu Asp Lys Ala Arg Gln Ala Glu Val Lys Arg Leu  
                               120                              125                              130  
 Phe Arg Pro Ile Glu Glu Leu Lys Lys Asp Phe Asp Glu Leu Asn Val  
                               135                              140                              145  
 Val Ile Glu Thr Asp Met Gln Ile Met Val Arg Leu Ile Asn Lys Phe  
           150                              155                              160  
 Asn Ser Ser Ser Ser Ser Leu Glu Glu Lys Ile Ala Ala Leu Phe Asp  
           165                              170                              175  
 Leu Glu Tyr Tyr Val His Gln Met Asp Asn Ala Gln Asp Leu Leu Ser  
 180                              185                              190                              195  
 Phe Gly Gly Leu Gln Val Val Ile Asn Gly Leu Asn Ser Thr Glu Pro  
                               200                              205                              210  
 Leu Val Lys Glu Tyr Ala Ala Phe Val Leu Gly Ala Ala Phe Ser Ser  
           215                              220                              225  
 Asn Pro Lys Val Gln Val Glu Ala Ile Glu Gly Gly Ala Leu Gln Lys  
           230                              235                              240  
 Leu Leu Val Ile Leu Ala Thr Glu Gln Pro Leu Thr Ala Lys Lys Lys  
           245                              250                              255  
 Val Leu Phe Ala Leu Cys Ser Leu Leu Arg His Phe Pro Tyr Ala Gln  
 260                              265                              270                              275  
 Arg Gln Phe Leu Lys Leu Gly Gly Leu Gln Val Leu Arg Thr Leu Val  
                               280                              285                              290  
 Gln Glu Lys Gly Thr Glu Val Leu Ala Val Arg Val Val Thr Leu Leu  
                               295                              300                              305



[illegible]

```
<220>  
<221> SIGNAL  
<222> -36..-1
```

262





<211> 138  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -15...-1

<400> 252  
 Met Lys Phe Thr Thr Leu Leu Phe Leu Ala Ala Val Ala Gly Ala Leu  
 -15 -10 -5 1  
 Val Tyr Ala Glu Asp Ala Ser Ser Asp Ser Thr Gly Ala Asp Pro Ala  
 5 10 15  
 Gln Glu Ala Gly Thr Ser Lys Pro Asn Glu Glu Ile Ser Gly Pro Ala  
 20 25 30  
 Glu Pro Ala Ser Pro Pro Glu Thr Thr Thr Thr Ala Gln Glu Thr Ser  
 35 40 45  
 Ala Ala Ala Val Gln Gly Thr Ala Lys Val Thr Ser Ser Arg Gln Glu  
 50 55 60 65  
 Leu Asn Pro Leu Lys Ser Ile Val Glu Lys Ser Ile Leu Leu Thr Glu  
 70 75 80  
 Gln Ala Leu Ala Lys Ala Gly Lys Gly Met His Gly Gly Val Pro Gly  
 85 90 95  
 Gly Lys Gln Phe Ile Glu Asn Gly Ser Glu Phe Ala Gln Lys Leu Leu  
 100 105 110  
 Lys Lys Phe Ser Leu Leu Lys Pro Trp Ala  
 115 120

<210> 253  
 <211> 108  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -31...-1

<220>  
 <221> UNSURE  
 <222> 45  
 <223> Xaa = Glu,Gln

<220>  
 <221> UNSURE  
 <222> 44  
 <223> Xaa = Lys,Asn

<400> 253  
 Met Trp Leu Trp Glu Asp Gln Gly Gly Leu Leu Gly Pro Phe Ser Phe  
 -30 -25 -20  
 Leu Leu Leu Val Leu Leu Leu Val Thr Arg Ser Pro Val Asn Ala Cys  
 -15 -10 -5 1  
 Leu Leu Thr Gly Ser Leu Phe Val Leu Leu Arg Val Phe Ser Phe Glu  
 5 10 15  
 Pro Val Pro Ser Cys Arg Ala Leu Gln Val Leu Lys Pro Arg Asp Arg  
 20 25 30  
 Ile Ser Ala Ile Ala His Arg Gly Gly Ser Xaa Xaa Ala Pro Glu Asn  
 35 40 45

Thr Leu Ala Ala Ile Arg Gln Leu Arg Met Glu Gln Gln Ala Trp Ser  
 50 55 60 65  
 Trp Thr Leu Ser Leu Leu Thr Gly Phe Leu Ser  
 70 75

<210> 254  
 <211> 147  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -24...-1

<400> 254  
 Met Val Met Gly Leu Gly Val Leu Leu Leu Val Phe Val Leu Gly Leu  
 -20 -15 -10  
 Gly Leu Thr Pro Pro Thr Leu Ala Gln Asp Asn Ser Arg Tyr Thr His  
 -5 1 5  
 Phe Leu Thr Gln His Tyr Asp Ala Lys Pro Gln Gly Arg Asp Asp Arg  
 10 15 20  
 Tyr Cys Glu Ser Ile Met Arg Arg Arg Gly Leu Thr Ser Pro Cys Lys  
 25 30 35 40  
 Asp Ile Asn Thr Phe Ile His Gly Asn Lys Arg Thr Ile Lys Ala Ile  
 45 50 55  
 Cys Glu Asn Lys Asn Gly Asn Pro His Arg Glu Asn Leu Arg Ile Ser  
 60 65 70  
 Lys Ser Ser Phe Gln Val Thr Thr Cys Lys Leu His Gly Gly Ser Pro  
 75 80 85  
 Trp Pro Pro Cys Gln Tyr Arg Ala Thr Ala Gly Phe Arg Asn Val Val  
 90 95 100  
 Val Ala Cys Glu Asn Gly Leu Pro Val His Leu Asp Gln Ser Ile Phe  
 105 110 115 120  
 Arg Arg Pro

<210> 255  
 <211> 381  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -33...-1

<400> 255  
 Met Ser Trp Thr Val Pro Val Val Arg Ala Ser Gln Arg Val Ser Ser  
 -30 -25 -20  
 Val Gly Ala Asn Phe Leu Cys Leu Gly Met Ala Leu Cys Pro Arg Gln  
 -15 -10 -5  
 Ala Thr Arg Ile Pro Leu Asn Gly Thr Trp Leu Phe Thr Pro Val Ser  
 1 5 10 15  
 Lys Met Ala Thr Val Lys Ser Glu Leu Ile Glu Arg Phe Thr Ser Glu  
 20 25 30  
 Lys Pro Val His Ser Lys Val Ser Ile Ile Gly Thr Gly Ser Val  
 35 40 45  
 Gly Met Ala Cys Ala Ile Ser Ile Leu Leu Lys Gly Leu Ser Asp Glu  
 50 55 60  
 Leu Ala Leu Val Asp Leu Asp Glu Asp Lys Leu Lys Gly Glu Thr Met

65	70	75
Asp Leu Gln His Gly Ser Pro Phe Thr Lys Met Pro Asn Ile Val Cys		
80	85	90
Ser Lys Asp Tyr Phe Val Thr Ala Asn Ser Asn Leu Val Ile Ile Thr		
	100	105
Ala Gly Ala Arg Gln Glu Lys Gly Glu Thr Arg Leu Asn Leu Val Gln		
	115	120
Arg Asn Val Ala Ile Phe Lys Leu Met Ile Ser Ser Ile Val Gln Tyr		
	130	135
Ser Pro His Cys Lys Leu Ile Ile Val Ser Asn Pro Val Asp Ile Leu		
	145	150
Thr Tyr Val Ala Trp Lys Leu Ser Ala Phe Pro Lys Asn Arg Ile Ile		
160	165	170
Gly Ser Gly Cys Asn Leu Asp Thr Ala Arg Phe Arg Phe Leu Ile Gly		
	180	185
Gln Lys Leu Gly Ile His Ser Glu Ser Cys His Gly Trp Ile Leu Gly		
	195	200
Glu His Gly Asp Ser Ser Val Pro Val Trp Ser Gly Val Asn Ile Ala		
	210	215
Gly Val Pro Leu Lys Asp Leu Asn Ser Asp Ile Gly Thr Asp Lys Asp		
	225	230
Pro Glu Gln Trp Lys Asn Val His Lys Glu Val Thr Ala Thr Ala Tyr		
240	245	250
Glu Ile Ile Lys Met Lys Gly Tyr Thr Ser Trp Ala Ile Gly Leu Ser		
	260	265
Val Ala Asp Leu Thr Glu Ser Ile Leu Lys Asn Leu Arg Arg Ile His		
	275	280
Pro Val Ser Thr Ile Ile Lys Gly Leu Tyr Gly Ile Asp Glu Glu Val		
	290	295
Phe Leu Ser Ile Pro Cys Ile Leu Gly Glu Asn Gly Ile Thr Asn Leu		
	305	310
Ile Lys Ile Lys Leu Thr Pro Glu Glu Glu Ala His Leu Lys Lys Ser		
320	325	330
Ala Lys Thr Leu Trp Glu Ile Gln Asn Lys Leu Lys Leu		
	340	345

<210> 256  
 <211> 139  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -33...-1

<400> 256

Met Ser Trp Thr Val Pro Val Val Arg Ala Ser Gln Arg Met Ser Ser	
	-30
Val Gly Ala Asn Phe Leu Cys Leu Gly Met Ala Leu Cys Leu Arg Gln	
	-15
Ala Thr Arg Ile Pro Leu Asn Gly Thr Trp Leu Phe Thr Pro Val Ser	
1	5
Lys Met Ala Thr Val Lys Ser Glu Leu Ile Glu Arg Phe Thr Ser Glu	
	20
Lys Pro Val His Ser Lys Val Ser Ile Ile Gly Thr Gly Ser Val	
	35
Gly Met Ala Cys Ala Ile Ser Ile Leu Leu Lys Gly Leu Ser Asp Glu	
	50
	55
	60

Leu Ala Leu Val Asp Leu Asp Glu Asp Lys Leu Lys Gly Glu Thr Met  
65 70 75  
Asp Leu Gln His Gly Ser Pro Phe Thr Lys Met Pro Ile Leu Phe Val  
80 85 90 95  
Ala Lys Ile Thr Leu Ser Gln Gln Thr Pro Thr  
100 105

<210> 257  
<211> 265  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -14...-1

<400> 257  
Met Asn Phe Ile Leu Phe Ile Phe Ile Pro Gly Val Phe Ser Leu Lys  
-10 -5 1  
Ser Ser Thr Leu Lys Pro Thr Ile Glu Ala Leu Pro Asn Val Leu Pro  
5 10 15  
Leu Asn Glu Asp Val Asn Lys Gln Glu Glu Lys Asn Glu Asp His Thr  
20 25 30  
Pro Asn Tyr Ala Pro Ala Asn Glu Lys Asn Gly Asn Tyr Tyr Lys Asp  
35 40 45 50  
Ile Lys Gln Tyr Val Phe Thr Thr Gln Asn Pro Asn Gly Thr Glu Ser  
55 60 65  
Glu Ile Ser Val Arg Ala Thr Thr Asp Leu Asn Phe Ala Leu Lys Asn  
70 75 80  
Gly Ser Thr Pro Asn Val Pro Ala Phe Trp Thr Met Leu Ala Lys Ala  
85 90 95  
Ile Asn Gly Thr Ala Val Val Met Asp Asp Lys Asp Gln Leu Phe His  
100 105 110  
Pro Ile Pro Glu Ser Asp Val Asn Ala Thr Gln Gly Glu Asn Gln Pro  
115 120 125 130  
Asp Leu Glu Asp Leu Lys Ile Lys Ile Met Leu Gly Ile Ser Leu Met  
135 140 145  
Thr Leu Leu Leu Phe Val Val Leu Leu Ala Phe Cys Ser Ala Thr Leu  
150 155 160  
Tyr Lys Leu Arg His Leu Ser Tyr Lys Ser Cys Glu Ser Gln Tyr Ser  
165 170 175  
Val Asn Pro Glu Leu Ala Thr Met Ser Tyr Phe His Pro Ser Glu Gly  
180 185 190  
Val Ser Asp Thr Ser Phe Ser Lys Ser Ala Glu Ser Ser Thr Phe Leu  
195 200 205 210  
Gly Thr Thr Ser Ser Asp Met Arg Arg Ser Gly Thr Arg Thr Ser Glu  
215 220 225  
Ser Lys Ile Met Thr Asp Ile Ile Ser Ile Gly Ser Asp Asn Glu Met  
230 235 240  
His Glu Asn Asp Glu Ser Val Thr Arg  
245 250

<210> 258  
<211> 200  
<212> PRT  
<213> Homo sapiens

<220>

<221> SIGNAL  
<222> -20...-1

<400> 258

Met	Asp	Ser	Ser	Thr	Ala	His	Ser	Pro	Val	Phe	Leu	Val	Phe	Pro	Pro
-20					-15					-10					-5
Glu	Ile	Thr	Ala	Ser	Glu	Tyr	Glu	Ser	Thr	Glu	Leu	Ser	Ala	Thr	Thr
				1				5					10		
Phe	Ser	Thr	Gln	Ser	Pro	Leu	Gln	Lys	Leu	Phe	Ala	Arg	Lys	Met	Lys
	15						20					25			
Ile	Leu	Gly	Thr	Ile	Gln	Ile	Leu	Phe	Gly	Ile	Met	Thr	Phe	Ser	Phe
	30					35					40				
Gly	Val	Ile	Phe	Leu	Phe	Thr	Leu	Leu	Lys	Pro	Tyr	Pro	Arg	Phe	Pro
45					50					55					60
Phe	Ile	Phe	Leu	Ser	Gly	Tyr	Pro	Phe	Trp	Gly	Ser	Val	Leu	Phe	Ile
				65					70					75	
Asn	Ser	Gly	Ala	Phe	Leu	Ile	Ala	Val	Lys	Arg	Lys	Thr	Thr	Glu	Thr
			80					85					90		
Leu	Ile	Ile	Leu	Ser	Arg	Ile	Met	Asn	Phe	Leu	Ser	Ala	Leu	Gly	Ala
	95						100					105			
Ile	Ala	Gly	Ile	Ile	Leu	Leu	Thr	Phe	Gly	Phe	Ile	Leu	Asp	Gln	Asn
	110					115					120				
Tyr	Ile	Cys	Gly	Tyr	Ser	His	Gln	Asn	Ser	Gln	Cys	Lys	Ala	Val	Thr
125					130					135					140
Val	Leu	Phe	Leu	Gly	Ile	Leu	Ile	Thr	Leu	Met	Thr	Phe	Ser	Ile	Ile
				145					150					155	
Glu	Leu	Phe	Ile	Ser	Leu	Pro	Phe	Ser	Ile	Leu	Gly	Cys	His	Ser	Glu
			160					165					170		
Asp	Cys	Asp	Cys	Glu	Gln	Cys	Cys								
	175						180								

<210> 259  
<211> 394  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -39...-1

<400> 259

Met	Ala	Thr	Ala	Gln	Leu	Gln	Arg	Thr	Pro	Met	Ser	Ala	Leu	Val	Phe
				-35					-30					-25	
Pro	Asn	Lys	Ile	Ser	Thr	Glu	His	Gln	Ser	Leu	Val	Leu	Val	Lys	Arg
		-20						-15					-10		
Leu	Leu	Ala	Val	Ser	Val	Ser	Cys	Ile	Thr	Tyr	Leu	Arg	Gly	Ile	Phe
		-5					1				5				
Pro	Glu	Cys	Ala	Tyr	Gly	Thr	Arg	Tyr	Leu	Asp	Asp	Leu	Cys	Val	Lys
10					15					20					25
Ile	Leu	Arg	Glu	Asp	Lys	Asn	Cys	Pro	Gly	Ser	Thr	Gln	Leu	Val	Lys
				30					35					40	
Trp	Ile	Leu	Gly	Cys	Tyr	Asp	Ala	Leu	Gln	Lys	Lys	Tyr	Leu	Arg	Met
			45					50					55		
Val	Val	Leu	Ala	Val	Tyr	Thr	Asn	Pro	Glu	Asp	Pro	Gln	Thr	Ile	Ser
		60					65					70			
Glu	Cys	Tyr	Gln	Phe	Lys	Phe	Lys	Tyr	Thr	Asn	Asn	Gly	Pro	Leu	Met
	75					80					85				
Asp	Phe	Ile	Ser	Lys	Asn	Gln	Ser	Asn	Glu	Ser	Ser	Met	Leu	Ser	Thr



90					95				100				105				
Asp	Thr	Lys	Lys	Ala	Ser	Ile	Leu	Leu	Ile	Arg	Lys	Ile	Tyr	Ile	Leu		
				110					115					120			
Met	Gln	Asn	Leu	Gly	Pro	Leu	Pro	Asn	Asp	Val	Cys	Leu	Thr	Met	Lys		
				125					130					135			
Leu	Phe	Tyr	Tyr	Asp	Glu	Val	Thr	Pro	Pro	Asp	Tyr	Gln	Pro	Pro	Gly		
				140					145					150			
Phe	Lys	Asp	Gly	Asp	Cys	Glu	Gly	Val	Ile	Phe	Glu	Gly	Glu	Pro	Met		
				155					160					165			
Tyr	Leu	Asn	Val	Gly	Glu	Val	Ser	Thr	Pro	Phe	His	Ile	Phe	Lys	Val		
170					175					180					185		
Lys	Val	Thr	Thr	Glu	Arg	Glu	Arg	Met	Glu	Asn	Ile	Asp	Ser	Thr	Ile		
				190					195					200			
Leu	Ser	Pro	Lys	Gln	Ile	Lys	Thr	Pro	Phe	Gln	Lys	Ile	Leu	Arg	Asp		
				205					210					215			
Lys	Asp	Val	Glu	Asp	Glu	Gln	Glu	His	Tyr	Thr	Ser	Asp	Asp	Leu	Asp		
				220					225					230			
Ile	Glu	Thr	Lys	Met	Glu	Glu	Gln	Glu	Lys	Asn	Pro	Ala	Ser	Ser	Glu		
				235					240					245			
Leu	Glu	Glu	Pro	Ser	Leu	Val	Cys	Glu	Glu	Asp	Glu	Ile	Met	Arg	Ser		
250					255					260					265		
Lys	Glu	Ser	Pro	Asp	Leu	Ser	Ile	Ser	His	Ser	Gln	Val	Glu	Gln	Leu		
				270					275					280			
Val	Asn	Lys	Thr	Ser	Glu	Leu	Asp	Met	Ser	Glu	Ser	Lys	Thr	Arg	Ser		
				285					290					295			
Gly	Lys	Val	Phe	Gln	Asn	Lys	Met	Ala	Asn	Gly	Asn	Gln	Pro	Val	Lys		
				300					305					310			
Ser	Ser	Lys	Glu	Asn	Arg	Lys	Arg	Ser	Gln	His	Glu	Ser	Gly	Arg	Ile		
				315					320					325			
Val	Leu	His	His	Phe	Asp	Ser	Ser	Ser	Gln	Glu	Ser	Val	Pro	Lys	Arg		
330					335					340					345		
Arg	Lys	Phe	Ser	Glu	Pro	Lys	Glu	His	Ile								
				350					355								

```
<220>  
<221> SIGNAL  
<222> -17..-1
```

270

Ser Thr Ser Arg Lys Ser Val Trp Leu Thr Pro Val Ser Thr Glu Asn  
 100 105 110  
 Glu Ile Lys Leu Asp Pro Ser Pro Phe Ile Ala Asp Phe Gln Thr Thr  
 115 120 125  
 Ala Glu Glu Leu Gly Leu Leu Ser Ser Ser Pro Asn Leu Leu  
 130 135 140

<210> 261  
 <211> 233  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -32...-1

<400> 261  
 Met Ala Thr Pro Pro Phe Arg Leu Ile Arg Lys Met Phe Ser Phe Lys  
 -30 -25 -20  
 Val Ser Arg Trp Met Gly Leu Ala Cys Phe Arg Ser Leu Ala Ala Ser  
 -15 -10 -5  
 Ser Pro Ser Ile Arg Gln Lys Lys Leu Met His Lys Leu Gln Glu Glu  
 1 5 10 15  
 Lys Ala Phe Arg Glu Glu Met Lys Ile Phe Arg Glu Lys Ile Glu Asp  
 20 25 30  
 Phe Arg Glu Glu Met Trp Thr Phe Arg Gly Lys Ile His Ala Phe Arg  
 35 40 45  
 Gly Gln Ile Leu Gly Phe Trp Glu Glu Glu Arg Pro Phe Trp Glu Glu  
 50 55 60  
 Glu Lys Thr Phe Trp Lys Glu Glu Lys Ser Phe Trp Glu Met Glu Lys  
 65 70 75 80  
 Ser Phe Arg Glu Glu Glu Lys Thr Phe Trp Lys Lys Tyr Arg Thr Phe  
 85 90 95  
 Trp Lys Glu Asp Lys Ala Phe Trp Lys Glu Asp Asn Ala Leu Trp Glu  
 100 105 110  
 Arg Asp Arg Asn Leu Leu Gln Glu Asp Lys Ala Leu Trp Glu Glu Glu  
 115 120 125  
 Lys Ala Leu Trp Val Glu Glu Arg Ala Leu Leu Glu Gly Glu Lys Ala  
 130 135 140  
 Leu Trp Glu Asp Lys Thr Ser Leu Trp Glu Glu Glu Asn Ala Leu Trp  
 145 150 155 160  
 Glu Glu Glu Arg Ala Phe Trp Met Glu Asn Asn Gly His Ile Ala Gly  
 165 170 175  
 Glu Gln Met Leu Glu Asp Gly Pro His Asn Ala Asn Arg Gly Gln Arg  
 180 185 190  
 Leu Leu Ala Phe Ser Arg Gly Arg Ala  
 195 200

<210> 262  
 <211> 67  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -20...-1

<400> 262

Met Asp Ser Ser Thr Ala His Ser Pro Val Phe Leu Val Phe Pro Pro  
 -20 -15 -10 -5  
 Glu Ile Thr Ala Ser Glu Tyr Glu Ser Thr Glu Leu Ser Ala Thr Thr  
 1 5 10  
 Phe Ser Thr Gln Ser Pro Leu Gln Lys Leu Phe Ala Arg Lys Met Lys  
 15 20 25  
 Ile Leu Gly Asp Ile His Ser Gly Ala Leu Phe Cys Ser Leu Ile Leu  
 30 35 40  
 Glu Pro Ser  
 45

<210> 263  
 <211> 94  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -25...-1

<400> 263  
 Met Cys Phe Leu Val Ser Phe Asn Leu Pro Ile His Ile Ser Leu Ser  
 -25 -20 -15 -10  
 His Leu Phe Leu Asp Leu Ser Arg Ser Leu Trp Phe Leu Ala Cys Pro  
 -5 1 5  
 Gly Leu Asn Leu Val Tyr Leu Ala Leu Asp Ser Phe Ser Asp Leu Arg  
 10 15 20  
 Pro Ser Leu Asn Leu Leu Phe Tyr Phe Val Pro Gly Phe Gly Val Ser  
 25 30 35  
 Lys Tyr Leu Thr Ser Ala Gln Pro Val Leu Gly Phe Leu Leu Leu Pro  
 40 45 50 55  
 Asp Ile Asp Asn Pro Ala Leu Leu Gly Thr Glu Arg Trp Ser  
 60 65

<210> 264  
 <211> 174  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -19...-1

<400> 264  
 Met Phe Leu Thr Val Lys Leu Leu Leu Gly Gln Arg Cys Ser Leu Lys  
 -15 -10 -5  
 Val Ser Gly Gln Glu Ser Val Ala Thr Leu Lys Arg Leu Val Ser Arg  
 1 5 10  
 Arg Leu Lys Val Pro Glu Glu Gln Gln His Leu Leu Phe Arg Gly Gln  
 15 20 25  
 Leu Leu Glu Asp Asp Lys His Leu Ser Asp Tyr Cys Ile Gly Pro Asn  
 30 35 40 45  
 Ala Ser Ile Asn Val Ile Met Gln Pro Leu Glu Lys Met Ala Leu Lys  
 50 55 60  
 Glu Ala His Gln Pro Gln Thr Gln Pro Leu Trp His Gln Leu Gly Leu  
 65 70 75  
 Val Leu Ala Lys His Phe Glu Pro Gln Asp Ala Lys Ala Val Leu Gln  
 80 85 90

Leu Leu Arg Gln Glu His Glu Glu Arg Leu Gln Lys Ile Ser Leu Glu  
 95 100 105  
 His Leu Glu Gln Leu Ala Glu Tyr Leu Leu Ala Glu Glu Pro His Val  
 110 115 120 125  
 Glu Pro Ala Gly Glu Arg Glu Leu Glu Ala Lys Ala Arg Pro Gln Ser  
 130 135 140  
 Ser Cys Asp Met Glu Glu Lys Glu Glu Ala Ala Ala Asp Gln  
 145 150 155

<210> 265  
 <211> 106  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -17...-1

<400> 265  
 Met Ala Leu Glu Val Leu Met Leu Leu Ala Val Leu Ile Trp Thr Gly  
 -15 -10 -5  
 Ala Glu Asn Leu His Val Lys Ile Ser Cys Ser Leu Asp Trp Leu Met  
 1 5 10 15  
 Val Ser Val Ile Pro Val Ala Glu Ser Arg Asn Leu Tyr Ile Phe Ala  
 20 25 30  
 Asp Glu Leu His Leu Gly Met Gly Cys Pro Ala Asn Arg Ile His Thr  
 35 40 45  
 Tyr Val Tyr Glu Phe Ile Tyr Leu Val Arg Asp Cys Gly Ile Arg Thr  
 50 55 60  
 Arg Val Arg Thr Val Ile Val Cys Lys Lys Tyr Cys Met Phe Cys Gln  
 65 70 75  
 Thr Phe Met Pro Ser Ile Lys Ile Val Phe  
 80 85

<210> 266  
 <211> 124  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -18...-1

<400> 266  
 Met Val Leu Cys Trp Leu Leu Leu Leu Val Met Ala Leu Pro Pro Gly  
 -15 -10 -5  
 Thr Thr Gly Val Lys Asp Cys Val Phe Cys Glu Leu Thr Asp Ser Met  
 1 5 10  
 Gln Cys Pro Gly Thr Tyr Met His Cys Gly Asp Asp Glu Asp Cys Phe  
 15 20 25 30  
 Thr Gly His Gly Val Ala Pro Gly Thr Gly Pro Val Ile Asn Lys Gly  
 35 40 45  
 Cys Leu Arg Ala Thr Ser Cys Gly Leu Glu Glu Pro Val Ser Tyr Arg  
 50 55 60  
 Gly Val Thr Tyr Ser Leu Thr Thr Asn Cys Cys Thr Gly Arg Leu Cys  
 65 70 75  
 Asn Arg Ala Pro Ser Ser Gln Thr Val Gly Ala Thr Thr Ser Leu Ala  
 80 85 90

	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99																																																																																																																																																												
0	00000000	00000001	00000010	00000011	00000100	00000101	00000110	00000111	00001000	00001001	00001010	00001011	00001100	00001101	00001110	00001111	00010000	00010001	00010010	00010011	00010100	00010101	00010110	00010111	00011000	00011001	00011010	00011011	00011100	00011101	00011110	00011111	00100000	00100001	00100010	00100011	00100100	00100101	00100110	00100111	00101000	00101001	00101010	00101011	00101100	00101101	00101110	00101111	00110000	00110001	00110010	00110011	00110100	00110101	00110110	00110111	00111000	00111001	00111010	00111011	00111100	00111101	00111110	00111111	01000000	01000001	01000010	01000011	01000100	01000101	01000110	01000111	01001000	01001001	01001010	01001011	01001100	01001101	01001110	01001111	01010000	01010001	01010010	01010011	01010100	01010101	01010110	01010111	01011000	01011001	01011010	01011011	01011100	01011101	01011110	01011111	01100000	01100001	01100010	01100011	01100100	01100101	01100110	01100111	01101000	01101001	01101010	01101011	01101100	01101101	01101110	01101111	01110000	01110001	01110010	01110011	01110100	01110101	01110110	01110111	01111000	01111001	01111010	01111011	01111100	01111101	01111110	01111111	10000000	10000001	10000010	10000011	10000100	10000101	10000110	10000111	10001000	10001001	10001010	10001011	10001100	10001101	10001110	10001111	10010000	10010001	10010010	10010011	10010100	10010101	10010110	10010111	10011000	10011001	10011010	10011011	10011100	10011101	10011110	10011111	10100000	10100001	10100010	10100011	10100100	10100101	10100110	10100111	10101000	10101001	10101010	10101011	10101100	10101101	10101110	10101111	10110000	10110001	10110010	10110011	10110100	10110101	10110110	10110111	10111000	10111001	10111010	10111011	10111100	10111101	10111110	10111111	11000000	11000001	11000010	11000011	11000100	11000101	11000110	11000111	11001000	11001001	11001010	11001011	11001100	11001101	11001110	11001111	11010000	11010001	11010010	11010011	11010100	11010101	11010110	11010111	11011000	11011001	11011010	11011011	11011100	11011101	11011110	11011111	11100000	11100001	11100010	11100011	11100100	11100101	11100110	11100111	11101000	11101001	11101010	11101011	11101100	11101101	11101110	11101111	11110000	11110001	11110010	11110011	11110100	11110101	11110110	11110111	11111000	11111001	11111010	11111011	11111100	11111101	11111110	11111111

```
<220>
<221> SIGNAL
<222> -16..-1
```

```
<210> 268
<211> 76
<212> PRT
<213> Homo sapiens
```

```
<220>
<221> SIGNAL
<222> -25..-1
```

274

Met Cys Met Ser Leu Ser Met Lys Val Pro Cys Cys Leu Cys Ala Leu  
 -25 -20 -15 -10  
 Leu Ser Asn Phe Cys Pro Ser Thr Thr Val Lys Gly Asp Val Val Thr  
 -5 1 5  
 Ser Phe Phe Arg Ala Asp Tyr Asp Leu Ala Ser Arg Ser Ala Asp Gln  
 10 15 20  
 Ser Ser Gln Lys Val Lys Leu Arg Met Phe Thr Gly Arg Leu Pro Ile  
 25 30 35  
 Gly Pro Phe Ala Ser Val Gly Asn Ala Ala Glu Leu  
 40 45 50

<210> 269  
 <211> 199  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -16...-1

<400> 269  
 Met Glu Thr Phe Pro Leu Leu Leu Leu Ser Leu Gly Leu Val Leu Ala  
 -15 -10 -5  
 Glu Ala Ser Glu Ser Thr Met Lys Ile Ile Lys Glu Glu Phe Thr Asp  
 1 5 10 15  
 Glu Glu Met Gln Tyr Asp Met Ala Lys Ser Gly Gln Glu Lys Gln Thr  
 20 25 30  
 Ile Glu Ile Leu Met Asn Pro Ile Leu Leu Val Lys Asn Thr Ser Leu  
 35 40 45  
 Ser Met Ser Lys Asp Asp Met Ser Ser Thr Leu Leu Thr Phe Arg Ser  
 50 55 60  
 Leu His Tyr Asn Asp Pro Lys Gly Asn Ser Ser Gly Asn Asp Lys Glu  
 65 70 75 80  
 Cys Cys Asn Asp Met Thr Val Trp Arg Lys Val Ser Glu Ala Asn Gly  
 85 90 95  
 Ser Cys Lys Trp Ser Asn Asn Phe Ile Arg Ser Ser Thr Glu Val Met  
 100 105 110  
 Arg Arg Val His Arg Ala Pro Ser Cys Lys Phe Val Gln Asn Pro Gly  
 115 120 125  
 Ile Ser Cys Cys Glu Ser Leu Glu Leu Glu Asn Thr Val Cys Gln Phe  
 130 135 140  
 Thr Thr Gly Lys Gln Phe Pro Arg Cys Gln Tyr His Ser Val Thr Ser  
 145 150 155 160  
 Leu Glu Lys Ile Leu Thr Val Leu Thr Gly His Ser Leu Met Ser Trp  
 165 170 175  
 Leu Val Cys Gly Ser Lys Leu  
 180

<210> 270  
 <211> 88  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -36...-1

<400> 270

09876997.060801

Met Ala Ser Val Val Pro Val Lys Asp Lys Lys Leu Leu Glu Val Lys  
 -35 -30 -25  
 Leu Gly Glu Leu Pro Ser Trp Ile Leu Met Arg Asp Phe Ser Pro Ser  
 -20 -15 -10 -5  
 Gly Ile Phe Gly Ala Phe Gln Arg Gly Tyr Tyr Arg Tyr Tyr Asn Lys  
 1 5 10  
 Tyr Ile Asn Val Lys Lys Gly Ser Ile Ser Gly Ile Thr Met Val Leu  
 15 20 25  
 Ala Cys Tyr Val Leu Phe Ser Tyr Ser Phe Ser Tyr Lys His Leu Lys  
 30 35 40  
 His Glu Arg Leu Arg Lys Tyr His  
 45 50

<210> 271  
 <211> 481  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -25...-1

<400> 271  
 Met Gly Ala Leu Ala Arg Ala Leu Pro Ser Ile Leu Leu Ala Leu Leu  
 -25 -20 -15 -10  
 Leu Thr Ser Thr Pro Glu Ala Leu Gly Ala Asn Pro Gly Leu Val Ala  
 -5 1 5  
 Arg Ile Thr Asp Lys Gly Leu Gln Tyr Ala Ala Gln Glu Gly Leu Leu  
 10 15 20  
 Ala Leu Gln Ser Glu Leu Leu Arg Ile Thr Leu Pro Asp Phe Thr Gly  
 25 30 35  
 Asp Leu Arg Ile Pro His Val Gly Arg Gly Arg Tyr Glu Phe His Ser  
 40 45 50 55  
 Leu Asn Ile His Ser Cys Glu Leu Leu His Ser Ala Leu Arg Pro Val  
 60 65 70  
 Pro Gly Gln Gly Leu Ser Leu Ser Ile Ser Asp Ser Ser Ile Arg Val  
 75 80 85  
 Gln Gly Arg Trp Lys Val Arg Lys Ser Phe Phe Lys Leu Gln Gly Ser  
 90 95 100  
 Phe Asp Val Ser Val Lys Gly Ile Ser Ile Ser Val Asn Leu Leu Leu  
 105 110 115  
 Gly Ser Asp Ser Ser Gly Arg Pro Thr Val Thr Ala Ser Ser Cys Ser  
 120 125 130 135  
 Ser Asp Ile Ala Asp Val Glu Val Asp Met Ser Gly Asp Leu Gly Trp  
 140 145 150  
 Leu Leu Asn Leu Phe His Asn Gln Ile Glu Ser Lys Phe Gln Lys Val  
 155 160 165  
 Leu Glu Ser Arg Ile Cys Glu Met Ile Gln Lys Ser Val Ser Ser Asp  
 170 175 180  
 Leu Gln Pro Tyr Leu Gln Thr Leu Thr Val Thr Thr Glu Ile Asp Ser  
 185 190 195  
 Phe Ala Asp Ile Asp Tyr Ser Leu Val Glu Ala Pro Arg Ala Thr Ala  
 200 205 210 215  
 Gln Met Leu Glu Val Met Phe Lys Gly Glu Ile Phe His Arg Asn His  
 220 225 230  
 Arg Ser Pro Val Thr Leu Leu Ala Ala Val Met Ser Leu Pro Glu Glu  
 235 240 245  
 His Asn Lys Met Val Tyr Phe Ala Ile Ser Asp Tyr Val Phe Asn Thr

Ala	Ser	Leu	Val	Tyr	His	Glu	Glu	Gly	Tyr	Leu	Asn	Phe	Ser	Ile	Thr
265						270					275				
Asp	Asp	Met	Ile	Pro	Pro	Asp	Ser	Asn	Ile	Arg	Leu	Thr	Thr	Lys	Ser
280						285				290					295
Phe	Arg	Pro	Phe	Val	Pro	Arg	Leu	Ala	Arg	Leu	Tyr	Pro	Asn	Met	Asn
				300					305					310	
Leu	Glu	Leu	Gln	Gly	Ser	Val	Pro	Ser	Ala	Pro	Leu	Leu	Asn	Phe	Ser
			315						320				325		
Pro	Gly	Asn	Leu	Ser	Val	Asp	Pro	Tyr	Met	Glu	Ile	Asp	Ala	Phe	Val
	330						335					340			
Leu	Leu	Pro	Ser	Ser	Ser	Lys	Glu	Pro	Val	Phe	Arg	Leu	Ser	Val	Ala
	345					350				355					
Thr	Asn	Val	Ser	Ala	Thr	Leu	Thr	Phe	Asn	Thr	Ser	Lys	Ile	Thr	Gly
360					365					370					375
Phe	Leu	Lys	Pro	Gly	Lys	Val	Lys	Val	Glu	Leu	Lys	Glu	Ser	Lys	Val
				380					385					390	
Gly	Leu	Phe	Asn	Ala	Glu	Leu	Leu	Glu	Ala	Leu	Leu	Asn	Tyr	Tyr	Ile
			395					400					405		
Leu	Asn	Thr	Phe	Tyr	Pro	Lys	Phe	Asn	Asp	Lys	Leu	Ala	Glu	Gly	Phe
	410						415					420			
Pro	Leu	Pro	Leu	Leu	Lys	Arg	Val	Gln	Leu	Tyr	Asp	Leu	Gly	Leu	Gln
	425					430					435				
Ile	His	Lys	Asp	Phe	Leu	Phe	Leu	Gly	Ala	Asn	Val	Gln	Tyr	Met	Arg
440					445					450					455
Val															

<210> 272

<211> 143

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -43...-1

<400> 272

Met	Ala	Lys	Tyr	Gln	Gly	Glu	Val	Gln	Ser	Leu	Lys	Leu	Asp	Asp	Asp
			-40					-35					-30		
Ser	Val	Ile	Glu	Gly	Val	Ser	Asp	Gln	Val	Leu	Val	Ala	Val	Val	Val
		-25					-20					-15			
Ser	Phe	Ala	Leu	Ile	Ala	Thr	Leu	Val	Tyr	Ala	Leu	Phe	Arg	Asn	Val
	-10					-5				1				5	
His	Gln	Asn	Ile	His	Pro	Glu	Asn	Gln	Glu	Leu	Val	Arg	Val	Leu	Arg
			10					15						20	
Glu	Gln	Leu	Gln	Thr	Glu	Gln	Asp	Ala	Pro	Ala	Ala	Thr	Arg	Gln	Gln
		25						30					35		
Phe	Tyr	Thr	Asp	Met	Tyr	Cys	Pro	Ile	Cys	Leu	His	Gln	Ala	Ser	Phe
		40					45					50			
Pro	Val	Glu	Thr	Asn	Cys	Gly	His	Leu	Phe	Cys	Gly	Ala	Cys	Ile	Ile
	55					60					65				
Ala	Tyr	Trp	Arg	Tyr	Gly	Ser	Trp	Leu	Gly	Ala	Ile	Ser	Cys	Pro	Ile
70					75					80					85
Cys	Arg	Gln	Thr	Arg	His	Gly	His	Ile	Ala	Leu	Ser	Arg	Thr	Ala	
				90					95					100	

<210> 273

<211> 82



<212> PRT  
 <213> Homo sapiens

<400> 273  
 Met Ala Lys Tyr Gln Gly Glu Val Gln Ser Leu Lys Leu Asp Asp Asp  
 1 5 10 15  
 Ser Val Ile Glu Gly Val Ser Asp Gln Val Leu Val Ala Val Val Val  
 20 25 30  
 Ser Phe Ala Leu Ile Ala Thr Leu Val Tyr Ala Leu Phe Arg Asn Val  
 35 40 45  
 His Gln Asn Ile His Pro Glu Asn Gln Glu Leu Val Arg Val Leu Arg  
 50 55 60  
 Glu Gln Leu Gln Thr Glu Gln Asp Ala Pro Ala Asp Ser Thr Ala Val  
 65 70 75 80  
 Leu His

<210> 274  
 <211> 373  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -27...-1

<400> 274  
 Met Ala Thr Gln Ala His Ser Leu Ser Tyr Ala Gly Cys Asn Phe Leu  
 -25 -20 -15  
 Cys Gln Arg Leu Val Leu Ser Thr Leu Ser Gly Arg Pro Val Lys Ile  
 -10 -5 1 5  
 Arg Lys Ile Arg Ala Arg Asp Asp Asn Pro Gly Leu Arg Asp Phe Glu  
 10 15 20  
 Ala Ser Phe Ile Arg Leu Leu Asp Lys Ile Thr Asn Gly Ser Arg Ile  
 25 30 35  
 Glu Ile Asn Gln Thr Gly Thr Thr Leu Tyr Tyr Gln Pro Gly Leu Leu  
 40 45 50  
 Tyr Gly Gly Ser Val Glu His Asp Cys Ser Val Leu Arg Gly Ile Gly  
 55 60 65  
 Tyr Tyr Leu Glu Ser Leu Leu Cys Leu Ala Pro Phe Met Lys His Pro  
 70 75 80 85  
 Leu Lys Ile Val Leu Arg Gly Val Thr Asn Asp Gln Ile Asp Pro Ser  
 90 95 100  
 Val Asp Val Leu Lys Ala Thr Ala Leu Pro Leu Leu Lys Gln Phe Gly  
 105 110 115  
 Ile Asp Gly Glu Ser Phe Glu Leu Lys Ile Val Arg Arg Gly Met Pro  
 120 125 130  
 Pro Gly Gly Gly Glu Val Phe Ser Cys Pro Val Arg Lys Val  
 135 140 145  
 Leu Lys Pro Ile Gln Leu Thr Asp Pro Gly Lys Ile Lys Arg Ile Arg  
 150 155 160 165  
 Gly Met Ala Tyr Ser Val Arg Val Ser Pro Gln Met Ala Asn Arg Ile  
 170 175 180  
 Val Asp Ser Ala Arg Ser Ile Leu Asn Lys Phe Ile Pro Asp Ile Tyr  
 185 190 195  
 Ile Tyr Thr Asp His Ile Lys Gly Val Asn Ser Gly Lys Ser Pro Gly  
 200 205 210  
 Phe Gly Leu Ser Leu Val Ala Glu Thr Thr Ser Gly Thr Phe Leu Ser  
 215 220 225

0087697-0608001

Ala Glu Leu Ala Ser Asn Pro Gln Gly Gln Gly Ala Ala Val Leu Pro  
 230 235 240 245  
 Glu Asp Leu Gly Arg Asn Cys Ala Arg Leu Leu Leu Glu Glu Ile Tyr  
 250 255 260  
 Arg Gly Gly Cys Val Asp Ser Thr Asn Gln Ser Leu Ala Leu Leu Leu  
 265 270 275  
 Met Thr Leu Gly Gln Gln Asp Val Ser Lys Val Leu Leu Gly Pro Leu  
 280 285 290  
 Ser Pro Tyr Thr Ile Glu Phe Leu Arg His Leu Lys Ser Phe Phe Gln  
 295 300 305  
 Ile Met Phe Lys Ile Glu Thr Lys Pro Cys Gly Glu Glu Leu Lys Gly  
 310 315 320 325  
 Gly Asp Lys Val Leu Met Thr Cys Val Gly Ile Gly Phe Ser Asn Leu  
 330 335 340  
 Ser Arg Thr Leu Lys  
 345

<210> 275  
 <211> 94  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -25...-1

<400> 275  
 Met Ala Ser Val Val Leu Ala Leu Arg Thr Arg Thr Ala Val Thr Ser  
 -25 -20 -15 -10  
 Leu Leu Ser Pro Thr Pro Ala Thr Ala Leu Ala Val Arg Tyr Ala Ser  
 -5 1 5  
 Lys Lys Ser Gly Gly Ser Ser Lys Asn Leu Gly Gly Lys Ser Ser Gly  
 10 15 20  
 Arg Arg Gln Gly Ile Lys Lys Met Glu Gly His Tyr Val His Ala Gly  
 25 30 35  
 Asn Ile Ile Ala Thr Gln Arg His Phe Arg Trp His Pro Gly Ala His  
 40 45 50 55  
 Val Ser Cys Ser Val Ala Ala Pro Leu Phe Pro Phe Leu Gly  
 60 65

<210> 276  
 <211> 197  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -20...-1

<400> 276  
 Met Thr Val Leu Glu Ile Thr Leu Ala Val Ile Leu Thr Leu Leu Gly  
 -20 -15 -10 -5  
 Leu Ala Ile Leu Ala Ile Leu Leu Thr Arg Trp Ala Arg Arg Lys Gln  
 1 5 10  
 Ser Glu Met Tyr Ile Ser Arg Tyr Ser Ser Glu Gln Ser Ala Arg Leu  
 15 20 25  
 Leu Asp Tyr Glu Asp Gly Arg Gly Ser Arg His Ala Tyr Ser Thr Gln  
 30 35 40

Ser Glu Arg Ser Lys Arg Asp Tyr Thr Pro Ser Thr Asn Ser Leu Ala  
 45 50 55 60  
 Leu Ser Arg Ser Ser Ile Ala Leu Pro Gln Gly Ser Met Ser Ser Ile  
 65 70 75  
 Lys Cys Leu Gln Thr Thr Glu Glu Pro Pro Ser Arg Thr Ala Gly Ala  
 80 85 90  
 Met Met Gln Phe Thr Ala Pro Ile Pro Gly Ala Thr Gly Pro Ile Lys  
 95 100 105  
 Leu Ser Gln Lys Thr Ile Val Gln Thr Leu Gly Pro Ile Val Gln Tyr  
 110 115 120  
 Pro Gly Ser Asn Gly Arg Ile Asn Ile Ser Gln Leu Thr Ser Glu Asp  
 125 130 135 140  
 Leu Thr Gly Ala Lys Gly Arg Val Thr Ser Gly Pro Gln Phe Pro Asn  
 145 150 155  
 Ser His His Val Pro Glu Asn Leu His Gly Tyr Met Asn Ser Leu Ser  
 160 165 170  
 Leu Phe Ser Pro Ala  
 175

<210> 277  
 <211> 344  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -29...-1

<400> 277  
 Met Asp Phe Leu Val Leu Phe Leu Phe Tyr Leu Ala Ser Val Leu Met  
 -25 -20 -15  
 Gly Leu Val Leu Ile Cys Val Cys Ser Lys Thr His Ser Leu Lys Gly  
 -10 -5 1  
 Leu Ala Arg Gly Gly Ala Gln Ile Phe Ser Cys Ile Ile Pro Glu Cys  
 5 10 15  
 Leu Gln Arg Ala Val His Gly Leu Leu His Tyr Leu Phe His Thr Arg  
 20 25 30 35  
 Asn His Thr Phe Ile Val Leu His Leu Val Leu Gln Gly Met Val Tyr  
 40 45 50  
 Thr Glu Tyr Thr Trp Glu Val Phe Gly Tyr Cys Gln Glu Leu Glu Leu  
 55 60 65  
 Ser Leu His Tyr Leu Leu Leu Pro Tyr Leu Leu Leu Gly Val Asn Leu  
 70 75 80  
 Phe Phe Phe Thr Leu Thr Cys Gly Thr Asn Pro Gly Ile Ile Thr Lys  
 85 90 95  
 Ala Asn Glu Leu Leu Phe Leu His Val Tyr Glu Phe Asp Glu Val Met  
 100 105 110 115  
 Phe Pro Lys Asn Val Arg Cys Ser Thr Cys Asp Leu Arg Lys Pro Ala  
 120 125 130  
 Arg Ser Lys His Cys Ser Val Cys Asn Trp Cys Val His Arg Phe Asp  
 135 140 145  
 His His Cys Val Trp Val Asn Asn Cys Ile Gly Ala Trp Asn Ile Arg  
 150 155 160  
 Tyr Phe Leu Ile Tyr Val Leu Thr Leu Thr Ala Ser Ala Ala Thr Val  
 165 170 175  
 Ala Ile Val Ser Thr Thr Phe Leu Val His Leu Val Val Met Ser Asp  
 180 185 190 195  
 Leu Tyr Gln Glu Thr Tyr Ile Asp Asp Leu Gly His Leu His Val Met



Thr	Glu	Gly	Glu	Arg	Tyr	Val	Met	Thr	Phe	Leu	Asn	Val	Leu	Asn	Phe
230						235					240				
Gly	Asp	Gln	Gly	Val	Tyr	Asp	Ile	Val	Asn	Asn	Leu	Gly	Ser	Leu	Val
245					250					255					260
Ala	Arg	Leu	Ile	Phe	Gln	Pro	Ile	Glu	Glu	Ser	Phe	Tyr	Ile	Phe	Phe
				265						270					275
Ala	Lys	Val	Leu	Glu	Arg	Gly	Lys	Asp	Ala	Thr	Leu	Gln	Lys	Gln	Glu
			280					285					290		
Asp	Val	Ala	Val	Ala	Ala	Ala	Val	Leu	Glu	Ser	Leu	Leu	Lys	Leu	Ala
		295					300					305			
Leu	Leu	Ala	Gly	Leu	Thr	Ile	Thr	Val	Phe	Gly	Phe	Ala	Tyr	Ser	Gln
	310					315					320				
Leu	Ala	Leu	Asp	Ile	Tyr	Gly	Gly	Thr	Met	Leu	Ser	Ser	Gly	Ser	Gly
325					330					335					340
Pro	Val	Leu	Leu	Arg	Ser	Tyr	Cys	Leu	Tyr	Val	Leu	Leu	Leu	Ala	Ile
				345					350					355	
Asn	Gly	Val	Thr	Glu	Cys	Phe	Thr	Phe	Ala	Ala	Met	Ser	Lys	Glu	Glu
			360					365					370		
Val	Asp	Arg	Tyr	Asn	Phe	Val	Met	Leu	Ala	Leu	Ser	Ser	Ser	Phe	Leu
		375					380					385			
Val	Leu	Ser	Tyr	Leu	Leu	Thr	Arg	Trp	Cys	Gly	Ser	Val	Gly	Phe	Ile
	390					395				400					
Leu	Ala	Asn	Cys	Phe	Asn	Met	Gly	Ile	Arg	Ile	Thr	Gln	Ser	Leu	Cys
405					410					415					420
Phe	Ile	His	Arg	Tyr	Tyr	Arg	Arg	Ser	Pro	His	Arg	Pro	Leu	Ala	Gly
				425					430					435	
Leu	His	Leu	Ser	Pro	Val	Leu	Leu	Gly	Thr	Phe	Ala	Leu	Ser	Gly	Gly
			440					445					450		
Val	Thr	Ala	Val	Ser	Glu	Val	Phe	Leu	Cys	Cys	Glu	Gln	Gly	Trp	Pro
		455					460					465			
Ala	Arg	Leu	Ala	His	Ile	Ala	Val	Gly	Ala	Phe	Cys	Leu	Gly	Ala	Thr
	470					475				480					
Leu	Gly	Thr	Ala	Phe	Leu	Thr	Glu	Thr	Lys	Leu	Ile	His	Phe	Leu	Arg
485					490					495					500
Thr	Gln	Leu	Gly	Val	Pro	Arg	Arg	Thr	Asp	Lys	Met	Thr			
				505					510						

```
<210> 279
<211> 267
<212> PRT
<213> Homo sapiens
```

```
<220>
<221> SIGNAL
<222> -24...-1
```

<400> 279															
Met	Ala	Arg	Phe	Leu	Thr	Leu	Cys	Thr	Trp	Leu	Leu	Leu	Leu	Gly	Pro
			-20						-15					-10	
Gly	Leu	Leu	Ala	Thr	Val	Arg	Ala	Glu	Cys	Ser	Gln	Asp	Cys	Ala	Thr
			-5					1				5			
Cys	Ser	Tyr	Arg	Leu	Val	Arg	Pro	Ala	Asp	Ile	Asn	Phe	Leu	Ala	Cys
	10					15					20				
Val	Met	Glu	Cys	Glu	Gly	Lys	Leu	Pro	Ser	Leu	Lys	Ile	Trp	Glu	Thr
25					30					35					40
Cys	Lys	Glu	Leu	Leu	Gln	Leu	Ser	Lys	Pro	Asp	Leu	Pro	Gln	Asp	Gly
				45					50					55	
Thr	Ser	Thr	Leu	Arg	Glu	Asn	Ser	Lys	Pro	Glu	Glu	Ser	His	Leu	Leu

			60					65					70			
Ala	Lys	Arg	Tyr	Gly	Gly	Phe	Met	Lys	Arg	Tyr	Gly	Gly	Phe	Met	Lys	
		75					80					85				
Lys	Met	Asp	Glu	Leu	Tyr	Pro	Met	Glu	Pro	Glu	Glu	Glu	Ala	Asn	Gly	
	90					95					100					
Ser	Glu	Ile	Leu	Ala	Lys	Arg	Tyr	Gly	Gly	Phe	Met	Lys	Lys	Asp	Ala	
105					110					115					120	
Glu	Glu	Asp	Asp	Ser	Leu	Ala	Asn	Ser	Ser	Asp	Leu	Leu	Lys	Glu	Leu	
				125					130					135		
Leu	Glu	Thr	Gly	Asp	Asn	Arg	Glu	Arg	Ser	His	His	Gln	Asp	Gly	Ser	
			140					145					150			
Asp	Asn	Glu	Glu	Glu	Val	Ser	Lys	Arg	Tyr	Gly	Gly	Phe	Met	Arg	Gly	
		155					160					165				
Leu	Lys	Arg	Ser	Pro	Gln	Leu	Glu	Asp	Glu	Ala	Lys	Glu	Leu	Gln	Lys	
	170					175					180					
Arg	Tyr	Gly	Gly	Phe	Met	Arg	Arg	Val	Gly	Arg	Pro	Glu	Trp	Trp	Met	
185					190					195					200	
Asp	Tyr	Gln	Lys	Arg	Tyr	Gly	Gly	Phe	Leu	Lys	Arg	Phe	Ala	Glu	Ala	
				205					210					215		
Leu	Pro	Ser	Asp	Glu	Glu	Gly	Glu	Ser	Tyr	Ser	Lys	Glu	Val	Pro	Glu	
			220					225					230			
Met	Glu	Lys	Arg	Tyr	Gly	Gly	Phe	Met	Arg	Phe						
		235					240									

```
<210> 280
<211> 362
<212> PRT
<213> Homo sapiens
```

```

<220>
<221> SIGNAL
<222> -40..-1

```

<400> 280																
Met	Pro	Phe	Ala	Tyr	Phe	Phe	Thr	Glu	Ser	Glu	Gly	Phe	Ala	Gly	Ser	
-40					-35					-30					-25	
Arg	Lys	Gly	Val	Leu	Gly	Arg	Val	Tyr	Glu	Thr	Val	Val	Met	Leu	Met	
				-20					-15					-10		
Leu	Leu	Thr	Leu	Leu	Val	Leu	Gly	Met	Val	Trp	Val	Ala	Ser	Ala	Ile	
			-5					1				5				
Val	Asp	Lys	Asn	Lys	Ala	Asn	Arg	Glu	Ser	Leu	Tyr	Asp	Phe	Trp	Glu	
	10					15					20					
Tyr	Tyr	Leu	Pro	Tyr	Leu	Tyr	Ser	Cys	Ile	Ser	Phe	Leu	Gly	Val	Leu	
25					30					35					40	
Leu	Leu	Leu	Val	Cys	Thr	Pro	Leu	Gly	Leu	Ala	Arg	Met	Phe	Ser	Val	
				45					50					55		
Thr	Gly	Lys	Leu	Leu	Val	Lys	Pro	Arg	Leu	Leu	Glu	Asp	Leu	Glu	Glu	
			60					65					70			
Gln	Leu	Tyr	Cys	Ser	Ala	Phe	Glu	Glu	Ala	Ala	Leu	Thr	Arg	Arg	Ile	
		75					80					85				
Cys	Asn	Pro	Thr	Ser	Cys	Trp	Leu	Pro	Leu	Asp	Met	Glu	Leu	Leu	His	
	90					95					100					
Arg	Gln	Val	Leu	Ala	Leu	Gln	Thr	Gln	Arg	Val	Leu	Leu	Glu	Lys	Arg	
105					110					115					120	
Arg	Lys	Ala	Ser	Ala	Trp	Gln	Arg	Asn	Leu	Gly	Tyr	Pro	Leu	Ala	Met	
				125					130					135		
Leu	Cys	Leu	Leu	Val	Leu	Thr	Gly	Leu	Ser	Val	Leu	Ile	Val	Ala	Ile	
			140					145					150			

His Ile Leu Glu Leu Leu Ile Asp Glu Ala Ala Met Pro Arg Gly Met  
 155 160 165  
 Gln Gly Thr Ser Leu Gly Gln Val Ser Phe Ser Lys Leu Gly Ser Phe  
 170 175 180  
 Gly Ala Val Ile Gln Val Val Leu Ile Phe Tyr Leu Met Val Ser Ser  
 185 190 195 200  
 Val Val Gly Phe Tyr Ser Ser Pro Leu Phe Arg Ser Leu Arg Pro Arg  
 205 210 215  
 Trp His Asp Thr Ala Met Thr Gln Ile Ile Gly Asn Cys Val Cys Leu  
 220 225 230  
 Leu Val Leu Ser Ser Ala Leu Pro Val Phe Ser Arg Thr Leu Gly Leu  
 235 240 245  
 Thr Arg Phe Asp Leu Leu Gly Asp Phe Gly Arg Phe Asn Trp Leu Gly  
 250 255 260  
 Asn Phe Tyr Ile Val Phe Leu Tyr Asn Ala Ala Phe Ala Gly Leu Thr  
 265 270 275 280  
 Thr Leu Tyr Leu Val Lys Thr Phe Thr Ala Ala Val Arg Ala Glu Leu  
 285 290 295  
 Ile Arg Ala Phe Gly Leu Asp Arg Leu Pro Leu Pro Val Ser Gly Phe  
 300 305 310  
 Pro Gln Ala Ser Arg Lys Thr Gln His Gln  
 315 320

<210> 281  
 <211> 81  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -21...-1

<400> 281  
 Met Ser Arg Ser Ser Lys Val Val Leu Gly Leu Ser Val Leu Leu Thr  
 -20 -15 -10  
 Ala Ala Thr Val Ala Gly Val His Val Lys Gln Gln Trp Asp Gln Gln  
 -5 1 5 10  
 Arg Leu Arg Asp Gly Val Ile Arg Asp Ile Glu Arg Gln Ile Arg Lys  
 15 20 25  
 Lys Glu Asn Ile Arg Leu Leu Gly Glu Gln Ile Ile Leu Thr Glu Gln  
 30 35 40  
 Leu Glu Ala Glu Arg Glu Lys Met Leu Leu Ala Lys Gly Ser Gln Lys  
 45 50 55  
 Ser  
 60

<210> 282  
 <211> 541  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -28...-1

<400> 282  
 Met Gly Ser Gln Glu Val Leu Gly His Ala Ala Arg Leu Ala Ser Ser  
 -25 -20 -15

Gly	Leu	Leu	Leu	Gln	Val	Leu	Phe	Arg	Leu	Ile	Thr	Phe	Val	Leu	Asn
		-10					-5					1			
Ala	Phe	Ile	Leu	Arg	Phe	Leu	Ser	Lys	Glu	Ile	Val	Gly	Val	Val	Asn
5					10					15					20
Val	Arg	Leu	Thr	Leu	Leu	Tyr	Ser	Thr	Thr	Leu	Phe	Leu	Ala	Arg	Glu
				25					30					35	
Ala	Phe	Arg	Arg	Ala	Cys	Leu	Ser	Gly	Gly	Thr	Gln	Arg	Asp	Trp	Ser
			40					45					50		
Gln	Thr	Leu	Asn	Leu	Leu	Trp	Leu	Thr	Val	Pro	Leu	Gly	Val	Phe	Trp
		55					60					65			
Ser	Leu	Phe	Leu	Gly	Trp	Ile	Trp	Leu	Gln	Leu	Leu	Glu	Val	Pro	Asp
	70					75					80				
Pro	Asn	Val	Val	Pro	His	Tyr	Ala	Thr	Gly	Val	Val	Leu	Phe	Gly	Leu
85					90					95					100
Ser	Ala	Val	Val	Glu	Leu	Leu	Gly	Glu	Pro	Phe	Trp	Val	Leu	Ala	Gln
				105					110					115	
Ala	His	Met	Phe	Val	Lys	Leu	Lys	Val	Ile	Ala	Glu	Ser	Leu	Ser	Val
			120					125					130		
Ile	Leu	Lys	Ser	Val	Leu	Thr	Ala	Phe	Leu	Val	Leu	Trp	Leu	Pro	His
		135					140					145			
Trp	Gly	Leu	Tyr	Ile	Phe	Ser	Leu	Ala	Gln	Leu	Phe	Tyr	Thr	Thr	Val
	150					155					160				
Leu	Val	Leu	Cys	Tyr	Val	Ile	Tyr	Phe	Thr	Lys	Leu	Leu	Gly	Ser	Pro
165					170					175					180
Glu	Ser	Thr	Lys	Leu	Gln	Thr	Leu	Pro	Val	Ser	Arg	Ile	Thr	Asp	Leu
				185					190					195	
Leu	Pro	Asn	Ile	Thr	Arg	Asn	Gly	Ala	Phe	Ile	Asn	Trp	Lys	Glu	Ala
		200						205					210		
Lys	Leu	Thr	Trp	Ser	Phe	Phe	Lys	Gln	Ser	Phe	Leu	Lys	Gln	Ile	Leu
	215						220					225			
Thr	Glu	Gly	Glu	Arg	Tyr	Val	Met	Thr	Phe	Leu	Asn	Val	Leu	Asn	Phe
	230					235					240				
Gly	Asp	Gln	Gly	Val	Tyr	Asp	Ile	Val	Asn	Asn	Leu	Gly	Ser	Leu	Val
245					250					255					260
Ala	Arg	Leu	Ile	Phe	Gln	Pro	Ile	Glu	Glu	Ser	Phe	Tyr	Ile	Phe	Phe
				265					270					275	
Ala	Lys	Val	Leu	Glu	Arg	Gly	Lys	Asp	Ala	Thr	Leu	Gln	Lys	Gln	Glu
			280					285					290		
Asp	Val	Ala	Val	Ala	Ala	Ala	Val	Leu	Glu	Ser	Leu	Leu	Lys	Leu	Ala
		295					300					305			
Leu	Leu	Ala	Gly	Leu	Thr	Ile	Thr	Val	Phe	Gly	Phe	Ala	Tyr	Ser	Gln
	310					315					320				
Leu	Ala	Leu	Asp	Ile	Asn	Gly	Gly	Thr	Met	Leu	Ser	Ser	Gly	Ser	Gly
325					330					335					340
Pro	Val	Leu	Leu	Arg	Ser	Tyr	Cys	Leu	Tyr	Val	Leu	Leu	Leu	Ala	Ile
				345					350					355	
Asn	Gly	Val	Thr	Glu	Cys	Phe	Thr	Phe	Ala	Ala	Met	Ser	Lys	Glu	Glu
			360					365					370		
Val	Asp	Arg	Tyr	Asn	Phe	Val	Met	Leu	Ala	Leu	Ser	Ser	Ser	Phe	Leu
		375					380					385			
Val	Leu	Ser	Tyr	Leu	Leu	Thr	Arg	Trp	Cys	Gly	Ser	Val	Gly	Phe	Ile
	390					395					400				
Leu	Ala	Asn	Cys	Phe	Asn	Met	Gly	Ile	Arg	Ile	Thr	Gln	Ser	Leu	Cys
405					410					415					420
Phe	Ile	His	Arg	Tyr	Tyr	Arg	Arg	Ser	Pro	His	Arg	Pro	Leu	Ala	Gly
				425					430					435	
Leu	His	Leu	Ser	Pro	Val	Leu	Leu	Gly	Thr	Phe	Ala	Leu	Ser	Gly	Gly
			440					445					450		





285		290		295
Cys Asp Ile Ala Gly Tyr Pro Leu Asp Val Val Thr Trp Thr				
300		305		310
Arg Glu Glu Leu Gly Gly Ser Pro Ala Gln Val Ser Gly Ala Ser Phe				
	320		325	330
Ser Ser Leu Arg Gln Ser Val Ala Gly Thr Tyr Ser Ile Ser Ser Ser				
	335		340	345
Leu Thr Ala Glu Pro Gly Ser Ala Gly Ala Thr Tyr Thr Cys Gln Val				
	350		355	360
Thr His Ile Ser Leu Glu Glu Pro Leu Gly Ala Ser Thr Gln Val Val				
	365		370	375
Pro Pro Glu Arg Arg Thr Ala Leu Gly Val Ile Phe Ala Ser Ser Leu				
380		385		390
Phe Leu Leu Ala Leu Met Phe Leu Gly Leu Gln Arg Arg Gln Ala Pro				
	400		405	410
Thr Gly Leu Gly Leu Leu Gln Ala Glu Arg Trp Glu Thr Thr Ser Cys				
	415		420	425
Ala Asp Thr Gln Ser Ser His Leu His Glu Asp Arg Thr Ala Arg Val				
	430		435	440
Ser Gln Pro Ser				
445				

<210> 284  
 <211> 406  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -31...-1

<400> 284
Met Val Arg Ile Gln Arg Arg Lys Leu Leu Ala Ser Cys Leu Cys Val
-30 -25 -20
Thr Ala Thr Val Phe Leu Leu Val Thr Leu Gln Ala Leu Asp Thr Val
-15 -10 -5 1
Glu Asn Leu Met Lys Val Thr Gly Pro Pro Gln Gly Val Thr Asp Ser
5 10 15
Met Gln Cys Phe Asn Asp Gln Trp Pro Leu Ser Asn Thr Arg Ser Ser
20 25 30
Glu His Ile Lys Glu Val Met Val Glu Leu Gly Lys Phe Glu Arg Lys
35 40 45
Glu Phe Lys Ser Ser Ser Leu Gln Asp Gly His Thr Lys Met Glu Glu
50 55 60 65
Ala Pro Thr His Leu Asn Ser Phe Leu Lys Lys Glu Gly Leu Thr Phe
70 75 80
Asn Arg Lys Arg Lys Trp Glu Leu Asp Ser Tyr Pro Ile Met Leu Trp
85 90 95
Trp Ser Pro Leu Thr Gly Glu Thr Gly Arg Leu Gly Gln Cys Gly Ala
100 105 110
Asp Ala Cys Phe Phe Thr Ile Asn Arg Thr Tyr Leu His His His Met
115 120 125
Thr Lys Ala Phe Leu Phe Tyr Gly Thr Asp Phe Asn Ile Asp Ser Leu
130 135 140 145
Pro Leu Pro Arg Lys Ala His His Asp Trp Ala Val Phe His Glu Glu
150 155 160
Ser Pro Lys Asn Asn Tyr Lys Leu Phe His Lys Pro Val Ile Thr Leu
165 170 175

Phe Asn Tyr Thr Ala Thr Phe Ser Arg His Ser His Leu Pro Leu Thr  
 180 185 190  
 Thr Gln Tyr Leu Glu Ser Ile Glu Val Leu Lys Ser Leu Arg Tyr Leu  
 195 200 205  
 Val Pro Leu Gln Ser Lys Asn Lys Leu Arg Lys Arg Leu Ala Pro Leu  
 210 215 220 225  
 Val Tyr Val Gln Ser Tyr Cys Asp Pro Pro Ser Asp Arg Asp Ser Tyr  
 230 235 240  
 Val Arg Glu Leu Met Thr Tyr Ile Glu Val Asp Ser Tyr Gly Glu Cys  
 245 250 255  
 Leu Arg Asn Lys Asp Leu Pro Gln Gln Leu Lys Asn Pro Ala Ser Met  
 260 265 270  
 Asp Ala Asp Gly Phe Tyr Arg Ile Ile Ala Gln Tyr Lys Phe Ile Leu  
 275 280 285  
 Ala Phe Glu Asn Ala Val Cys Asp Asp Tyr Ile Thr Glu Lys Phe Trp  
 290 295 300 305  
 Arg Pro Leu Lys Leu Gly Val Val Pro Val Tyr Tyr Gly Ser Pro Ser  
 310 315 320  
 Ile Thr Asp Trp Leu Pro Ser Asn Lys Ser Ala Ile Leu Val Ser Glu  
 325 330 335  
 Phe Ser His Pro Arg Glu Leu Ala Ser Tyr Ile Arg Arg Leu Asp Ser  
 340 345 350  
 Asp Asp Arg Leu Tyr Glu Ala Tyr Val Glu Trp Lys Leu Lys Gly Arg  
 355 360 365  
 Ser Leu Thr Ser Asp Phe  
 370 375

<210> 285  
 <211> 305  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -26...-1

<400> 285  
 Met Gly Ile Gln Thr Ser Pro Val Leu Leu Ala Ser Leu Gly Val Gly  
 -25 -20 -15  
 Leu Val Thr Leu Leu Gly Leu Ala Val Gly Ser Tyr Leu Val Arg Arg  
 -10 -5 1 5  
 Ser Arg Arg Pro Gln Val Thr Leu Leu Asp Pro Asn Glu Lys Tyr Leu  
 10 15 20  
 Leu Arg Leu Leu Asp Lys Thr Thr Val Ser His Asn Thr Lys Arg Phe  
 25 30 35  
 Arg Phe Ala Leu Pro Thr Ala His His Thr Leu Gly Leu Pro Val Gly  
 40 45 50  
 Lys His Ile Tyr Leu Ser Thr Arg Ile Asp Gly Ser Leu Val Ile Arg  
 55 60 65 70  
 Pro Tyr Thr Pro Val Thr Ser Asp Glu Asp Gln Gly Tyr Val Asp Leu  
 75 80 85  
 Val Ile Lys Val Tyr Leu Lys Gly Val His Pro Lys Phe Pro Glu Gly  
 90 95 100  
 Gly Lys Met Ser Gln Tyr Leu Asp Ser Leu Lys Val Gly Asp Val Val  
 105 110 115  
 Glu Phe Arg Gly Pro Ser Gly Leu Leu Thr Tyr Thr Gly Lys Gly His  
 120 125 130  
 Phe Asn Ile Gln Pro Asn Lys Lys Ser Pro Pro Glu Pro Arg Val Ala

09876997.060804

135 140 145 150  
 Lys Lys Leu Gly Met Ile Ala Gly Gly Thr Gly Ile Thr Pro Met Leu  
 155 160 165  
 Gln Leu Ile Arg Ala Ile Leu Lys Val Pro Glu Asp Pro Thr Gln Cys  
 170 175 180  
 Phe Leu Leu Phe Ala Asn Gln Thr Glu Lys Asp Ile Ile Leu Arg Glu  
 185 190 195  
 Asp Leu Glu Glu Leu Gln Ala Arg Tyr Pro Asn Arg Phe Lys Leu Trp  
 200 205 210  
 Phe Thr Leu Asp His Pro Pro Lys Asp Trp Ala Tyr Ser Lys Gly Phe  
 215 220 225 230  
 Val Thr Ala Asp Met Ile Arg Glu His Leu Pro Ala Pro Gly Asp Asp  
 235 240 245  
 Val Leu Val Leu Leu Cys Gly Pro Pro Met Val Gln Leu Ala Cys  
 250 255 260  
 His Pro Asn Leu Asp Lys Leu Gly Tyr Ser Gln Lys Met Arg Phe Thr  
 265 270 275  
 Tyr

<210> 286  
 <211> 442  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -21..-1

<220>  
 <221> UNSURE  
 <222> 132  
 <223> Xaa = Pro,Arg

<400> 286  
 Met Gly Thr Gln Glu Gly Trp Cys Leu Leu Leu Cys Leu Ala Leu Ser  
 -20 -15 -10  
 Gly Ala Ala Glu Thr Lys Pro His Pro Ala Glu Gly Gln Leu Arg Ala  
 -5 1 5 10  
 Val Asp Val Val Leu Asp Cys Phe Leu Ala Lys Asp Gly Ala His Arg  
 15 20 25  
 Gly Ala Leu Ala Ser Ser Glu Asp Arg Ala Arg Ala Ser Leu Val Leu  
 30 35 40  
 Lys Gln Val Pro Val Leu Asp Asp Gly Ser Leu Glu Asp Phe Thr Asp  
 45 50 55  
 Phe Gln Gly Gly Thr Leu Ala Gln Asp Asp Pro Pro Ile Ile Phe Glu  
 60 65 70 75  
 Ala Ser Val Asp Leu Val Gln Ile Pro Gln Ala Glu Ala Leu Leu His  
 80 85 90  
 Ala Asp Cys Ser Gly Lys Glu Val Thr Cys Glu Ile Ser Arg Tyr Phe  
 95 100 105  
 Leu Gln Met Thr Glu Thr Thr Val Lys Thr Ala Ala Trp Phe Met Ala  
 110 115 120  
 Asn Met Gln Val Ser Gly Gly Gly Xaa Ser Ile Ser Leu Val Met Lys  
 125 130 135  
 Thr Pro Arg Val Thr Lys Asn Glu Ala Leu Trp His Pro Thr Leu Asn  
 140 145 150 155  
 Leu Pro Leu Ser Pro Gln Gly Thr Val Arg Thr Ala Val Glu Phe Gln  
 160 165 170

Val	Met	Thr	Gln	Thr	Gln	Ser	Leu	Ser	Phe	Leu	Leu	Gly	Ser	Ser	Ala
			175					180					185		
Ser	Leu	Asp	Cys	Gly	Phe	Ser	Met	Ala	Pro	Gly	Leu	Asp	Leu	Ile	Ser
		190					195					200			
Val	Glu	Trp	Arg	Leu	Gln	His	Lys	Gly	Arg	Gly	Gln	Leu	Val	Tyr	Ser
	205					210					215				
Trp	Thr	Ala	Gly	Gln	Gly	Gln	Ala	Val	Arg	Lys	Gly	Ala	Thr	Leu	Glu
220					225					230					235
Pro	Ala	Gln	Leu	Gly	Met	Ala	Arg	Asp	Ala	Ser	Leu	Thr	Leu	Pro	Gly
				240					245					250	
Leu	Thr	Ile	Gln	Asp	Glu	Gly	Thr	Tyr	Ile	Cys	Gln	Ile	Thr	Thr	Ser
			255					260					265		
Leu	Tyr	Arg	Ala	Gln	Gln	Ile	Ile	Gln	Leu	Asn	Ile	Gln	Ala	Ser	Pro
	270						275					280			
Lys	Val	Arg	Leu	Ser	Leu	Ala	Asn	Glu	Ala	Leu	Leu	Pro	Thr	Leu	Ile
	285					290					295				
Cys	Asp	Ile	Ala	Gly	Tyr	Tyr	Pro	Leu	Asp	Val	Val	Val	Thr	Trp	Thr
300					305					310					315
Arg	Glu	Glu	Leu	Gly	Gly	Ser	Pro	Ala	Gln	Val	Ser	Gly	Ala	Ser	Phe
				320					325					330	
Ser	Ser	Leu	Arg	Gln	Ser	Val	Ala	Gly	Thr	Tyr	Ser	Ile	Ser	Ser	Ser
			335					340					345		
Leu	Thr	Ala	Glu	Pro	Gly	Ser	Ala	Gly	Ala	Thr	Tyr	Thr	Cys	Gln	Val
		350					355					360			
Thr	His	Ile	Ser	Leu	Glu	Glu	Pro	Leu	Gly	Ala	Ser	Thr	Gln	Val	Val
	365					370					375				
Pro	Pro	Glu	Arg	Arg	Thr	Ala	Leu	Gly	Val	Ile	Phe	Ala	Ser	Ser	Leu
380					385					390					395
Phe	Leu	Leu	Ala	Leu	Met	Phe	Leu	Gly	Leu	Gln	Arg	Arg	Gln	Ala	Pro
				400					405					410	
Thr	Gly	Leu	Gly	Leu	Leu	Gln	Ala	Glu	Arg						
			415					420							

```
<210> 287
<211> 286
<212> PRT
<213> Homo sapiens
```

```
<220>  
<221> SIGNAL  
<222> -48..-1
```

```
<400> 287
Met Asn Pro Ala Ser Asp Gly Gly Thr Ser Glu Ser Ile Phe Asp Leu
      -45                    -40                -35
Asp Tyr Ala Ser Trp Gly Ile Arg Ser Thr Leu Met Val Ala Gly Phe
      -30                    -25                -20
Val Phe Tyr Leu Gly Val Phe Val Val Cys His Gln Leu Ser Ser Ser
      -15                    -10                -5
Leu Asn Ala Thr Tyr Arg Ser Leu Val Ala Arg Glu Lys Val Phe Trp
   1          5                      10        15
Asp Leu Ala Ala Thr Arg Ala Val Phe Gly Val Gln Ser Thr Ala Ala
      20                    25
Gly Leu Trp Ala Leu Leu Gly Asp Pro Val Leu His Ala Asp Lys Ala
      35                    40                45
Arg Gly Gln Gln Asn Trp Cys Trp Phe His Ile Thr Thr Ala Thr Gly
      50                    55                60
Phe Phe Cys Phe Glu Asn Val Ala Val His Leu Ser Asn Leu Ile Phe
```

65		70		75		80
Arg	Thr	Phe	Asp	Leu	Phe	Leu
			85		90	
Gly	Phe	Leu	Gly	Cys	Leu	Val
			100		105	
Met	Thr	Thr	Leu	Leu	Leu	Glu
			115		120	
Trp	Met	Leu	Leu	Lys	Ala	Gly
			130		135	
Asn	Gln	Trp	Leu	Met	Ile	His
			145		150	
Tyr	His	Met	Trp	Trp	Val	Cys
			165		170	
Ser	Leu	Tyr	Leu	Pro	His	Leu
			180		185	
Leu	Thr	Leu	Ile	Ile	Asn	Pro
			195		200	
Leu	Leu	Asn	Pro	Val	Asp	Trp
			210		215	
Arg	Pro	Glu	Gly	Asn	Gly	Gln
			225		230	

<210> 288  
 <211> 398  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -21...-1

<400> 288
Met Val Asn Asp Pro Pro Val Pro Ala Leu Leu Trp Ala Gln Glu Val
-20 -15 -10
Gly Gln Val Leu Ala Gly Arg Ala Arg Arg Leu Leu Leu Gln Phe Gly
-5 1 5 10
Val Leu Phe Cys Thr Ile Leu Leu Leu Trp Val Ser Val Phe Leu
15 20 25
Tyr Gly Ser Phe Tyr Tyr Ser Tyr Met Pro Thr Val Ser His Leu Ser
30 35 40
Pro Val His Phe Tyr Tyr Arg Thr Asp Cys Asp Ser Ser Thr Thr Ser
45 50 55
Leu Cys Ser Phe Pro Val Ala Asn Val Ser Leu Thr Lys Gly Gly Arg
60 65 70 75
Asp Arg Val Leu Met Tyr Gly Gln Pro Tyr Arg Val Thr Leu Glu Leu
80 85 90
Glu Leu Pro Glu Ser Pro Val Asn Gln Asp Leu Gly Met Phe Leu Val
95 100 105
Thr Ile Ser Cys Tyr Thr Arg Gly Gly Arg Ile Ile Ser Thr Ser Ser
110 115 120
Arg Ser Val Met Leu His Tyr Arg Ser Asp Leu Leu Gln Met Leu Asp
125 130 135
Thr Leu Val Phe Ser Ser Leu Leu Leu Phe Gly Phe Ala Glu Gln Lys
140 145 150 155
Gln Leu Leu Glu Val Glu Leu Tyr Ala Asp Tyr Arg Glu Asn Ser Tyr
160 165 170
Val Pro Thr Thr Gly Ala Ile Ile Glu Ile His Ser Lys Arg Ile Gln
175 180 185

Leu	Tyr	Gly	Ala	Tyr	Leu	Arg	Ile	His	Ala	His	Phe	Thr	Gly	Leu	Arg
		190					195					200			
Tyr	Leu	Leu	Tyr	Asn	Phe	Pro	Met	Thr	Cys	Ala	Phe	Ile	Gly	Val	Ala
		205				210					215				
Ser	Asn	Phe	Thr	Phe	Leu	Ser	Val	Ile	Val	Leu	Phe	Ser	Tyr	Met	Gln
220				225						230					235
Trp	Val	Trp	Gly	Gly	Ile	Trp	Pro	Arg	His	Arg	Phe	Ser	Leu	Gln	Val
				240					245					250	
Asn	Ile	Arg	Lys	Arg	Asp	Asn	Ser	Arg	Lys	Glu	Val	Gln	Arg	Arg	Ile
			255					260					265		
Ser	Ala	His	Gln	Pro	Gly	Pro	Glu	Gly	Gln	Glu	Glu	Ser	Thr	Pro	Gln
			270				275					280			
Ser	Asp	Val	Thr	Glu	Asp	Gly	Glu	Ser	Pro	Glu	Asp	Pro	Ser	Gly	Thr
		285				290					295				
Glu	Gly	Gln	Leu	Ser	Glu	Glu	Glu	Lys	Pro	Asp	Gln	Gln	Pro	Leu	Ser
300					305					310					315
Gly	Glu	Glu	Glu	Leu	Glu	Pro	Glu	Ala	Ser	Asp	Gly	Ser	Gly	Ser	Trp
				320					325					330	
Glu	Asp	Ala	Ala	Leu	Leu	Thr	Glu	Ala	Asn	Leu	Pro	Ala	Pro	Ala	Pro
			335					340					345		
Ala	Ser	Ala	Ser	Ala	Pro	Val	Leu	Glu	Thr	Leu	Gly	Ser	Ser	Glu	Pro
		350					355					360			
Ala	Gly	Gly	Ala	Leu	Arg	Gln	Arg	Pro	Thr	Cys	Ser	Ser	Ser		
		365				370					375				

```
<210> 289
<211> 130
<212> PRT
<213> Homo sapiens
```

```
<220>
<221> SIGNAL
<222> -20..-1
```

<400>	289
Met Arg Gln Lys Ala Val Ser Leu Phe Phe Cys Tyr Leu Leu Leu Phe -20                        -15                        -10                        -5	
Thr Cys Ser Gly Val Glu Ala Gly Lys Lys Lys Cys Ser Glu Ser Ser 1                        5                        10	
Asp Ser Gly Ser Gly Phe Trp Lys Ala Leu Thr Phe Met Ala Val Gly 15                        20                        25	
Gly Gly Leu Ala Val Ala Gly Leu Pro Ala Leu Gly Phe Thr Gly Ala 30                        35                        40	
Gly Ile Ala Ala Asn Ser Val Ala Ala Ser Leu Met Ser Trp Ser Ala 45                        50                        55                        60	
Ile Leu Asn Gly Gly Gly Val Pro Ala Gly Gly Leu Val Ala Thr Leu 65                        70                        75	
Gln Ser Leu Gly Ala Gly Gly Ser Ser Val Val Ile Gly Asn Ile Gly 80                        85                        90	
Ala Leu Met Gly Tyr Ala Thr His Lys Tyr Leu Asp Ser Glu Glu Asp 95                        100                        105	
Glu Glu 110	

```
<210> 290
<211> 86
<212> PRT
<213> Homo sapiens
```

<220>

<221> SIGNAL

<222> -20...-1

<400> 290

Met Ala Val Gly Gly Gly Leu Ala Val Ala Gly Leu Pro Ala Leu Gly  
 -20 -15 -10 -5  
 Phe Thr Gly Ala Gly Ile Ala Ala Asn Ser Val Ala Ala Ser Leu Met  
 1 5 10  
 Ser Trp Ser Ala Ile Leu Asn Gly Gly Val Pro Ala Gly Gly Leu  
 15 20 25  
 Val Ala Thr Leu Gln Ser Leu Gly Ala Gly Gly Ser Ser Val Val Ile  
 30 35 40  
 Gly Asn Ile Gly Ala Leu Met Gly Tyr Ala Thr His Lys Tyr Leu Asp  
 45 50 55 60  
 Ser Glu Glu Asp Glu Glu  
 65

<210> 291

<211> 207

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -23...-1

<400> 291

Met Ala Pro Phe Glu Pro Leu Ala Ser Gly Ile Leu Leu Leu Leu Trp  
 -20 -15 -10  
 Leu Ile Ala Pro Ser Arg Ala Cys Thr Cys Val Pro Pro His Pro Gln  
 -5 1 5  
 Thr Ala Phe Cys Asn Ser Asp Leu Val Ile Arg Ala Lys Phe Val Gly  
 10 15 20 25  
 Thr Pro Glu Val Asn Gln Thr Thr Leu Tyr Gln Arg Tyr Glu Ile Lys  
 30 35 40  
 Met Thr Lys Met Tyr Lys Gly Phe Gln Ala Leu Gly Asp Ala Ala Asp  
 45 50 55  
 Ile Arg Phe Val Tyr Thr Pro Ala Met Glu Ser Val Cys Gly Tyr Phe  
 60 65 70  
 His Arg Ser His Asn Arg Ser Glu Glu Phe Leu Ile Ala Gly Lys Leu  
 75 80 85  
 Gln Asp Gly Leu Leu His Ile Thr Thr Cys Ser Phe Val Ala Pro Trp  
 90 95 100 105  
 Asn Ser Leu Ser Leu Ala Gln Arg Arg Gly Phe Thr Lys Thr Tyr Thr  
 110 115 120  
 Val Gly Cys Glu Glu Cys Thr Val Phe Pro Cys Leu Ser Phe Pro Cys  
 125 130 135  
 Lys Leu Gln Ser Gly Thr His Cys Leu Trp Thr Asp Gln Leu Leu Gln  
 140 145 150  
 Gly Ser Glu Lys Gly Phe Gln Ser Arg His Leu Ala Cys Leu Pro Arg  
 155 160 165  
 Glu Pro Gly Leu Cys Thr Trp Gln Ser Leu Arg Ser Gln Ile Ala  
 170 175 180

<210> 292

<211> 111



[illegible][illegible][illegible][illegible][illegible][illegible][illegible][illegible]

	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523</
--	---	---	---	---	---	---	---	---	---	---	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-------

Met	Gln	Arg	Val	Ser	Gly	Leu	Leu	Ser	Trp	Thr	Leu	Ser	Arg	Val	Leu
		-25					-20					-15			
Trp	Leu	Ser	Gly	Leu	Ser	Glu	Pro	Gly	Ala	Ala	Arg	Gln	Pro	Arg	Ile
	-10					-5					1				5
Met	Glu	Glu	Lys	Ala	Leu	Glu	Val	Tyr	Asp	Leu	Ile	Arg	Thr	Ile	Arg
			10					15						20	
Asp	Pro	Glu	Lys	Pro	Asn	Thr	Leu	Glu	Glu	Leu	Glu	Val	Val	Ser	Glu
			25					30					35		
Ser	Cys	Val	Glu	Val	Gln	Glu	Ile	Asn	Glu	Glu	Glu	Tyr	Leu	Val	Ile
		40					45					50			
Ile	Arg	Phe	Thr	Pro	Thr	Val	Pro	His	Cys	Ser	Leu	Ala	Thr	Leu	Ile
	55					60					65				
Gly	Leu	Cys	Leu	Arg	Val	Lys	Leu	Gln	Arg	Cys	Leu	Pro	Phe	Lys	His
70					75				80					85	
Lys	Leu	Glu	Ile	Tyr	Ile	Ser	Glu	Gly	Thr	His	Ser	Thr	Glu	Glu	Asp
			90					95						100	
Ile	Asn	Lys	Gln	Ile	Asn	Asp	Lys	Glu	Arg	Val	Ala	Ala	Ala	Met	Glu
			105					110				115			
Asn	Pro	Asn	Leu	Arg	Glu	Ile	Val	Glu	Gln	Cys	Val	Leu	Glu	Pro	Asp
		120					125					130			

```
<220>  
<221> SIGNAL  
<222> -16..-1
```

[illegible]

```
<220>
<221> SIGNAL
<222> -18..-1
```

```
<210> 297
<211> 132
<212> PRT
<213> Homo sapiens
```

```

<400> 297
Met Glu Gly Gly Ala Tyr Gly Ala Gly Lys Ala Gly Gly Ala Phe Asp
   -40                               -35                               -30
Pro Tyr Thr Leu Val Arg Gln Pro His Thr Ile Leu Arg Val Val Ser

```



<210> 299  
 <211> 137  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -22...-1

<400> 299  
 Met Leu Ser Gly Arg Leu Val Leu Gly Leu Val Ser Met Ala Gly Arg  
           -20                  -15                  -10  
 Val Cys Leu Cys Gln Gly Ser Ala Gly Ser Gly Ala Ile Gly Pro Val  
       -5                  1                  5                  10  
 Glu Ala Ala Ile Arg Thr Lys Leu Glu Glu Ala Leu Ser Pro Glu Val  
                   15                  20                  25  
 Leu Glu Leu Arg Asn Glu Ser Gly Gly His Ala Val Pro Pro Gly Ser  
                   30                  35                  40  
 Glu Thr His Phe Arg Val Ala Val Val Ser Ser Arg Phe Glu Gly Leu  
           45                  50                  55  
 Ser Pro Leu Gln Arg His Arg Leu Val His Ala Ala Leu Ala Glu Glu  
       60                  65                  70  
 Leu Gly Gly Pro Val His Ala Leu Ala Ile Gln Ala Arg Thr Pro Ala  
 75                  80                  85                  90  
 Gln Trp Arg Glu Asn Ser Gln Leu Asp Thr Ser Pro Pro Cys Leu Gly  
                   95                  100                  105  
 Gly Asn Lys Lys Thr Leu Gly Thr Pro  
           110                  115

<210> 300  
 <211> 541  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -28...-1

<400> 300  
 Met Gly Ser Gln Glu Val Leu Gly His Ala Ala Arg Leu Ala Ser Ser  
           -25                  -20                  -15  
 Gly Leu Leu Leu Gln Val Leu Phe Arg Leu Ile Thr Phe Val Leu Asn  
       -10                  -5                  1  
 Ala Phe Ile Leu Arg Phe Leu Ser Lys Glu Ile Val Gly Val Val Asn  
 5                  10                  15                  20  
 Val Arg Leu Thr Leu Leu Tyr Ser Thr Thr Leu Phe Leu Ala Arg Glu  
                   25                  30                  35  
 Ala Phe Arg Arg Ala Cys Leu Ser Gly Gly Thr Gln Arg Asp Trp Ser  
                   40                  45                  50  
 Gln Thr Leu Asn Leu Leu Trp Leu Thr Val Pro Leu Gly Val Phe Trp  
       55                  60                  65  
 Ser Leu Phe Leu Gly Trp Ile Trp Leu Gln Leu Leu Glu Val Pro Asp  
       70                  75                  80  
 Pro Asn Val Val Pro His Tyr Ala Thr Gly Val Val Leu Phe Gly Leu  
 85                  90                  95                  100  
 Ser Ala Val Val Glu Leu Leu Gly Glu Pro Phe Trp Val Leu Ala Gln  
                   105                  110                  115

Ala	His	Met	Phe	Val	Lys	Leu	Lys	Val	Ile	Ala	Glu	Ser	Leu	Ser	Val
			120					125					130		
Ile	Leu	Lys	Ser	Val	Leu	Thr	Ala	Phe	Leu	Val	Leu	Trp	Leu	Pro	His
		135					140					145			
Trp	Gly	Leu	Tyr	Ile	Phe	Ser	Leu	Ala	Gln	Leu	Phe	Tyr	Thr	Thr	Val
	150					155					160				
Leu	Val	Leu	Cys	Tyr	Val	Ile	Tyr	Phe	Thr	Lys	Leu	Leu	Gly	Ser	Pro
165				170						175					180
Glu	Ser	Thr	Lys	Leu	Gln	Thr	Leu	Pro	Val	Ser	Arg	Ile	Thr	Asp	Leu
			185					190						195	
Leu	Pro	Asn	Ile	Thr	Arg	Asn	Gly	Ala	Phe	Ile	Asn	Trp	Lys	Glu	Ala
			200					205					210		
Lys	Leu	Thr	Trp	Ser	Phe	Phe	Lys	Gln	Ser	Phe	Leu	Lys	Gln	Ile	Leu
		215					220					225			
Thr	Glu	Gly	Glu	Arg	Tyr	Val	Met	Thr	Phe	Leu	Asn	Val	Leu	Asn	Phe
	230					235					240				
Gly	Asp	Gln	Gly	Val	Tyr	Asp	Ile	Val	Asn	Asn	Leu	Gly	Ser	Leu	Val
245				250						255					260
Ala	Arg	Leu	Ile	Phe	Gln	Pro	Ile	Glu	Glu	Ser	Phe	Tyr	Ile	Phe	Phe
			265					270						275	
Ala	Lys	Val	Leu	Glu	Arg	Gly	Lys	Asp	Ala	Thr	Leu	Gln	Lys	Gln	Glu
		280						285					290		
Asp	Val	Ala	Val	Ala	Ala	Ala	Val	Leu	Glu	Ser	Leu	Leu	Lys	Leu	Ala
		295					300					305			
Leu	Leu	Ala	Gly	Leu	Thr	Ile	Thr	Val	Phe	Gly	Phe	Ala	Tyr	Ser	Gln
	310					315					320				
Leu	Ala	Leu	Asp	Ile	Tyr	Gly	Gly	Thr	Met	Leu	Ser	Ser	Gly	Ser	Gly
325				330						335					340
Pro	Val	Leu	Leu	Arg	Ser	Tyr	Cys	Leu	Tyr	Val	Leu	Leu	Leu	Ala	Ile
			345					350						355	
Asn	Gly	Val	Thr	Glu	Cys	Leu	Thr	Phe	Ala	Ala	Met	Ser	Lys	Glu	Glu
		360						365					370		
Val	Asp	Arg	Tyr	Asn	Phe	Val	Met	Leu	Ala	Leu	Ser	Ser	Ser	Phe	Leu
	375						380					385			
Val	Leu	Ser	Tyr	Leu	Leu	Thr	Arg	Trp	Cys	Gly	Ser	Val	Gly	Phe	Ile
	390					395					400				
Leu	Ala	Asn	Cys	Phe	Asn	Met	Gly	Ile	Arg	Ile	Thr	Gln	Ser	Leu	Cys
405				410						415					420
Phe	Ile	His	Arg	Tyr	Tyr	Arg	Arg	Ser	Pro	His	Arg	Pro	Leu	Ala	Gly
			425						430					435	
Leu	His	Leu	Ser	Pro	Val	Leu	Leu	Gly	Thr	Phe	Ala	Leu	Ser	Gly	Gly
		440						445					450		
Val	Thr	Ala	Val	Ser	Glu	Val	Phe	Leu	Cys	Cys	Asp	Gln	Gly	Trp	Pro
	455						460					465			
Ala															

```
<210> 301
<211> 287
<212> PRT
<213> Homo sapiens
```

299

<222> -17...-1

<400> 301

Met	Glu	Leu	Glu	Arg	Ile	Val	Ser	Ala	Ala	Leu	Leu	Ala	Phe	Val	Gln
	-15						-10					-5			
Thr	His	Leu	Pro	Glu	Ala	Asp	Leu	Ser	Gly	Leu	Asp	Glu	Val	Ile	Phe
1					5				10					15	
Ser	Tyr	Val	Leu	Gly	Val	Leu	Glu	Asp	Leu	Gly	Pro	Ser	Gly	Pro	Ser
			20						25					30	
Glu	Glu	Asn	Phe	Asp	Met	Glu	Ala	Phe	Thr	Glu	Met	Met	Glu	Ala	Tyr
		35						40					45		
Val	Pro	Gly	Phe	Ala	His	Ile	Pro	Arg	Gly	Thr	Ile	Gly	Asp	Met	Met
	50						55					60			
Gln	Lys	Leu	Ser	Gly	Gln	Leu	Ser	Asp	Ala	Arg	Asn	Lys	Glu	Asn	Leu
65					70						75				
Gln	Pro	Gln	Ser	Ser	Gly	Val	Gln	Gly	Gln	Val	Pro	Ile	Ser	Pro	Glu
80					85					90					95
Pro	Leu	Gln	Arg	Pro	Glu	Met	Leu	Lys	Glu	Glu	Thr	Arg	Ser	Ser	Ala
				100					105					110	
Ala	Ala	Ala	Ala	Asp	Thr	Gln	Asp	Glu	Ala	Thr	Gly	Ala	Glu	Glu	Glu
			115					120					125		
Leu	Leu	Pro	Gly	Val	Asp	Val	Leu	Leu	Glu	Val	Phe	Pro	Thr	Cys	Ser
		130					135					140			
Val	Glu	Gln	Ala	Gln	Trp	Val	Leu	Ala	Lys	Ala	Arg	Gly	Asp	Leu	Glu
	145					150					155				
Glu	Ala	Val	Gln	Met	Leu	Val	Glu	Gly	Lys	Glu	Glu	Gly	Pro	Ala	Ala
160					165					170					175
Trp	Glu	Gly	Pro	Asn	Gln	Asp	Leu	Pro	Arg	Arg	Leu	Arg	Gly	Pro	Gln
				180					185					190	
Lys	Asp	Glu	Leu	Lys	Ser	Phe	Ile	Leu	Gln	Lys	Tyr	Met	Met	Val	Asp
		195						200					205		
Ser	Ala	Glu	Asp	Gln	Lys	Ile	His	Arg	Pro	Met	Ala	Pro	Lys	Glu	Ala
	210						215					220			
Pro	Lys	Lys	Leu	Ile	Arg	Tyr	Ile	Asp	Asn	Gln	Val	Val	Ser	Thr	Lys
	225					230					235				
Gly	Glu	Arg	Phe	Lys	Asp	Val	Arg	Asn	Pro	Glu	Ala	Glu	Glu	Met	Lys
240					245					250					255
Ala	Thr	Tyr	Ile	Asn	Leu	Lys	Pro	Ala	Arg	Lys	Tyr	Arg	Phe	His	
			260						265					270	

<210> 302

<211> 165

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -35...-1

<400> 302

Met	Met	Arg	Cys	Cys	Arg	Arg	Arg	Cys	Cys	Cys	Arg	Gln	Pro	Pro	His
-35					-30					-25					-20
Ala	Leu	Arg	Pro	Leu	Leu	Leu	Leu	Pro	Leu	Val	Leu	Leu	Pro	Pro	Leu
				-15					-10						-5
Ala	Ala	Ala	Ala	Ala	Gly	Pro	Asn	Arg	Cys	Asp	Thr	Ile	Tyr	Gln	Gly
		1				5					10				
Phe	Ala	Glu	Cys	Leu	Ile	Arg	Leu	Gly	Asp	Ser	Met	Gly	Arg	Gly	Gly
15						20					25				

00076997 060801

Glu Leu Glu Thr Ile Cys Arg Ser Trp Asn Tyr Phe His Ala Cys Ala  
 30 35 40 45  
 Ser Gln Val Leu Ser Gly Cys Pro Glu Glu Ala Ala Val Trp Glu  
 50 55 60  
 Ser Leu Gln Gln Glu Ala Arg Gln Ala Pro Arg Pro Asn Asn Leu His  
 65 70 75  
 Thr Leu Cys Gly Ala Pro Val His Val Arg Glu Arg Gly Thr Gly Ser  
 80 85 90  
 Glu Thr Asn Gln Glu Thr Leu Arg Ala Thr Ala Pro Ala Leu Pro Met  
 95 100 105  
 Ala Pro Ala Pro Pro Leu Leu Ala Ala Leu Ala Leu Ala Tyr Leu  
 110 115 120 125  
 Leu Arg Pro Leu Ala  
 130

<210> 303  
 <211> 148  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -25...-1

<400> 303  
 Met Ala Ser Val Val Leu Ala Leu Arg Thr Arg Thr Ala Val Thr Ser  
 -25 -20 -15 -10  
 Leu Leu Ser Pro Thr Pro Ala Thr Ala Leu Ala Val Arg Tyr Ala Ser  
 -5 1 5  
 Lys Lys Ser Gly Gly Ser Ser Lys Asn Leu Gly Gly Lys Ser Ser Gly  
 10 15 20  
 Arg Arg Gln Gly Ile Lys Lys Met Glu Gly His Tyr Val His Ala Gly  
 25 30 35  
 Asn Ile Ile Ala Thr Gln Arg His Phe Arg Trp His Pro Gly Ala His  
 40 45 50 55  
 Val Gly Val Gly Lys Asn Lys Cys Leu Tyr Ala Leu Glu Glu Gly Ile  
 60 65 70  
 Val Arg Tyr Thr Lys Glu Val Tyr Val Pro His Pro Arg Asn Thr Glu  
 75 80 85  
 Ala Val Asp Leu Ile Thr Arg Leu Pro Lys Gly Ala Val Leu Tyr Lys  
 90 95 100  
 Thr Phe Val His Val Val Pro Ala Lys Pro Glu Gly Thr Phe Lys Leu  
 105 110 115  
 Val Ala Met Leu  
 120

<210> 304  
 <211> 291  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -34...-1

<400> 304  
 Met Glu Ser Glu Arg Ser Lys Arg Met Gly Asn Ala Cys Ile Pro Leu  
 -30 -25 -20



Lys Arg Ile Ala Tyr Phe Leu Cys Leu Leu Ser Ala Leu Leu Leu Thr  
 -15 -10 -5  
 Glu Gly Lys Lys Pro Ala Lys Pro Lys Cys Pro Ala Val Cys Thr Cys  
 1 5 10  
 Thr Lys Asp Asn Ala Leu Cys Glu Asn Ala Arg Ser Ile Pro Arg Thr  
 15 20 25 30  
 Val Pro Pro Asp Val Ile Ser Leu Ser Phe Val Arg Ser Gly Phe Thr  
 35 40 45  
 Glu Ile Ser Glu Gly Ser Phe Leu Phe Thr Pro Ser Leu Gln Leu Leu  
 50 55 60  
 Leu Phe Thr Ser Asn Ser Phe Asp Val Ile Ser Asp Asp Ala Phe Ile  
 65 70 75  
 Gly Leu Pro His Leu Glu Tyr Leu Phe Ile Glu Asn Asn Asn Ile Lys  
 80 85 90  
 Ser Ile Ser Arg His Thr Phe Arg Gly Leu Lys Ser Leu Ile His Leu  
 95 100 105 110  
 Ser Leu Ala Asn Asn Asn Leu Gln Thr Leu Pro Lys Asp Ile Phe Lys  
 115 120 125  
 Gly Leu Asp Ser Leu Thr Asn Val Asp Leu Arg Gly Asn Ser Phe Asn  
 130 135 140  
 Cys Asp Cys Lys Leu Lys Trp Leu Val Glu Trp Leu Gly His Thr Asn  
 145 150 155  
 Ala Thr Val Glu Asp Ile Tyr Cys Glu Gly Pro Pro Glu Tyr Lys Lys  
 160 165 170  
 Arg Lys Ile Asn Ser Leu Ser Ser Lys Asp Phe Asp Cys Ile Ile Thr  
 175 180 185 190  
 Glu Phe Ala Lys Ser Gln Asp Leu Pro Tyr Gln Ser Leu Ser Ile Asp  
 195 200 205  
 Thr Phe Ser Tyr Leu Asn Asp Glu Tyr Val Val Ile Ala Gln Pro Phe  
 210 215 220  
 Thr Gly Lys Cys Ile Phe Leu Glu Trp Asp His Val Glu Lys Thr Phe  
 225 230 235  
 Arg Asn Tyr Asp Asn Ile Thr Val Leu Arg Glu Ile His Arg Phe Thr  
 240 245 250  
 Asn Met Ser  
 255

<210> 305  
 <211> 81  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -49..-1

<400> 305  
 Met Glu Gly Ala Gly Ala Gly Ser Gly Phe Arg Lys Glu Leu Val Ser  
 -45 -40 -35  
 Arg Leu Leu His Leu His Phe Lys Asp Asp Lys Thr Lys Val Ser Gly  
 -30 -25 -20  
 Asp Ala Leu Gln Leu Met Val Glu Leu Leu Lys Val Phe Val Val Glu  
 -15 -10 -5  
 Ala Ala Val Arg Gly Val Arg Gln Ala Gln Ala Glu Asp Ala Leu Arg  
 1 5 10 15  
 Val Asp Val Asp Gln Leu Glu Lys Val Leu Pro Gln Leu Leu Leu Asp  
 20 25 30  
 Phe

<210> 306  
 <211> 233  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -30...-1

<400> 306  
 Met Ala Ala Thr Ser Gly Thr Asp Glu Pro Val Ser Gly Glu Leu Val  
 -30 -25 -20 -15  
 Ser Val Ala His Ala Leu Ser Leu Pro Ala Glu Ser Tyr Gly Asn Asp  
 -10 -5 1  
 Pro Asp Ile Glu Met Ala Trp Ala Met Arg Ala Met Gln His Ala Glu  
 5 10 15  
 Val Tyr Tyr Lys Leu Ile Ser Ser Val Asp Pro Gln Phe Leu Lys Leu  
 20 25 30  
 Thr Lys Val Asp Asp Gln Ile Tyr Ser Glu Phe Arg Lys Asn Phe Glu  
 35 40 45 50  
 Thr Leu Arg Ile Asp Val Leu Asp Pro Glu Glu Leu Lys Ser Glu Ser  
 55 60 65  
 Ala Lys Glu Lys Trp Arg Pro Phe Cys Leu Lys Phe Asn Gly Ile Val  
 70 75 80  
 Glu Asp Phe Asn Tyr Gly Thr Leu Leu Arg Leu Asp Cys Ser Gln Gly  
 85 90 95  
 Tyr Thr Glu Glu Asn Thr Ile Phe Ala Pro Arg Ile Gln Phe Phe Ala  
 100 105 110  
 Ile Glu Ile Ala Arg Asn Arg Glu Gly Tyr Asn Lys Ala Val Tyr Ile  
 115 120 125 130  
 Ser Val Gln Asp Lys Glu Gly Glu Lys Gly Val Asn Asn Gly Gly Glu  
 135 140 145  
 Lys Arg Ala Asp Ser Gly Glu Glu Glu Asn Thr Lys Asn Gly Gly Glu  
 150 155 160  
 Lys Gly Ala Asp Ser Gly Glu Glu Lys Glu Glu Gly Ile Asn Arg Glu  
 165 170 175  
 Asp Lys Thr Asp Lys Gly Gly Glu Lys Gly Lys Glu Ala Asp Lys Glu  
 180 185 190  
 Ile Asn Lys Ser Gly Glu Lys Ala Met  
 195 200

<210> 307  
 <211> 85  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -20...-1

<400> 307  
 Met Arg Gln Lys Ala Val Ser Leu Phe Leu Cys Tyr Leu Leu Leu Phe  
 -20 -15 -10 -5  
 Thr Cys Ser Gly Val Glu Ala Gly Lys Lys Cys Ser Glu Ser Ser  
 1 5 10  
 Asp Ser Gly Ser Gly Phe Trp Lys Ala Leu Thr Phe Met Ala Val Gly  
 15 20 25





165					170					175					180		
Leu	Thr	Ser	Arg	Tyr	Glu	Val	Pro	Cys	Val	Leu	Asp	Leu	Lys	Met	Gly		
				185					190					195			
Thr	Arg	Gln	His	Gly	Asp	Asp	Ala	Ser	Glu	Glu	Lys	Ala	Ala	Asn	Gln		
				200					205					210			
Ile	Arg	Lys	Cys	Gln	Gln	Ser	Thr	Ser	Ala	Val	Ile	Gly	Val	Arg	Val		
				215					220					225			
Cys	Gly	Met	Gln	Val	Tyr	Gln	Ala	Gly	Ser	Gly	Gln	Leu	Met	Phe	Met		
				230					235					240			
Asn	Lys	Tyr	His	Gly	Arg	Lys	Leu	Ser	Met	Gln	Gly	Phe	Lys	Glu	Ala		
245					250					255					260		
Leu	Phe	Gln	Phe	Phe	His	Asn	Gly	Arg	Tyr	Leu	Arg	Arg	Glu	Leu	Leu		
				265					270					275			
Gly	Pro	Val	Leu	Lys	Lys	Leu	Thr	Glu	Leu	Lys	Ala	Val	Leu	Glu	Arg		
				280					285					290			
Gln	Glu	Ser	Tyr	Arg	Phe	Tyr	Ser	Ser	Ser	Leu	Leu	Val	Ile	Tyr	Asp		
				295					300					305			
Gly	Lys	Glu	Arg	Pro	Glu	Val	Val	Leu	Asp	Ser	Asp	Ala	Glu	Asp	Leu		
				310					315					320			
Glu	Asp	Leu	Ser	Glu	Glu	Ser	Ala	Asp	Glu	Ser	Ala	Gly	Ala	Tyr	Ala		
325					330					335					340		
Tyr	Lys	Pro	Ile	Gly	Ala	Ser	Ser	Val	Asp	Val	Arg	Met	Ile	Asp	Phe		
				345					350					355			
Ala	His	Thr	Thr	Cys	Arg	Leu	Tyr	Gly	Glu	Asp	Thr	Val	Val	His	Glu		
				360					365					370			
Gly	Gln	Asp	Ala	Gly	Tyr	Ile	Phe	Gly	Leu	Gln	Ser	Leu	Ile	Asp	Ile		
				375					380					385			
Val	Thr	Glu	Ile	Ser	Glu	Glu	Ser	Gly	Glu								
				390					395								

```
<210> 311
<211> 466
<212> PRT
<213> Homo sapiens
```

```
<220>  
<221> SIGNAL  
<222> -16..-1
```

<400> 311																
Met	Gly	Leu	Tyr	Ala	Ala	Ala	Ala	Gly	Val	Leu	Ala	Gly	Val	Glu	Ser	
	-15					-10					-5					
Arg	Gln	Gly	Ser	Ile	Lys	Gly	Leu	Val	Tyr	Ser	Ser	Asn	Phe	Gln	Asn	
1				5					10					15		
Val	Lys	Gln	Leu	Tyr	Ala	Leu	Val	Cys	Glu	Thr	Gln	Arg	Tyr	Ser	Ala	
			20					25					30			
Val	Leu	Asp	Ala	Val	Ile	Ala	Ser	Ala	Gly	Leu	Leu	Arg	Ala	Glu	Lys	
		35					40					45				
Lys	Leu	Arg	Pro	His	Leu	Ala	Lys	Val	Leu	Val	Tyr	Glu	Leu	Leu	Leu	
	50					55					60					
Gly	Lys	Gly	Phe	Arg	Gly	Gly	Gly	Gly	Arg	Trp	Lys	Ala	Leu	Leu	Gly	
65					70				75						80	
Arg	His	Gln	Ala	Arg	Leu	Lys	Ala	Glu	Leu	Ala	Arg	Leu	Lys	Val	His	
				85					90					95		
Arg	Gly	Val	Ser	Arg	Asn	Glu	Asp	Leu	Leu	Glu	Val	Gly	Ser	Arg	Pro	
			100					105					110			
Gly	Pro	Ala	Ser	Gln	Leu	Pro	Arg	Phe	Val	Arg	Val	Asn	Thr	Leu	Lys	
		115					120					125				

Thr Cys Ser Asp Asp Val Val Asp Tyr Phe Lys Arg Gln Gly Phe Ser  
 130 135 140  
 Tyr Gln Gly Arg Ala Ser Ser Leu Asp Asp Leu Arg Ala Leu Lys Gly  
 145 150 155 160  
 Lys His Phe Leu Leu Asp Pro Leu Met Pro Glu Leu Leu Val Phe Pro  
 165 170 175  
 Ala Gln Thr Asp Leu His Glu His Pro Leu Tyr Arg Ala Gly His Leu  
 180 185 190  
 Ile Leu Gln Asp Arg Ala Ser Cys Leu Pro Ala Met Leu Leu Asp Pro  
 195 200 205  
 Pro Pro Gly Ser His Val Ile Asp Ala Cys Ala Ala Pro Gly Asn Lys  
 210 215 220  
 Thr Ser His Leu Ala Ala Leu Leu Lys Asn Gln Gly Lys Ile Phe Ala  
 225 230 235 240  
 Phe Asp Leu Asp Ala Lys Arg Leu Ala Ser Met Ala Thr Leu Leu Ala  
 245 250 255  
 Arg Ala Gly Val Ser Cys Cys Glu Leu Ala Glu Glu Asp Phe Leu Ala  
 260 265 270  
 Val Ser Pro Ser Asp Pro Arg Tyr His Glu Val His Tyr Ile Leu Leu  
 275 280 285  
 Asp Pro Ser Cys Ser Gly Ser Gly Met Pro Ser Arg Gln Leu Glu Glu  
 290 295 300  
 Pro Gly Ala Gly Thr Pro Ser Pro Val Arg Leu His Ala Leu Ala Gly  
 305 310 315 320  
 Phe Gln Gln Arg Ala Leu Cys His Ala Leu Thr Phe Pro Ser Leu Gln  
 325 330 335  
 Arg Leu Val Tyr Ser Thr Cys Ser Leu Cys Gln Glu Glu Asn Glu Asp  
 340 345 350  
 Val Val Arg Asp Ala Leu Gln Gln Asn Pro Gly Ala Phe Arg Leu Ala  
 355 360 365  
 Pro Ala Leu Pro Ala Trp Pro His Arg Gly Leu Ser Thr Phe Pro Gly  
 370 375 380  
 Ala Glu His Cys Leu Arg Ala Ser Pro Glu Thr Thr Leu Ser Ser Gly  
 385 390 395 400  
 Phe Phe Val Ala Val Ile Glu Arg Val Glu Val Pro Ser Ser Ala Ser  
 405 410 415  
 Gln Ala Lys Ala Ser Ala Pro Glu Arg Thr Pro Ser Pro Ala Pro Lys  
 420 425 430  
 Arg Lys Lys Arg Gln Gln Arg Ala Ala Ala Gly Ala Cys Thr Pro Pro  
 435 440 445  
 Cys Thr  
 450

<210> 312  
 <211> 382  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -16..-1

<400> 312  
 Met Gly Leu Tyr Ala Ala Ala Ala Gly Val Leu Ala Gly Val Glu Ser  
 -15 -10 -5  
 Arg Gln Gly Ser Ile Lys Gly Leu Val Tyr Ser Ser Asn Phe Gln Asn  
 1 5 10 15  
 Val Lys Gln Leu Tyr Ala Leu Val Cys Glu Thr Gln Arg Tyr Ser Ala

			20				25				30					
Val	Leu	Asp	Ala	Val	Ile	Ala	Ser	Ala	Gly	Leu	Leu	Arg	Ala	Glu	Lys	
		35					40					45				
Lys	Leu	Arg	Pro	His	Leu	Ala	Lys	Val	Leu	Val	Tyr	Glu	Leu	Leu	Leu	
	50					55					60					
Gly	Lys	Gly	Phe	Arg	Gly	Gly	Gly	Gly	Arg	Trp	Lys	Ala	Leu	Leu	Gly	
65					70					75					80	
Arg	His	Gln	Ala	Arg	Leu	Lys	Ala	Glu	Leu	Ala	Arg	Leu	Lys	Val	His	
				85						90				95		
Arg	Gly	Val	Ser	Arg	Asn	Glu	Asp	Leu	Leu	Glu	Val	Gly	Ser	Arg	Pro	
			100					105					110			
Gly	Pro	Ala	Ser	Gln	Leu	Pro	Arg	Phe	Val	Arg	Val	Asn	Thr	Leu	Lys	
		115					120					125				
Thr	Cys	Ser	Asp	Asp	Val	Val	Asp	Tyr	Phe	Lys	Arg	Gln	Gly	Phe	Ser	
	130					135					140					
Tyr	Gln	Gly	Arg	Ala	Ser	Ser	Leu	Asp	Asp	Leu	Arg	Ala	Leu	Lys	Gly	
145					150					155					160	
Lys	His	Phe	Leu	Leu	Asp	Pro	Leu	Met	Pro	Glu	Leu	Leu	Val	Phe	Pro	
				165					170					175		
Ala	Gln	Thr	Asp	Leu	His	Glu	His	Pro	Leu	Tyr	Arg	Ala	Gly	His	Leu	
			180					185					190			
Ile	Leu	Gln	Asp	Arg	Ala	Ser	Cys	Leu	Pro	Ala	Met	Leu	Leu	Asp	Pro	
		195					200					205				
Pro	Pro	Gly	Ser	His	Val	Ile	Asp	Ala	Cys	Ala	Ala	Pro	Gly	Asn	Lys	
	210					215					220					
Thr	Ser	His	Leu	Ala	Ala	Leu	Leu	Lys	Asn	Gln	Gly	Lys	Ile	Phe	Ala	
225					230					235					240	
Phe	Asp	Leu	Asp	Ala	Lys	Arg	Leu	Ala	Ser	Met	Ala	Thr	Leu	Leu	Ala	
			245						250					255		
Arg	Ala	Gly	Val	Ser	Cys	Cys	Glu	Leu	Ala	Glu	Glu	Asp	Phe	Leu	Ala	
			260					265					270			
Val	Ser	Pro	Ser	Asp	Pro	Arg	Tyr	His	Glu	Val	His	Tyr	Ile	Leu	Leu	
		275					280					285				
Asp	Pro	Ser	Cys	Ser	Gly	Ser	Gly	Met	Pro	Ser	Arg	Gln	Leu	Glu	Glu	
	290					295					300					
Pro	Gly	Ala	Gly	Thr	Pro	Ser	Pro	Val	Arg	Leu	His	Ala	Leu	Ala	Ala	
305					310					315					320	
Ser	Ser	Ser	Glu	Pro	Cys	Ala	Thr	Arg	Ser	Leu	Ser	Leu	Pro	Cys	Ser	
			325						330					335		
Gly	Ser	Ser	Thr	Pro	Arg	Ala	Pro	Ser	Ala	Arg	Arg	Arg	Met	Lys	Thr	
			340					345					350			
Trp	Cys	Glu	Met	Arg	Cys	Ser	Arg	Thr	Arg	Ala	Pro	Ser	Gly			
		355					360					365				

```
<210> 313
<211> 258
<212> PRT
<213> Homo sapiens
```

```
<220>  
<221> SIGNAL  
<222> -36..-1
```

<400> 313  
Met Glu Glu Leu Gln Glu Pro Leu Arg Gly Glu Leu Arg Leu Cys Phe  
-35 -30 -25  
Thr Gln Ala Ala Arg Thr Ser Leu Leu Leu Leu Arg Leu Asn Asp Ala  
-20 -15 -10 -5

[illegible]

```
<210> 314
<211> 280
<212> PRT
<213> Homo sapiens
```

```
<220>  
<221> SIGNAL  
<222> -33..-1
```

<400> 314															
Met	Lys	Ser	Cys	Gly	Ser	Met	Leu	Gly	Leu	Trp	Gly	Gln	Arg	Leu	Pro
			-30					-25					-20		
Ala	Ala	Trp	Val	Leu	Leu	Leu	Leu	Pro	Phe	Leu	Pro	Leu	Leu	Leu	Leu
		-15					-10					-5			
Ala	Ala	Pro	Ala	Pro	His	Arg	Ala	Ser	Tyr	Lys	Pro	Val	Ile	Val	Val
1					5					10				15	
His	Gly	Leu	Phe	Asp	Ser	Ser	Tyr	Ser	Phe	Arg	His	Leu	Leu	Glu	Tyr
			20						25					30	
Ile	Asn	Glu	Thr	His	Pro	Gly	Thr	Val	Val	Thr	Val	Leu	Asp	Leu	Phe
			35				40						45		
Asp	Gly	Arg	Glu	Ser	Leu	Arg	Pro	Leu	Trp	Glu	Gln	Val	Gln	Gly	Phe
		50					55					60			
Arg	Glu	Ala	Val	Val	Pro	Ile	Met	Ala	Lys	Ala	Pro	Gln	Gly	Val	His
	65					70					75				
Leu	Ile	Cys	Tyr	Ser	Gln	Gly	Gly	Leu	Val	Cys	Arg	Ala	Leu	Leu	Ser
80					85					90				95	
Val	Met	Asp	Asp	His	Asn	Val	Asp	Ser	Phe	Ile	Ser	Leu	Ser	Ser	Pro
				100					105					110	



Gln Met Gly Gln Tyr Gly Asp Thr Asp Tyr Leu Lys Trp Leu Phe Pro  
 115 120 125  
 Thr Ser Met Arg Ser Asn Leu Tyr Arg Ile Cys Tyr Ser Pro Leu Ile  
 130 135 140  
 Asn Gly Glu Arg Asp His Pro Asn Ala Thr Val Trp Arg Lys Asn Phe  
 145 150 155  
 Leu Arg Val Gly His Leu Val Leu Ile Gly Gly Pro Asp Asp Gly Val  
 160 165 170 175  
 Ile Thr Pro Trp Gln Ser Ser Phe Phe Gly Phe Tyr Asp Ala Asn Glu  
 180 185 190  
 Thr Val Leu Glu Met Glu Glu Gln Leu Val Tyr Leu Arg Asp Ser Phe  
 195 200 205  
 Gly Leu Lys Thr Leu Leu Ala Arg Gly Ala Ile Val Arg Cys Pro Met  
 210 215 220  
 Ala Gly Ile Ser His Thr Ala Trp His Ser Asn Arg Thr Leu Tyr Glu  
 225 230 235  
 Thr Cys Ile Glu Pro Trp Leu Ser  
 240 245

<210> 315  
 <211> 174  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -33...-1

<400> 315  
 Met Lys Ser Cys Gly Ser Met Leu Gly Leu Trp Gly Gln Arg Leu Pro  
 -30 -25 -20  
 Ala Ala Trp Val Leu Leu Leu Leu Pro Phe Leu Pro Leu Leu Leu Leu  
 -15 -10 -5  
 Ala Ala Pro Ala Pro His Arg Ala Ser Tyr Lys Pro Val Ile Val Val  
 1 5 10 15  
 His Gly Leu Phe Asp Ser Ser Tyr Ser Phe Arg His Leu Leu Glu Tyr  
 20 25 30  
 Ile Asn Glu Thr His Pro Gly Thr Val Val Thr Val Leu Asp Leu Phe  
 35 40 45  
 Asp Gly Arg Glu Ser Leu Arg Pro Leu Trp Glu Gln Val Gln Gly Phe  
 50 55 60  
 Arg Glu Ala Val Val Pro Ile Met Ala Lys Ala Pro Gln Gly Val His  
 65 70 75  
 Leu Ile Cys Tyr Ser Gln Gly Gly Leu Val Cys Arg Ala Leu Leu Ser  
 80 85 90 95  
 Val Met Asp Asp His Asn Val Asp Ser Phe Ile Ser Leu Ser Ser Pro  
 100 105 110  
 Gln Met Gly Gln Tyr Gly Asp Thr Asp Tyr Leu Lys Trp Leu Phe Pro  
 115 120 125  
 Thr Ser Met Arg Ser Asn Leu Tyr Arg Ile Cys Tyr Ser Pro  
 130 135 140

<210> 316  
 <211> 160  
 <212> PRT  
 <213> Homo sapiens

<220>

<221> SIGNAL  
<222> -17...-1

<400> 316  
Met Ala Phe Thr Phe Ala Ala Phe Cys Tyr Met Leu Ser Leu Val Leu  
-15 -10 -5  
Cys Ala Ala Leu Ile Phe Phe Ala Ile Trp His Ile Ile Ala Phe Asp  
1 5 10 15  
Glu Leu Arg Thr Asp Phe Lys Ser Pro Ile Asp Gln Cys Asn Pro Val  
20 25 30  
His Ala Arg Glu Arg Leu Arg Asn Ile Glu Arg Ile Cys Phe Leu Leu  
35 40 45  
Arg Lys Leu Val Leu Pro Glu Tyr Ser Ile His Ser Leu Phe Cys Ile  
50 55 60  
Met Phe Leu Cys Ala Gln Glu Trp Leu Thr Leu Gly Leu Asn Val Pro  
65 70 75  
Leu Leu Phe Tyr His Phe Trp Arg Tyr Phe His Cys Pro Ala Asp Ser  
80 85 90 95  
Ser Glu Leu Ala Tyr Asp Pro Pro Val Val Met Asn Pro Asp Thr Leu  
100 105 110  
Ser Tyr Cys Gln Lys Glu Ala Trp Cys Lys Leu Ala Phe Tyr Leu Leu  
115 120 125  
Ser Phe Phe Tyr Tyr Leu Tyr Cys Met Ile Tyr Thr Leu Val Ser Ser  
130 135 140

<210> 317  
<211> 426  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -28...-1

<400> 317  
Met Ser Pro Ala Phe Arg Ala Met Asp Val Glu Pro Arg Ala Lys Gly  
-25 -20 -15  
Val Leu Leu Glu Pro Phe Val His Gln Val Gly Gly His Ser Cys Val  
-10 -5 1  
Leu Arg Phe Asn Glu Thr Thr Leu Cys Lys Pro Leu Val Pro Arg Glu  
5 10 15 20  
His Gln Phe Tyr Glu Thr Leu Pro Ser Glu Met Arg Lys Phe Thr Pro  
25 30 35  
Gln Tyr Lys Gly Val Val Ser Val Arg Phe Glu Glu Asp Glu Asp Arg  
40 45 50  
Asn Leu Cys Leu Ile Ala Tyr Pro Leu Lys Gly Asp His Gly Ile Val  
55 60 65  
Asp Ile Val Asp Asn Ser Asp Cys Glu Pro Lys Ser Lys Leu Leu Arg  
70 75 80  
Trp Thr Thr Asn Lys Lys His His Val Leu Glu Thr Glu Lys Thr Pro  
85 90 95 100  
Lys Asp Trp Val Arg Gln His Arg Lys Glu Glu Lys Met Lys Ser His  
105 110 115  
Lys Leu Glu Glu Glu Phe Glu Trp Leu Lys Lys Ser Glu Val Leu Tyr  
120 125 130  
Tyr Thr Val Glu Lys Lys Gly Asn Ile Ser Ser Gln Leu Lys His Tyr  
135 140 145  
Asn Pro Trp Ser Met Lys Cys His Gln Gln Gln Leu Gln Arg Met Lys

	150					155					160					
Glu 165	Asn	Ala	Lys	His	Arg	Asn	Gln	Tyr	Lys	Phe	Ile	Leu	Leu	Glu	Asn	
Leu	Thr	Ser	Arg	Tyr	Glu	Val	Pro	Cys	Val	Leu	Asp	Leu	Lys	Met	Gly	
				185					190					195		
Thr	Arg	Gln	His	Gly	Asp	Asp	Ala	Ser	Glu	Glu	Lys	Ala	Ala	Asn	Gln	
			200					205					210			
Ile	Arg	Lys	Cys	Gln	Gln	Ser	Thr	Ser	Ala	Val	Ile	Gly	Val	Arg	Val	
		215					220					225				
Cys	Gly	Met	Gln	Val	Tyr	Gln	Ala	Gly	Ser	Gly	Gln	Leu	Met	Phe	Met	
	230					235					240					
Asn 245	Lys	Tyr	His	Gly	Arg	Lys	Leu	Ser	Val	Gln	Gly	Phe	Lys	Glu	Ala	
				250						255				260		
Leu	Phe	Gln	Phe	Phe	His	Asn	Gly	Arg	Tyr	Leu	Arg	Arg	Glu	Leu	Leu	
				265					270					275		
Gly	Pro	Val	Leu	Lys	Lys	Leu	Thr	Glu	Leu	Lys	Ala	Val	Leu	Glu	Arg	
			280					285					290			
Gln	Glu	Ser	Tyr	Arg	Phe	Tyr	Ser	Ser	Ser	Leu	Leu	Val	Ile	Tyr	Asp	
		295					300					305				
Gly	Lys	Glu	Arg	Pro	Glu	Val	Val	Leu	Asp	Ser	Asp	Ala	Glu	Asp	Leu	
	310					315					320					
Glu 325	Asp	Leu	Ser	Glu	Glu	Ser	Ala	Asp	Glu	Ser	Ala	Gly	Ala	Tyr	Ala	
				330						335				340		
Tyr	Lys	Pro	Ile	Gly	Ala	Ser	Ser	Val	Asp	Val	Arg	Met	Ile	Asp	Phe	
				345					350					355		
Ala	His	Thr	Thr	Cys	Arg	Leu	Tyr	Gly	Glu	Asp	Thr	Val	Val	His	Glu	
			360					365					370			
Gly	Gln	Asp	Ala	Gly	Tyr	Ile	Phe	Gly	Leu	Gln	Ser	Leu	Ile	Asp	Ile	
		375					380					385				
Val	Thr	Glu	Ile	Ser	Glu	Glu	Ser	Gly	Glu							
	390					395										

```
<210> 318
<211> 301
<212> PRT
<213> Homo sapiens
```

```
<220>  
<221> SIGNAL  
<222> -20..-1
```

<400>	318														
Met	Ala	Arg	His	Gly	Leu	Pro	Leu	Leu	Pro	Leu	Leu	Ser	Leu	Leu	Val
-20					-15					-10					-5
Gly	Ala	Trp	Leu	Lys	Leu	Gly	Asn	Gly	Gln	Ala	Thr	Ser	Met	Val	Gln
			1				5					10			
Leu	Gln	Gly	Gly	Arg	Phe	Leu	Met	Gly	Thr	Asn	Ser	Pro	Asp	Ser	Arg
		15				20						25			
Asp	Gly	Glu	Gly	Pro	Val	Arg	Glu	Ala	Thr	Val	Lys	Pro	Phe	Ala	Ile
	30					35					40				
Asp	Ile	Phe	Pro	Val	Thr	Asn	Lys	Asp	Phe	Arg	Asp	Phe	Val	Arg	Glu
45					50					55					60
Lys	Lys	Tyr	Arg	Thr	Glu	Ala	Glu	Met	Phe	Gly	Leu	Ser	Phe	Val	Phe
				65					70					75	
Glu	Asp	Phe	Val	Ser	Asp	Glu	Leu	Arg	Asn	Lys	Ala	Thr	Gln	Pro	Met
			80					85					90		
Lys	Ser	Val	Leu	Trp	Trp	Leu	Pro	Val	Glu	Lys	Ala	Phe	Trp	Arg	Gln
		95					100					105			

Pro	Ala	Gly	Pro	Gly	Ser	Gly	Ile	Arg	Glu	Arg	Leu	Glu	His	Pro	Val
	110					115					120				
Leu	His	Val	Ser	Trp	Asn	Asp	Ala	Arg	Ala	Tyr	Cys	Ala	Trp	Arg	Gly
125					130					135					140
Lys	Arg	Leu	Pro	Thr	Glu	Glu	Glu	Trp	Glu	Phe	Ala	Ala	Arg	Gly	Gly
				145					150					155	
Leu	Lys	Gly	Gln	Val	Tyr	Pro	Trp	Gly	Asn	Trp	Phe	Gln	Pro	Asn	Arg
			160					165					170		
Thr	Asn	Leu	Trp	Gln	Gly	Lys	Phe	Pro	Lys	Gly	Asp	Lys	Ala	Glu	Asp
		175					180					185			
Gly	Phe	His	Gly	Val	Ser	Pro	Val	Asn	Ala	Phe	Pro	Ala	Gln	Asn	Asn
	190				195					200					
Tyr	Gly	Leu	Tyr	Asp	Leu	Leu	Gly	Asn	Val	Trp	Glu	Trp	Thr	Ala	Ser
205					210					215					220
Pro	Tyr	Gln	Ala	Ala	Glu	Gln	Asp	Met	Arg	Val	Leu	Arg	Gly	Ala	Ser
			225						230					235	
Trp	Ile	Asp	Thr	Ala	Asp	Gly	Ser	Ala	Asn	His	Arg	Ala	Arg	Val	Thr
			240					245					250		
Thr	Arg	Met	Gly	Asn	Thr	Pro	Asp	Ser	Ala	Ser	Asp	Asn	Leu	Gly	Phe
		255					260				265				
Arg	Cys	Ala	Ala	Asp	Ala	Gly	Arg	Pro	Pro	Gly	Glu	Leu			
	270					275					280				

```

<220>
<221> SIGNAL
<222> -17..-1

```

```
<210> 320
<211> 95
<212> PRT
<213> Homo sapiens
```

313

<400> 320  
 Met Asp Tyr Ser Arg Val Phe Gln Gly Val Phe Phe Thr Phe Lys His  
                   -35                  -30                  -25  
 Ala Phe Ala Asp Gly Ala Trp Asp Leu Ser Phe Leu Cys Ala Leu Cys  
                   -20                  -15                  -10  
 Ser Phe Cys Pro Ile Ser Ala Ala Ser Gly Arg Pro Tyr Arg Tyr Leu  
                   -5                  1                  5  
 Glu Phe Trp Arg Leu Tyr Leu Ser Pro Ser Ser Met Glu Asn Gly Val  
 10                  15                  20                  25  
 Gln Lys Phe His Glu Thr Phe Phe Ile Val Phe Leu Leu Leu Phe Asp  
                   30                  35                  40  
 Ile Glu Arg Lys Gly Lys Ser Ser Val Cys Pro Phe Cys Tyr Arg  
                   45                  50                  55

<210> 321  
 <211> 191  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -39...-1

<400> 321  
 Met Met Thr Ile Thr Phe Leu Pro Tyr Thr Phe Ser Leu Met Val Thr  
                   -35                  -30                  -25  
 Phe Pro Asp Val Pro Leu Gly Ile Phe Leu Phe Cys Val Cys Val Ile  
                   -20                  -15                  -10  
 Ala Ile Gly Val Val Gln Ala Leu Ile Val Gly Tyr Ala Phe His Phe  
                   -5                  1                  5  
 Pro His Leu Leu Ser Pro Gln Ile Gln Arg Ser Ala His Arg Ala Leu  
 10                  15                  20                  25  
 Tyr Arg Arg His Val Leu Gly Ile Val Leu Gln Gly Pro Ala Leu Cys  
                   30                  35                  40  
 Phe Ala Ala Ala Ile Phe Ser Leu Phe Phe Val Pro Leu Ser Tyr Leu  
                   45                  50                  55  
 Leu Met Val Thr Val Ile Leu Leu Pro Tyr Val Ser Lys Val Thr Gly  
                   60                  65                  70  
 Trp Cys Arg Asp Arg Leu Leu Gly His Arg Glu Pro Ser Ala His Pro  
                   75                  80                  85  
 Val Glu Val Phe Ser Phe Asp Leu His Glu Pro Leu Ser Lys Glu Arg  
 90                  95                  100                  105  
 Val Glu Ala Phe Ser Asp Gly Val Tyr Ala Ile Val Ala Thr Leu Leu  
                   110                  115                  120  
 Ile Leu Asp Ile Cys Pro Ser Cys Ser Leu Trp Leu Ala Val Ala Ser  
                   125                  130                  135  
 Phe Gln Arg Leu Leu Leu Arg Gly Leu Ile Cys Leu Phe Val Cys  
                   140                  145                  150

<210> 322  
 <211> 89  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -41...-1



Asp Leu Val Val Ala Met Leu Ile Ala Pro Val Ala Gly Leu Ile Ala  
                   75                  80                  85  
 Ala Pro Ala Ile Ala Thr Ser Val Leu Gly Pro Val Ala Val Pro Ala  
           90                  95                  100  
 Thr Ala Met Pro Pro Ala Val Leu Ala Ala Pro Pro Ser Ala Ala Pro  
       105                  110                  115  
 Gly Val Leu Val Asp Gly Glu Ala Ala Leu Ala Val Pro Trp Glu Ala  
 120                  125                  130                  135  
 Cys Trp Ile Pro Ser Pro Pro Ala  
                   140

<210> 325  
 <211> 166  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -15...-1

<400> 325  
 Met Leu Pro Leu Leu Ile Ile Cys Leu Leu Pro Ala Ile Glu Gly Lys  
 -15                  -10                  -5                  1  
 Asn Cys Leu Arg Cys Trp Pro Glu Leu Ser Ala Leu Ile Asp Tyr Asp  
           5                  10                  15  
 Leu Gln Ile Leu Trp Val Thr Pro Gly Pro Pro Thr Glu Leu Ser Gln  
       20                  25                  30  
 Asn Arg Asp His Leu Glu Glu Thr Ala Lys Phe Phe Thr Gln Val  
       35                  40                  45  
 His Gln Ala Ile Lys Thr Leu Arg Asp Asp Lys Thr Val Leu Leu Glu  
 50                  55                  60                  65  
 Glu Ile Tyr Thr His Lys Asn Leu Phe Thr Glu Arg Leu Asn Lys Ile  
           70                  75                  80  
 Ser Asp Gly Leu Lys Glu Lys Asp Ile Gln Ser Thr Leu Lys Val Thr  
       85                  90                  95  
 Ser Cys Ala Asp Cys Arg Thr His Phe Leu Ser Cys Asn Asp Pro Thr  
       100                  105                  110  
 Phe Cys Pro Ala Arg Asn Arg Arg Thr Ser Leu Trp Ala Val Ser Leu  
       115                  120                  125  
 Ser Ser Ala Leu Leu Leu Ala Ile Ala Gly Asp Val Ser Phe Thr Gly  
 130                  135                  140                  145  
 Lys Gly Arg Arg Arg Gln  
                   150

<210> 326  
 <211> 156  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -15...-1

<400> 326  
 Met Asn Ile Leu Met Leu Thr Phe Ile Ile Cys Gly Leu Leu Thr Arg  
 -15                  -10                  -5                  1  
 Val Thr Lys Gly Ser Phe Glu Pro Gln Lys Cys Trp Lys Asn Asn Val  
       5                  10                  15





Lys Thr Ser Lys Gln Ala Tyr Tyr Trp Ala Ile Ala Ser Ile Thr Val  
                   25                  30                  35  
 Gly Ile Leu Gly Thr Ile Leu Tyr Thr Tyr Leu Ile Tyr Leu Leu Arg  
                   40                  45                  50  
 Leu

<210> 329  
 <211> 95  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -27...-1

<400> 329  
 Met Thr Asp Gln Asp Arg Ile Ile Asn Leu Val Val Gly Ser Leu Thr  
           -25                  -20                  -15  
 Ser Leu Leu Ile Leu Val Thr Leu Ile Ser Ala Phe Val Phe Pro Gln  
           -10                  -5                  1                  5  
 Leu Pro Pro Lys Pro Leu Asn Ile Phe Phe Ala Val Cys Ile Ser Leu  
                   10                  15                  20  
 Ser Ser Ile Thr Ala Cys Ile Ile Tyr Trp Tyr Arg Gln Gly Asp Leu  
                   25                  30                  35  
 Glu Pro Lys Phe Arg Lys Leu Ile Tyr Tyr Ile Ile Phe Ser Ile Ile  
           40                  45                  50  
 Met Leu Cys Ile Cys Ala Asn Leu Tyr Phe His Asp Val Gly Arg  
           55                  60                  65

<210> 330  
 <211> 84  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -20...-1

<400> 330  
 Met Ala Ala Ala Ala Val Pro Ser Leu Leu Leu Ser Leu Pro Pro His  
           -20                  -15                  -10                  -5  
 Gln Gly Leu Thr Phe Ser Asn Lys Ile Gln Pro Phe Gly Ala Gln Gly  
                   1                  5                  10  
 Val Leu His Pro Glu Pro Gly Leu Arg Asp Trp Leu Leu Pro Thr Cys  
           15                  20                  25  
 Ser Arg Gln Leu Arg Val Ala Leu Pro Glu Lys Gly Ser Glu Gly Ser  
           30                  35                  40  
 Leu Cys Gln Thr Gln Leu Pro Ala Thr Pro Cys Phe Leu Pro Ser Asn  
           45                  50                  55                  60  
 Thr Val Arg Thr

<210> 331  
 <211> 124  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL

<222> -32...-1

<400> 331

Met Val Val Val Glu Pro Gly Ala Ser Leu Phe Pro Asn Gly Val Pro  
 -30 -25 -20  
 Trp Leu Tyr Ala Val Phe Ala Val Leu Phe Val Phe Phe Leu Phe Ala  
 -15 -10 -5  
 Met Leu Ser Pro Phe Leu Leu Glu Ile Asp Gln His Ile Lys Lys Phe  
 1 5 10 15  
 Leu Ile Arg Cys Arg Tyr Ser Leu His Asn Thr Val His Lys Asp Lys  
 20 25 30  
 Lys Asn Ser Glu Ile Lys Met Asp His Leu Glu Arg Pro Gly Cys Pro  
 35 40 45  
 Leu Glu Ser Pro Arg Arg Gly Val Leu Gly Gly Lys Lys Asn Gly Met  
 50 55 60  
 Gly Asn Asp Pro Leu Leu Phe Val Lys Val Thr Lys Glu Pro Arg Asp  
 65 70 75 80  
 Ser Glu Ala Glu Ile Tyr Thr Pro Gly Pro Ser Val  
 85 90

<210> 332

<211> 62

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -46...-1

<400> 332

Met Asp Gln Leu Val Phe Lys Glu Thr Ile Trp Asn Asp Ala Phe Trp  
 -45 -40 -35  
 Gln Asn Pro Trp Asp Gln Gly Gly Leu Ala Val Ile Ile Leu Phe Ile  
 -30 -25 -20 -15  
 Thr Ala Val Leu Leu Leu Ile Leu Phe Ala Ile Val Phe Gly Leu Leu  
 -10 -5 1  
 Thr Ser Thr Glu Asn Thr Gln Cys Glu Ala Gly Glu Glu  
 5 10 15

<210> 333

<211> 150

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -23...-1

<400> 333

Met Ser Asn Gln Arg Leu Pro Leu Ile Phe Ser Leu Leu Phe Ile Cys  
 -20 -15 -10  
 Phe Phe Gly Glu Ser Phe Cys Ile Cys Asp Gly Thr Val Trp Thr Lys  
 -5 1 5  
 Val Gly Trp Glu Ile Leu Pro Glu Glu Val His Tyr Trp Lys Gly Cys  
 10 15 20 25  
 Leu Tyr Leu Ile Tyr Asn Leu Leu Gln Ala Val Phe Phe Val Leu Phe  
 30 35 40  
 Val Leu Ser Val His Tyr Leu Trp Lys Lys Trp Lys Lys His Gln Lys

45 50 55  
 Lys Leu Lys Lys Gln Ala Ser Leu Glu Lys Pro Gly Asn Asp Leu Glu  
 60 65 70  
 Ser Pro Leu Ile Asn Asn Ile Asp Gln Thr Leu His Arg Val Ala Thr  
 75 80 85  
 Thr Ala Ser Val Ile Tyr Lys Ile Trp Glu His Arg Ser His His Pro  
 90 95 100 105  
 Ser Ser Lys Lys Ile Lys His Cys Lys Leu Lys Lys Lys Ser Lys Glu  
 110 115 120  
 Glu Gly Ala Arg Arg Tyr  
 125

<210> 334  
 <211> 198  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -13...-1

<400> 334  
 Met Leu Leu Gly Arg Leu Thr Ser Gln Leu Leu Arg Ala Val Pro Trp  
 -10 -5 1  
 Ala Gly Gly Arg Pro Pro Trp Pro Val Ser Gly Val Leu Gly Ser Arg  
 5 10 15  
 Val Cys Gly Pro Leu Tyr Ser Thr Ser Pro Ala Gly Pro Gly Arg Ala  
 20 25 30 35  
 Ala Ser Leu Pro Arg Lys Gly Ala Gln Leu Glu Leu Glu Glu Met Val  
 40 45 50  
 Pro Arg Lys Met Ser Val Ser Pro Leu Glu Ser Trp Leu Thr Ala Arg  
 55 60 65  
 Cys Phe Leu Pro Arg Leu Asp Thr Gly Thr Ala Gly Thr Val Ala Pro  
 70 75 80  
 Pro Gln Ser Tyr Gln Cys Pro Pro Ser Gln Ile Gly Glu Gly Ala Glu  
 85 90 95  
 Gln Gly Asp Glu Gly Val Ala Asp Ala Pro Gln Ile Gln Cys Lys Asn  
 100 105 110 115  
 Val Leu Lys Ile Arg Arg Arg Lys Met Asn His His Lys Tyr Arg Lys  
 120 125 130  
 Leu Val Lys Lys Thr Arg Phe Leu Arg Arg Lys Val Gln Glu Gly Arg  
 135 140 145  
 Leu Arg Arg Lys Gln Ile Lys Phe Glu Lys Asp Leu Arg Arg Ile Trp  
 150 155 160  
 Leu Lys Ala Gly Leu Lys Glu Ala Pro Glu Gly Trp Gln Thr Pro Lys  
 165 170 175  
 Ile Tyr Leu Arg Gly Lys  
 180 185

<210> 335  
 <211> 88  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -24...-1





Ala Gln Pro Ser Ser Leu Ala Phe Cys Gln Val Gly Phe Leu Thr Ala  
 -15 -10 -5  
 Gln Pro Ser Pro Pro Arg Arg Arg Asn Gly Lys Asp Arg Tyr Thr Leu  
 1 5 10 15  
 Val Leu Gln His Gln Glu Cys Gln Asp Asp Leu Ala Thr Ser Ser Leu  
 20 25 30  
 Val Tyr Leu Ser Leu Pro Cys Phe Lys Asp Leu Gly Arg Ser Lys His  
 35 40 45  
 Gln Ser Ile Thr Val Ala Asp Thr Asn Lys  
 50 55

<210> 340  
 <211> 80  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -35...-1

<400> 340  
 Met Pro Phe Gln Phe Gly Thr Gln Pro Arg Arg Phe Pro Val Glu Gly  
 -35 -30 -25 -20  
 Gly Asp Ser Ser Ile Glu Leu Glu Pro Gly Leu Ser Ser Ser Ala Ala  
 -15 -10 -5  
 Cys Asn Gly Lys Glu Met Ser Pro Thr Arg Gln Leu Arg Arg Cys Pro  
 1 5 10  
 Gly Ser His Cys Leu Thr Ile Thr Asp Val Pro Val Thr Val Tyr Ala  
 15 20 25  
 Thr Thr Arg Lys Pro Pro Ala Gln Ser Ser Lys Glu Met His Pro Lys  
 30 35 40 45

<210> 341  
 <211> 131  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -15...-1

<400> 341  
 Met Ser Leu Leu Met Phe Thr Gln Leu Leu Leu Cys Gly Phe Leu Tyr  
 -15 -10 -5 1  
 Val Arg Val Asp Gly Ser Arg Leu Arg Gln Glu Asp Phe Pro Pro Arg  
 5 10 15  
 Ile Val Glu His Pro Ser Asp Val Ile Val Ser Lys Gly Glu Pro Thr  
 20 25 30  
 Thr Leu Asn Cys Lys Ala Glu Gly Arg Pro Thr Pro Thr Ile Glu Trp  
 35 40 45  
 Tyr Lys Asp Gly Glu Arg Val Glu Thr Asp Lys Asp Asp Pro Arg Ser  
 50 55 60 65  
 His Arg Met Leu Leu Pro Ser Gly Ser Leu Phe Phe Leu Arg Ile Val  
 70 75 80  
 His Gly Arg Arg Ser Lys Pro Asp Glu Gly Ser Tyr Val Cys Val Ala  
 85 90 95  
 Arg Asn Tyr Leu Gly Glu Ala Val Ser Arg Asn Ala Ser Leu Glu Val  
 100 105 110

Ala Cys Lys  
115

<210> 342  
<211> 99  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -39...-1

<400> 342  
Met Asp Leu Ile Gly Phe Gly Tyr Ala Ala Leu Val Thr Phe Gly Ser  
                  -35                  -30                  -25  
Ile Phe Gly Tyr Lys Arg Arg Gly Gly Val Pro Ser Leu Ile Ala Gly  
                  -20                  -15                  -10  
Leu Phe Val Gly Cys Leu Ala Gly Tyr Gly Ala Tyr Arg Val Ser Asn  
                  -5                  1                  5  
Asp Lys Arg Asp Val Lys Val Ser Leu Phe Thr Ala Phe Phe Leu Ala  
10                  15                  20                  25  
Thr Ile Met Gly Val Arg Phe Lys Arg Ser Lys Lys Ile Met Pro Ala  
                  30                  35                  40  
Gly Leu Val Ala Gly Leu Ser Leu Met Met Ile Leu Arg Leu Val Leu  
                  45                  50                  55  
Leu Leu Leu  
60

<210> 343  
<211> 98  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -43...-1

<400> 343  
Met Cys Glu Thr Leu Leu Thr Ser Lys Trp Ala Ser Val Ser Pro Ile  
                  -40                  -35                  -30  
Pro Ala Leu Leu Gln Glu Gly Glu Asn Arg Asp Ser Arg Arg Leu Gly  
                  -25                  -20                  -15  
Asp Ala Leu Leu Phe Leu Arg Pro Ala Gly Ser Cys Ala Leu Gln Val  
-10                  -5                  1                  5  
Ser Trp Pro Ala Ala Leu Ala Gly Pro Arg Ser His Thr Gly Gln Leu  
                  10                  15                  20  
Thr Gln His Phe Cys His Leu Lys Asn Asp Thr Cys Ile Pro Pro Ser  
                  25                  30                  35  
Leu Gly Pro Pro Arg Asn Ser Gly Ser Leu Glu Ser Leu Arg Ser Lys  
40                  45                  50  
Arg Tyr  
55

<210> 344  
<211> 217  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -19...-1

<220>  
<221> UNSURE  
<222> 185  
<223> Xaa = Phe,Val

<400> 344  
Met Val Gly Ile Leu Pro Leu Cys Cys Ser Gly Cys Val Pro Ser Leu  
-15 -10 -5  
Cys Cys Ser Ser Tyr Val Pro Ser Val Ala Pro Thr Ala Ala His Ser  
1 5 10  
Val Arg Val Pro His Ser Ala Gly His Cys Gly Gln Arg Val Leu Ala  
15 20 25  
Cys Ser Leu Pro Gln Val Phe Leu Lys Pro Trp Ile Phe Val Glu His  
30 35 40 45  
Phe Ser Ser Trp Leu Ser Leu Glu Leu Phe Ser Phe Leu Arg Tyr Leu  
50 55 60  
Gly Thr Leu Leu Cys Ala Cys Gly His Arg Leu Arg Glu Gly Arg Leu  
65 70 75  
Leu Pro Cys Leu Leu Gly Val Gly Ser Trp Leu Leu Phe Asn Asn Trp  
80 85 90  
Thr Gly Gly Ser Trp Phe Ser Leu His Leu Gln Gln Val Ser Leu Ser  
95 100 105  
Gln Gly Ser His Val Ala Ala Phe Leu Pro Glu Ala Ile Gly Pro Gly  
110 115 120 125  
Val Pro Val Pro Val Ser Gly Glu Ser Thr Ser Ala Gln Gln Ser His  
130 135 140  
Ala Gly Trp Gln Leu Ser Ala Glu Ala Asp Ala Cys Pro Ser Val Leu  
145 150 155  
Tyr Ser Glu Val Leu Glu Trp Asn Lys Asn Ile Asn Thr Tyr Thr Ser  
160 165 170  
Phe His Asp Phe Cys Leu Ile Leu Gly Ile Phe Xaa Val Leu Phe Cys  
175 180 185  
Phe Gly Gly Asp Arg Leu Thr Leu His  
190 195

<210> 345  
<211> 183  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -20...-1

<400> 345  
Met Lys Leu Leu Ser Leu Val Ala Val Val Gly Cys Leu Leu Val Pro  
-20 -15 -10 -5  
Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys Cys Ile  
1 5 10  
Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn Gln Asn Val  
15 20 25  
Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu Pro Met Pro Val  
30 35 40  
Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu Cys Glu Cys Arg Tyr



45 50 55 60  
 Glu Glu Arg Ser Thr Thr Thr Ile Lys Val Ile Ile Val Ile Tyr Leu  
 65 70 75  
 Ser Val Val Gly Ala Leu Leu Leu Tyr Met Ala Phe Leu Met Leu Val  
 80 85 90  
 Asp Pro Leu Ile Arg Lys Pro Asp Ala Tyr Thr Glu Gln Leu His Asn  
 95 100 105  
 Glu Glu Glu Asn Glu Asp Ala Arg Ser Met Ala Ala Ala Ala Ala Ser  
 110 115 120  
 Leu Gly Gly Pro Arg Ala Asn Thr Val Leu Glu Arg Val Glu Gly Ala  
 125 130 135 140  
 Gln Gln Arg Trp Lys Leu Gln Val Gln Glu Gln Arg Lys Thr Val Phe  
 145 150 155  
 Asp Arg His Lys Met Leu Ser  
 160

<210> 346  
 <211> 247  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -13...-1

<400> 346  
 Met Leu Val Leu Arg Ser Ala Leu Thr Arg Ala Leu Ala Ser Arg Thr  
 -10 -5 1  
 Leu Ala Pro Gln Met Cys Ser Ser Phe Ala Thr Gly Pro Arg Gln Tyr  
 5 10 15  
 Asp Gly Ile Phe Tyr Glu Phe Arg Ser Tyr Tyr Leu Lys Pro Ser Lys  
 20 25 30 35  
 Met Asn Glu Phe Leu Glu Asn Phe Glu Lys Asn Ala His Leu Arg Thr  
 40 45 50  
 Ala His Ser Glu Leu Val Gly Tyr Trp Ser Val Glu Phe Gly Gly Arg  
 55 60 65  
 Met Asn Thr Val Phe His Ile Trp Lys Tyr Asp Asn Phe Ala His Arg  
 70 75 80  
 Thr Glu Val Gln Lys Ala Leu Ala Lys Asp Lys Glu Trp Gln Glu Gln  
 85 90 95  
 Phe Leu Ile Pro Asn Leu Ala Leu Ile Asp Lys Gln Glu Ser Glu Ile  
 100 105 110 115  
 Thr Tyr Leu Val Pro Trp Cys Lys Leu Glu Lys Pro Pro Lys Glu Gly  
 120 125 130  
 Val Tyr Glu Leu Ala Thr Phe Gln Met Lys Pro Gly Gly Pro Ala Leu  
 135 140 145  
 Trp Gly Asp Ala Phe Lys Arg Ala Val His Ala His Val Asn Leu Gly  
 150 155 160  
 Tyr Thr Lys Leu Val Gly Val Phe His Thr Glu Tyr Gly Ala Leu Asn  
 165 170 175  
 Arg Val His Val Leu Trp Trp Asn Glu Ser Ala Asp Ser Arg Ala Ala  
 180 185 190 195  
 Gly Arg His Lys Ser His Glu Asp Pro Arg Val Val Ala Ala Val Arg  
 200 205 210  
 Glu Ser Val Asn Tyr Leu Val Ser Gln Asn Met Leu Leu Ile Pro  
 215 220 225  
 Thr Ser Phe Ser Pro Leu Lys  
 230

<210> 347  
 <211> 104  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL .  
 <222> -47...-1

<400> 347  
 Met Phe Ser Pro Arg Gln Ala Leu Thr Pro Asp Pro Leu His Ser Pro  
           -45                          -40                          -35  
 Ala Tyr Ser Pro Val Leu Gly Gly Trp Ser Arg Phe Arg Ser Val Asp  
           -30                          -25                          -20  
 Phe Arg Phe Leu Tyr Leu Thr Leu Asn Gln Ser Cys Ile Phe Ala Asn  
           -15                          -10                          -5                          1  
 Tyr Lys Glu Ala His Ala Asn Arg Tyr Cys Thr Glu Gly Arg Tyr Thr  
                           5                          10                          15  
 Arg Glu Ile Gln Arg Leu Thr Ser Pro Ala Ala Trp Pro Thr Arg Asp  
                           20                          25                          30  
 Lys Asn Arg Met Ile Ser Asn Gly Met Ala Leu Asn Ser Pro Ala Glu  
           35                          40                          45  
 Gly Leu Ala Phe Gln Cys Arg Phe  
           50                          55

<210> 348  
 <211> 125  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -21...-1

<400> 348  
 Met Ala Lys Tyr Leu Ala Gln Ile Ile Val Met Gly Val Gln Val Val  
           -20                          -15                          -10  
 Gly Arg Ala Phe Ala Arg Ala Leu Arg Gln Glu Phe Ala Ala Ser Arg  
           -5                          1                          5                          10  
 Ala Ala Ala Asp Ala Arg Gly Arg Ala Gly His Arg Ser Ala Ala Ala  
                           15                          20                          25  
 Ser Asn Leu Ser Gly Leu Ser Leu Gln Glu Ala Gln Gln Ile Leu Asn  
           30                          35                          40  
 Val Ser Lys Leu Ser Pro Glu Val Gln Lys Asn Tyr Glu His Leu  
           45                          50                          55  
 Phe Lys Val Asn Asp Lys Ser Val Gly Gly Ser Phe Tyr Leu Gln Ser  
           60                          65                          70                          75  
 Lys Val Val Arg Ala Lys Glu Arg Leu Asp Glu Glu Leu Lys Ile Gln  
                           80                          85                          90  
 Ala Gln Glu Asp Arg Glu Lys Gly Gln Met Pro His Thr  
           95                          100

<210> 349  
 <211> 302  
 <212> PRT  
 <213> Homo sapiens

[illegible]

Met	Ala	Pro	Asn -15	Ser	Ile	Thr	Leu	Leu -10	Gly	Leu	Ala	Val	Asn -5	Val	Val
Thr	Thr	Leu	Val	Leu	Ile	Ser	Tyr	Cys	Pro	Thr	Ala	Thr	Glu	Glu	Ala
		1				5				10					
Pro	Tyr	Trp	Thr	Tyr	Leu	Leu	Cys	Ala	Leu	Gly	Leu	Phe	Ile	Tyr	Gln
15					20					25					30
Ser	Leu	Asp	Ala	Ile	Asp	Gly	Lys	Gln	Ala	Arg	Arg	Thr	Asn	Ser	Cys
				35				40						45	
Ser	Pro	Leu	Gly	Glu	Leu	Phe	Asp	His	Gly	Cys	Asp	Ser	Leu	Ser	Thr
			50					55					60		
Val	Phe	Met	Ala	Val	Gly	Ala	Ser	Ile	Ala	Ala	Arg	Leu	Gly	Thr	Tyr
		65					70				75				
Pro	Asp	Trp	Phe	Phe	Phe	Cys	Ser	Phe	Ile	Gly	Met	Phe	Val	Phe	Tyr
		80				85					90				
Cys	Ala	His	Trp	Gln	Thr	Tyr	Val	Ser	Gly	Met	Leu	Arg	Phe	Gly	Lys
95					100					105					110
Val	Asp	Val	Thr	Glu	Ile	Gln	Ile	Ala	Leu	Val	Ile	Val	Phe	Val	Leu
				115					120					125	
Ser	Ala	Phe	Gly	Gly	Ala	Thr	Met	Trp	Asp	Tyr	Thr	Gly	Thr	Ser	Val
			130					135					140		
Leu	Ser	Pro	Gly	Leu	His	Ile	Gly	Leu	Ile	Ile	Ile	Leu	Ala	Ile	Met
		145					150					155			
Ile	Tyr	Lys	Lys	Ser	Ala	Thr	Asp	Val	Phe	Glu	Lys	His	Pro	Cys	Leu
		160				165					170				
Tyr	Ile	Leu	Met	Phe	Gly	Cys	Val	Phe	Ala	Lys	Val	Ser	Gln	Lys	Leu
175					180					185					190
Val	Val	Ala	His	Met	Thr	Lys	Ser	Glu	Leu	Tyr	Leu	Gln	Asp	Thr	Val
				195					200					205	
Phe	Leu	Gly	Pro	Gly	Leu	Leu	Phe	Leu	Asp	Gln	Tyr	Phe	Asn	Asn	Phe
			210					215					220		
Ile	Asp	Glu	Tyr	Val	Val	Leu	Trp	Met	Ala	Met	Val	Ile	Ser	Ser	Phe
		225					230					235			
Asp	Met	Val	Ile	Tyr	Phe	Ser	Ala	Leu	Cys	Leu	Gln	Ile	Ser	Arg	His
		240				245					250				
Leu	His	Leu	Asn	Ile	Phe	Lys	Thr	Ala	Cys	His	Gln	Ala	Pro	Glu	Gln
255					260					265					270
Val	Gln	Val	Leu	Ser	Ser	Lys	Ser	His	Gln	Asn	Asn	Met	Asp		
				275					280						

```
<220>
<221> SIGNAL
<222> -14..-1
```

Met Ile Leu Val Thr Val Pro Gly Val Cys Pro Ala Gln Cys Cys Trp  
-10 -5 1  
Ala Glu Gln Arg Gly Arg Gly Ser Gly Met Tyr Phe Ile Asp Lys Trp  
5 10 15

Ala	Arg	Pro	Ser	Trp	Val	Pro	His	Trp	Leu	Asn	Asp	Leu	Phe	Ile	Val
20						25				30					
Lys	Ser	Gly	Tyr	Leu	Val	Cys	Ile	Arg	Thr	Thr	Val	Ile	Arg	Gln	Gly
35				40					45					50	
Ile	Val	Arg	Ile	Gly	Arg	Asn	Lys	Ile	Ser	Glu	Ser	Gly	Arg	Ser	Ala
			55					60					65		
Leu	Tyr	Thr	Ile	Ala	Lys	Asn	Lys	Met	Val	Ile	Phe	Lys	Val	Pro	Asp
		70					75					80			
Cys	Met	His	Leu	Asn	Ala	Asp	Tyr	Phe	Gly	Val					
	85						90								

<210> 351  
 <211> 229  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -34...-1

<400>	351														
Met	Ser	Phe	Leu	Gln	Asp	Pro	Ser	Phe	Phe	Thr	Met	Gly	Met	Trp	Ser
			-30					-25					-20		
Ile	Gly	Ala	Gly	Ala	Leu	Gly	Ala	Ala	Ala	Leu	Ala	Leu	Leu	Leu	Ala
		-15					-10					-5			
Asn	Thr	Asp	Val	Phe	Leu	Ser	Lys	Pro	Gln	Lys	Ala	Ala	Leu	Glu	Tyr
	1				5				10						
Leu	Glu	Asp	Ile	Asp	Leu	Lys	Thr	Leu	Glu	Lys	Glu	Pro	Arg	Thr	Phe
15				20					25					30	
Lys	Ala	Lys	Glu	Leu	Trp	Glu	Lys	Asn	Gly	Ala	Val	Ile	Met	Ala	Val
			35					40					45		
Arg	Arg	Pro	Gly	Cys	Phe	Leu	Cys	Arg	Glu	Glu	Ala	Ala	Asp	Leu	Ser
		50					55					60			
Ser	Leu	Lys	Ser	Met	Leu	Asp	Gln	Leu	Gly	Val	Pro	Leu	Tyr	Ala	Val
	65					70				75					
Val	Lys	Glu	His	Ile	Arg	Thr	Glu	Val	Lys	Asp	Phe	Gln	Pro	Tyr	Phe
	80				85					90					
Lys	Gly	Glu	Ile	Phe	Leu	Asp	Glu	Lys	Lys	Lys	Phe	Tyr	Gly	Pro	Gln
95					100				105					110	
Arg	Arg	Lys	Met	Met	Phe	Met	Gly	Phe	Ile	Arg	Leu	Gly	Val	Trp	Tyr
			115					120						125	
Asn	Phe	Phe	Arg	Ala	Trp	Asn	Gly	Gly	Phe	Ser	Gly	Asn	Leu	Glu	Gly
			130				135						140		
Glu	Gly	Phe	Ile	Leu	Gly	Gly	Val	Phe	Val	Val	Gly	Ser	Gly	Lys	Gln
		145				150						155			
Gly	Ile	Leu	Leu	Glu	His	Arg	Glu	Lys	Glu	Phe	Gly	Asp	Lys	Val	Asn
	160					165				170					
Leu	Leu	Ser	Val	Leu	Glu	Ala	Ala	Lys	Met	Ile	Lys	Pro	Gln	Thr	Leu
175					180					185					190
Ala	Ser	Glu	Lys	Lys											
				195											

<210> 352  
 <211> 206  
 <212> PRT  
 <213> Homo sapiens

<220>

<221> SIGNAL  
<222> -34...-1

<400> 352

Met	Ser	Phe	Leu	Gln	Asp	Pro	Ser	Phe	Phe	Thr	Met	Gly	Met	Trp	Ser
				-30					-25					-20	
Ile	Gly	Ala	Gly	Ala	Leu	Gly	Ala	Ala	Ala	Leu	Ala	Leu	Leu	Leu	Ala
			-15					-10					-5		
Asn	Thr	Asp	Val	Phe	Leu	Ser	Lys	Pro	Gln	Lys	Ala	Ala	Leu	Glu	Tyr
	1					5					10				
Leu	Glu	Asp	Ile	Asp	Leu	Lys	Thr	Leu	Glu	Lys	Glu	Pro	Arg	Thr	Phe
15					20					25					30
Lys	Ala	Lys	Glu	Leu	Trp	Glu	Lys	Asn	Gly	Ala	Val	Ile	Met	Ala	Val
				35					40					45	
Arg	Arg	Pro	Gly	Cys	Phe	Leu	Cys	Arg	Glu	Glu	Ala	Ala	Asp	Leu	Ser
			50					55					60		
Ser	Leu	Lys	Ser	Met	Leu	Asp	Gln	Leu	Gly	Val	Pro	Leu	Tyr	Ala	Val
		65					70					75			
Val	Lys	Glu	His	Ile	Arg	Thr	Glu	Val	Lys	Asp	Phe	Gln	Pro	Tyr	Phe
	80					85					90				
Lys	Gly	Glu	Ile	Phe	Leu	Asp	Glu	Lys	Lys	Lys	Phe	Tyr	Gly	Pro	Gln
95					100					105					110
Arg	Arg	Lys	Met	Met	Phe	Met	Gly	Phe	Ile	Arg	Leu	Gly	Val	Trp	Tyr
				115					120					125	
Asn	Phe	Phe	Arg	Ala	Trp	Asn	Gly	Gly	Phe	Ser	Gly	Asn	Leu	Glu	Gly
			130					135					140		
Glu	Gly	Phe	Ile	Leu	Gly	Gly	Val	Phe	Val	Val	Gly	Ser	Gly	Ser	Arg
		145				150					155				
Ala	Phe	Phe	Leu	Ser	Thr	Glu	Lys	Lys	Asn	Leu	Glu	Thr	Lys		
		160				165					170				

<210> 353  
<211> 88  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -44...-1

<400> 353

Met	Ala	Ala	Glu	Gly	Trp	Ile	Trp	Arg	Trp	Gly	Trp	Gly	Arg	Arg	Cys
				-40					-35					-30	
Leu	Gly	Arg	Pro	Gly	Leu	Leu	Gly	Pro	Gly	Pro	Gly	Pro	Thr	Thr	Pro
			-25					-20					-15		
Leu	Phe	Leu	Leu	Leu	Leu	Leu	Gly	Ser	Val	Thr	Ala	Asp	Ile	Thr	Asp
		-10					-5					1			
Gly	Asn	Ile	Glu	His	Leu	Lys	Arg	Glu	His	Ser	Leu	Ile	Lys	Pro	Tyr
5					10					15				20	
Gln	Gly	Val	Gly	Ser	Ser	Ser	Pro	Ser	Gly	Thr	Ser	Arg	Ala	Ala	Leu
				25					30					35	
Cys	Ser	Arg	Ala	Ser	Thr	Tyr	Val								
				40											

<210> 354  
<211> 151  
<212> PRT  
<213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -32...-1

<400> 354  
 Met Asp Ser Ala Ser Asn Pro Thr Asn Leu Val Ser Thr Ser Gln Arg  
           -30                              -25                              -20  
 His Arg Pro Leu Leu Ser Ser Cys Gly Leu Pro Pro Ser Thr Ala Ser  
           -15                              -10                              -5  
 Ala Val Arg Arg Leu Cys Ser Arg Gly Val Leu Lys Gly Ser Asn Glu  
  1                              5                              10                              15  
 Arg Arg Asp Met Glu Ser Phe Trp Lys Leu Asn Arg Ser Pro Gly Ser  
                               20                              25                              30  
 Asp Arg Tyr Leu Glu Ser Arg Asp Ala Ser Arg Leu Ser Gly Arg Asp  
                               35                              40                              45  
 Pro Ser Ser Trp Thr Val Glu Asp Val Met Gln Phe Val Arg Glu Ala  
                               50                              55                              60  
 Asp Pro Gln Leu Gly Pro His Ala Asp Leu Phe Arg Lys His Glu Ile  
  65                              70                              75                              80  
 Asp Gly Lys Ala Leu Leu Leu Arg Ser Asp Met Met Met Lys Tyr  
                               85                              90                              95  
 Met Gly Leu Lys Leu Gly Pro Ala Leu Lys Leu Ser Tyr His Ile Asp  
                               100                              105                              110  
 Arg Leu Lys Gln Gly Lys Phe  
                               115

<210> 355  
 <211> 65  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -16...-1

<400> 355  
 Met Ala Glu Leu Ala Cys Val Arg Glu Ser Thr Ser Val Ala Trp Ala  
           -15                              -10                              -5  
 Cys Lys Val Arg Gly Gly Thr Ala Pro Ser Pro Ser Gly Ala Glu Gly  
  1                              5                              10                              15  
 His Val Met Leu Asn Lys Ser Arg Glu Val Glu Ser Pro Val Ser Ser  
                               20                              25                              30  
 Arg Pro Arg Cys Gly Met Pro Thr Val Pro Pro Gly Ser Leu Lys Thr  
                               35                              40                              45  
 Leu

<210> 356  
 <211> 189  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -24...-1

<220>  
 <221> UNSURE







100 105 110 115  
 Leu Val Leu Cys Ser Val Lys Asn Gln Glu Arg Ile Leu Arg Glu Val  
 120 125 130  
 Cys Arg Val Leu Arg Pro Gly Gly Ala Phe Tyr Phe Met Glu His Val  
 135 140 145  
 Ala Ala Glu Cys Ser Thr Trp Asn Tyr Phe Trp Gln Gln Val Leu Asp  
 150 155 160  
 Pro Ala Trp His Leu Leu Phe Asp Gly Cys Asn Leu Thr Arg Glu Ser  
 165 170 175  
 Trp Lys Ala Leu Glu Arg Ala Ser Phe Ser Lys Leu Lys Leu Gln His  
 180 185 190 195  
 Ile Gln Ala Pro Leu Ser Trp Glu Leu Val Arg Pro His Ile Tyr Gly  
 200 205 210  
 Tyr Ala Val Lys  
 215

<210> 360  
 <211> 177  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -23...-1

<400> 360  
 Met Ser Asn Gln Arg Leu Pro Leu Ile Phe Ser Leu Leu Phe Ile Cys  
 -20 -15 -10  
 Phe Phe Gly Glu Ser Phe Cys Ile Cys Asp Gly Thr Val Trp Thr Lys  
 -5 1 5  
 Val Gly Trp Glu Ile Leu Pro Glu Glu Val His Tyr Trp Lys Val Lys  
 10 15 20 25  
 Gly Ser Pro Ser His Cys Leu Pro Tyr Leu Leu Asp Lys Leu Cys Cys  
 30 35 40  
 Asp Phe Ala Asn Met Asp Ile Phe Gln Gly Cys Leu Tyr Leu Ile Tyr  
 45 50 55  
 Asn Leu Leu Gln Ala Val Phe Phe Val Leu Phe Val Leu Ser Val His  
 60 65 70  
 Tyr Leu Trp Lys Lys Trp Lys Lys His Gln Lys Lys Leu Lys Lys Gln  
 75 80 85  
 Ala Ser Leu Glu Lys Pro Gly Asn Asp Leu Glu Ser Pro Leu Ile Asn  
 90 95 100 105  
 Asn Ile Asp Gln Thr Leu His Arg Val Ala Thr Thr Ala Ser Val Ile  
 110 115 120  
 Tyr Lys Ile Trp Glu His Arg Ser His His Pro Ser Ser Lys Lys Ile  
 125 130 135  
 Lys His Cys Lys Leu Lys Lys Lys Ser Lys Glu Glu Gly Ala Arg Arg  
 140 145 150  
 Tyr

<210> 361  
 <211> 158  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -21...-1



<210> 363  
 <211> 150  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -47...-1

<400> 363  
 Met Gly Asp Arg Val Lys Gly Ser Lys Ser Arg Ala Phe Val Ser Pro  
           -45                  -40                  -35  
 Trp Pro His Thr Pro Met Ala Ser Gly Leu Arg Asp Pro Trp Leu Gln  
           -30                  -25                  -20  
 Pro Thr Ala Leu Gly Leu Ala Leu Cys Ser Thr Lys Ala Leu Ser Val  
           -15                  -10                  -5                  1  
 Gly Ser Ala Pro Leu Pro Pro Arg Asn Ser Asn Thr Met Ala Ala Ala  
                   5                  10                  15  
 Ala Leu Ala Ala Pro Ser Leu Gly Phe Asp Gly Val Ile Gly Val Leu  
           20                  25                  30  
 Val Ala Asp Thr Ser Leu Thr Asp Met His Val Val Asp Val Glu Leu  
           35                  40                  45  
 Ser Gly Pro Arg Gly Pro Thr Gly Arg Ser Phe Ala Val His Thr Arg  
           50                  55                  60                  65  
 Arg Glu Asn Pro Ala Glu Pro Gly Ala Val Thr Gly Ser Ala Thr Val  
                   70                  75                  80  
 Thr Ala Phe Trp Arg Ser Leu Leu Ala Cys Cys Gln Leu Pro Ser Arg  
                   85                  90                  95  
 Pro Gly Ile His Leu Cys  
           100

<210> 364  
 <211> 95  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -45...-1

<400> 364  
 Met Leu His His Val Ile Thr Ala Gly Pro Val Leu Leu Leu His Leu  
           -45                  -40                  -35                  -30  
 Pro Arg Pro Asp Thr Ser Thr Arg Leu Leu Leu Thr Ser Val Ser Ala  
                   -25                  -20                  -15  
 Phe Ile Leu Leu Leu Leu Ser Gly Pro Ala Glu Met Ser Ala Ser  
                   -10                  -5                  1  
 Gln Glu Ser Phe Pro Gly Ser Leu Gln Gln Glu Ile Ala Ser Leu Ile  
           5                  10                  15  
 Thr Val Ala Leu Gly Ser Leu Ile Ser Leu Ser Cys Ser Thr Leu Leu  
           20                  25                  30                  35  
 Tyr Phe Ser Cys Glu Leu Lys Ile Pro Cys Glu Asp Val Asn Leu  
                   40                  45                  50

<210> 365  
 <211> 94  
 <212> PRT  
 <213> Homo sapiens

00076997-060804



Met Asp Pro Gly Trp Pro His Phe Lys Leu Thr His Ser Arg Cys Met  
 -35 -30 -25 -20  
 Ala Val Leu Phe Leu Gly Thr Leu Pro Leu Cys Pro Val Thr Ser Pro  
 -15 -10 -5  
 Val Trp Gly Trp Ser Pro Gly  
 1

<210> 368  
 <211> 78  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -41...-1

<400> 368  
 Met Ser Ala Ser Val Val Ser Val Ile Ser Arg Phe Leu Glu Glu Tyr  
 -40 -35 -30  
 Leu Ser Ser Thr Pro Gln Arg Leu Lys Leu Leu Asp Ala Tyr Leu Leu  
 -25 -20 -15 -10  
 Tyr Ile Leu Leu Thr Gly Ala Leu Gln Phe Gly Tyr Cys Leu Leu Val  
 -5 1 5  
 Gly Thr Phe Pro Phe Asn Ser Phe Leu Ser Gly Phe Ile Ser Cys Val  
 10 15 20  
 Gly Ser Phe Ile Leu Ala Gly Ser Leu Phe Glu Phe Pro Gly  
 25 30 35

<210> 369  
 <211> 83  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -40...-1

<400> 369  
 Met Gly Leu Thr Ser Thr Trp Arg Tyr Gly Arg Gly Pro Gly Ile Gly  
 -40 -35 -30 -25  
 Thr Val Thr Met Val Ser Trp Gly Arg Phe Ile Cys Leu Val Val Val  
 -20 -15 -10  
 Thr Met Ala Thr Leu Ser Leu Ala Arg Pro Ser Phe Ser Leu Val Glu  
 -5 1 5  
 Asp Thr Thr Leu Glu Pro Glu Asp Ala Ile Ser Ser Gly Asp Asp Glu  
 10 15 20  
 Asp Asp Thr Asp Gly Ala Glu Asp Phe Val Ser Glu Asn Ser Asn Asn  
 25 30 35 40  
 Lys Ser Lys

<210> 370  
 <211> 92  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -15...-1

<400> 370

Met Ala Val Leu Ala Gly Ser Leu Leu Gly Pro Thr Ser Arg Ser Ala  
 -15 -10 -5 1  
 Ala Leu Leu Gly Gly Arg Trp Leu Gln Pro Arg Ala Trp Leu Gly Phe  
 5 10 15  
 Pro Asp Ala Trp Gly Leu Pro Thr Pro Gln Gln Ala Arg Gly Lys Ala  
 20 25 30  
 Arg Gly Asn Glu Tyr Gln Pro Ser Asn Ile Lys Arg Lys Asn Lys His  
 35 40 45  
 Gly Trp Val Arg Arg Leu Ser Thr Pro Ala Gly Val Gln Val Ile Leu  
 50 55 60 65  
 Arg Arg Met Leu Lys Gly Arg Lys Ser Leu Ser His  
 70 75

<210> 371

<211> 279

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -42...-1

<400> 371

Met Ala Ala Pro Val Arg Arg Thr Leu Leu Gly Val Ala Gly Gly Trp  
 -40 -35 -30  
 Arg Arg Phe Glu Arg Leu Trp Ala Gly Ser Leu Ser Arg Ser Leu  
 -25 -20 -15  
 Ala Leu Ala Ala Ala Pro Ser Ser Asn Gly Ser Pro Trp Arg Leu Leu  
 -10 -5 1 5  
 Gly Ala Leu Cys Leu Gln Arg Pro Pro Val Val Ser Lys Pro Leu Thr  
 10 15 20  
 Pro Leu Gln Glu Glu Met Ala Ser Leu Leu Gln Gln Ile Glu Ile Glu  
 25 30 35  
 Arg Ser Leu Tyr Ser Asp His Glu Leu Arg Ala Leu Asp Glu Asn Gln  
 40 45 50  
 Arg Leu Ala Lys Lys Lys Ala Asp Leu His Asp Glu Glu Asp Glu Gln  
 55 60 65 70  
 Asp Ile Leu Leu Ala Gln Asp Leu Glu Asp Met Trp Glu Gln Lys Phe  
 75 80 85  
 Leu Gln Phe Lys Leu Gly Ala Arg Ile Thr Glu Ala Asp Glu Lys Asn  
 90 95 100  
 Asp Arg Thr Ser Leu Asn Arg Asn Leu Asp Arg Asn Leu Val Leu Leu  
 105 110 115  
 Val Arg Glu Lys Phe Gly Asp Gln Asp Val Trp Ile Leu Pro Gln Ala  
 120 125 130  
 Glu Trp Gln Pro Gly Glu Thr Leu Arg Gly Thr Ala Glu Arg Thr Leu  
 135 140 145 150  
 Ala Thr Leu Ser Glu Asn Asn Met Glu Ala Lys Phe Leu Gly Asn Ala  
 155 160 165  
 Pro Cys Gly His Tyr Thr Phe Lys Phe Pro Gln Ala Met Arg Thr Glu  
 170 175 180  
 Ser Asn Leu Gly Ala Lys Val Phe Phe Lys Ala Leu Leu Leu Thr  
 185 190 195  
 Gly Asp Phe Ser Gln Ala Gly Asn Lys Gly His His Val Trp Val Ile  
 200 205 210  
 Lys Asp Glu Leu Gly Asp Tyr Leu Lys Pro Lys Tyr Leu Ala Gln Val

215                      220                      225                      230  
 Arg Arg Phe Val Ser Asp Leu  
                          235

<210> 372  
 <211> 184  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -31...-1

<400> 372  
 Met Ala Cys Thr Thr Thr Ala Pro Ala Gln Glu His Met Leu Leu Thr  
          -30                      -25                      -20  
 Pro Leu Thr Ala Leu Met Val Gly Ala Ala Ser Leu Leu Glu Gly Arg  
          -15                      -10                      -5                      1  
 Pro Gln Ile Ser Ala Pro Tyr Ser Arg Ala Ala Cys Cys Ser Pro Gly  
                          5                      10                      15  
 Ala Leu Gly Cys Pro Ala Ala Arg Val Gly Ile Leu Asp Leu Met Tyr  
                          20                      25                      30  
 Ser Trp Val Ala Arg Lys Val Leu Arg Cys Ser Asn Thr Gly Leu Gln  
                          35                      40                      45  
 Gly Leu His Cys Ala Pro Ala Tyr Ala Ala Gln Leu Gly Met Asp Pro  
                          50                      55                      60                      65  
 Gly Arg Gly Gln Arg Ala Gly Gly Pro Val Glu Gln Thr Tyr Phe Ser  
    70                      75                      80  
 Pro Met Gly Lys Leu Pro Thr Leu Ser Trp Leu Glu Gly Cys Thr Ala  
    85                      90                      95  
 Val Met Thr Leu Ala Ser Ala Trp Leu Leu Gly Ser Pro Arg Glu Thr  
    100                      105                      110  
 Tyr Asn His Glu Lys Val Lys Glu Lys Gln Cys Pro Phe Ser Ser Met  
    115                      120                      125  
 Val Leu Gly Glu Tyr Gly Phe Leu Pro Thr Val Asp His Leu Ser Thr  
    130                      135                      140                      145  
 Leu Gly Cys Asn Met Arg Glu Leu  
    150

<210> 373  
 <211> 101  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -42...-1

<400> 373  
 Met Ala His Val Ala Glu Lys Asp Gly Leu Asp Trp Ala Ser Gly Cys  
          -40                      -35                      -30  
 Ile Pro Gly Leu Gln Thr Gly Ile Cys Leu Phe Gly Ser Gln Leu Cys  
          -25                      -20                      -15  
 Phe His Leu Ser Trp Leu Tyr Ser Trp Ala Ser Gln Cys Gly Pro Thr  
          -10                      -5                      1                      5  
 Ala Pro Val Ile Asp Lys Lys Ser Ser Pro Leu Leu Thr Glu Leu Leu  
    10                      15                      20  
 Asp Leu Val Leu Ile Gly Pro Asp Glu Glu Gly Ile Gln Pro Gln Val

25 30 35  
 Ile Ile Val Ala Arg Lys Met Glu Tyr Thr Lys Trp Thr Gly Leu Ala  
 40 45 50  
 Cys Thr His Arg Asp  
 55

<210> 374  
 <211> 85  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -20...-1

<400> 374  
 Met Gly Pro Asn Thr Lys Asn Leu Leu Leu Val Thr Leu Val Ala Ser  
 -20 -15 -10 -5  
 Thr Val Pro Gly Asn Ser Leu Gly Gln Asp Phe Thr Phe Ala His Leu  
 1 5 10  
 Glu Arg Ser Cys Thr Arg Glu Asn Arg Ser Pro Gly Glu Val Phe Gln  
 15 20 25  
 Gln Pro Cys Lys Ser Gly Gly Gly Gly Val Gly Glu Pro Asn Ala Gln  
 30 35 40  
 Gly Gln Leu Leu Ser Gln His Pro Leu Pro Ala Phe Ile Asn Cys Ser  
 45 50 55 60  
 His Gly Gln Ala Phe  
 65

<210> 375  
 <211> 90  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -28...-1

<400> 375  
 Met Ala Phe Pro Gly Gln Ser Asp Thr Lys Met Gln Trp Pro Glu Val  
 -25 -20 -15  
 Pro Ala Leu Pro Leu Leu Ser Ser Leu Cys Met Ala Met Val Arg Lys  
 -10 -5 1  
 Ser Ser Ala Leu Gly Lys Glu Val Gly Arg Arg Val Lys Glu Met Val  
 5 10 15 20  
 Met Leu Val Ala Pro Phe Arg Gln Ser Ser Ser Leu Ser Arg Thr Phe  
 25 30 35  
 Ser Ser Arg Lys Val Val Lys Ala His Ala Ser Leu His Gly Ala Arg  
 40 45 50  
 Leu Ser Pro Leu Ser Arg Asn Ile Arg Gly  
 55 60

<210> 376  
 <211> 89  
 <212> PRT  
 <213> Homo sapiens

<220>



<221> SIGNAL  
<222> -33...-1

<220>  
<221> UNSURE  
<222> 47  
<223> Xaa = Ala,Pro,Ser,Thr

<400> 376  
Met Ala Gln Pro Ala Ala Pro Ser Leu Thr Arg Pro Phe Leu Ala Glu  
                  -30                  -25                  -20  
Ala Pro Thr Ala Leu Val Pro His Ser Pro Leu Pro Gly Ala Leu Ser  
                  -15                  -10                  -5  
Ser Ala Pro Gly Pro Lys Gln Pro Pro Thr Ala Ser Thr Gly Pro Glu  
          1                  5                  10                  15  
Leu Leu Leu Leu Pro Leu Ser Ser Phe Met Pro Cys Gly Ala Ala Ala  
                  20                  25                  30  
Pro Ala Arg Val Ser Ser Gln Arg Ala Thr Pro Arg Asp Lys Pro Xaa  
                  35                  40                  45  
Gly Pro Leu Ile Pro Gly Gln Cys Pro  
          50                  55

<210> 377  
<211> 132  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -15...-1

<400> 377  
Met Asn Arg Val Leu Cys Ala Pro Ala Ala Gly Ala Val Arg Ala Leu  
-15                  -10                  -5                  1  
Arg Leu Ile Gly Trp Ala Ser Arg Ser Leu His Pro Leu Pro Gly Ser  
          5                  10                  15  
Arg Asp Arg Ala His Pro Ala Ala Glu Glu Glu Asp Asp Pro Asp Arg  
          20                  25                  30  
Pro Ile Glu Phe Ser Ser Ser Lys Ala Asn Pro His Arg Trp Ser Val  
          35                  40                  45  
Gly His Thr Met Gly Lys Gly His Gln Arg Pro Trp Trp Lys Val Leu  
50                  55                  60                  65  
Pro Leu Ser Cys Phe Leu Val Ala Leu Ile Trp Cys Tyr Leu Arg  
                  70                  75                  80  
Glu Glu Ser Glu Ala Asp Gln Trp Leu Arg Gln Val Trp Gly Glu Val  
          85                  90                  95  
Pro Glu Pro Ser Asp Arg Ser Glu Glu Pro Glu Thr Pro Ala Ala Tyr  
          100                  105                  110  
Arg Ala Arg Thr  
          115

<210> 378  
<211> 102  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL

<222> -14...-1

<220>

<221> UNSURE

<222> 50

<223> Xaa = Ala,Gly

<220>

<221> UNSURE

<222> 51

<223> Xaa = Leu,Met,Val

<400> 378

Met Phe Leu Thr Ala Leu Leu Trp Arg Gly Arg Ile Pro Gly Arg Gln  
                    -10                    -5                    1  
Trp Ile Gly Lys His Arg Arg Pro Arg Phe Val Ser Leu Arg Ala Lys  
          5                    10                    15  
Gln Asn Met Ile Arg Arg Leu Glu Ile Asp Ala Glu Asn His Tyr Trp  
      20                    25                    30  
Leu Ser Met Pro Tyr Met Thr Arg Glu Gln Glu Arg Gly His Ala Xaa  
35                    40                    45                    50  
Xaa Arg Arg Arg Glu Ala Phe Glu Ala Ile Lys Ala Ala Ala Thr Ser  
          55                    60                    65  
Lys Phe Pro Pro His Arg Phe Ile Ala Asp Gln Leu Asp His Leu Asn  
          70                    75                    80  
Val Thr Lys Lys Trp Ser  
          85

<210> 379

<211> 504

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -24...-1

<400> 379

Met Gly Ile Lys Thr Ala Leu Pro Ala Ala Glu Leu Gly Leu Tyr Ser  
                    -20                    -15                    -10  
Leu Val Leu Ser Gly Ala Leu Ala Tyr Ala Gly Arg Gly Leu Leu Glu  
          -5                    1                    5  
Ala Ser Gln Asp Gly Ala His Arg Lys Ala Phe Arg Glu Ser Val Arg  
      10                    15                    20  
Pro Gly Trp Glu Tyr Ile Gly Arg Lys Met Asp Val Ala Asp Phe Glu  
25                    30                    35                    40  
Trp Val Met Trp Phe Thr Ser Phe Arg Asn Val Ile Ile Phe Ala Leu  
          45                    50                    55  
Ser Gly His Val Leu Phe Ala Lys Leu Cys Thr Met Val Ala Pro Lys  
          60                    65                    70  
Leu Arg Ser Trp Met Tyr Ala Val Tyr Gly Ala Leu Ala Val Met Gly  
      75                    80                    85  
Thr Met Gly Pro Trp Tyr Leu Leu Leu Leu Leu Gly His Cys Val Gly  
      90                    95                    100  
Leu Tyr Val Ala Ser Leu Leu Gly Gln Pro Trp Leu Cys Leu Gly Leu  
105                    110                    115                    120  
Gly Leu Ala Ser Leu Ala Ser Phe Lys Met Asp Pro Leu Ile Ser Trp  
          125                    130                    135

Gln Ser Gly Phe Val Thr Gly Thr Phe Asp Leu Gln Glu Val Leu Phe  
 140 145 150  
 His Gly Gly Ser Ser Phe Thr Val Leu Arg Cys Thr Ser Phe Ala Leu  
 155 160 165  
 Glu Ser Cys Ala His Pro Asp Arg His Tyr Ser Leu Ala Asp Leu Leu  
 170 175 180  
 Lys Tyr Ser Phe Tyr Leu Pro Phe Phe Phe Phe Gly Pro Ile Met Thr  
 185 190 195 200  
 Phe Asp Arg Phe His Ala Gln Val Ser Gln Val Glu Pro Val Arg Arg  
 205 210 215  
 Glu Gly Glu Leu Trp His Ile Arg Ala Gln Ala Gly Leu Ser Val Val  
 220 225 230  
 Ala Ile Met Ala Val Asp Ile Phe Phe His Phe Phe Tyr Ile Leu Thr  
 235 240 245  
 Ile Pro Ser Asp Leu Lys Phe Ala Asn Arg Leu Pro Asp Ile Ala Leu  
 250 255 260  
 Ala Gly Leu Ala Tyr Ser Asn Leu Val Tyr Asp Trp Val Lys Ala Ala  
 265 270 275 280  
 Val Leu Phe Gly Val Val Asn Thr Val Ala Cys Leu Asp His Leu Asp  
 285 290 295  
 Pro Pro Gln Pro Pro Lys Cys Ile Thr Ala Leu Tyr Val Phe Ala Glu  
 300 305 310  
 Thr His Phe Asp Arg Gly Ile Asn Asp Trp Leu Cys Lys Tyr Val Tyr  
 315 320 325  
 Asn His Ile Gly Gly Glu His Ser Ala Val Ile Pro Glu Leu Ala Ala  
 330 335 340  
 Thr Val Ala Thr Phe Ala Ile Thr Thr Leu Trp Leu Gly Pro Cys Asp  
 345 350 355 360  
 Ile Val Tyr Leu Trp Ser Phe Leu Asn Cys Phe Gly Leu Asn Phe Glu  
 365 370 375  
 Leu Trp Met Gln Lys Leu Ala Glu Trp Gly Pro Leu Ala Arg Ile Glu  
 380 385 390  
 Ala Ser Leu Ser Val Gln Met Ser Arg Arg Val Arg Ala Leu Phe Gly  
 395 400 405  
 Ala Met Asn Phe Trp Ala Ile Ile Met Tyr Asn Leu Val Ser Leu Asn  
 410 415 420  
 Ser Leu Lys Phe Thr Glu Leu Val Ala Arg Arg Leu Leu Leu Thr Gly  
 425 430 435 440  
 Phe Pro Gln Thr Thr Leu Ser Ile Leu Phe Val Thr Tyr Cys Gly Val  
 445 450 455  
 Gln Leu Val Lys Glu Arg Glu Arg Thr Leu Ala Leu Glu Glu Glu Gln  
 460 465 470  
 Lys Gln Asp Lys Glu Lys Pro Glu  
 475 480

<210> 380

<211> 152

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -26...-1

<400> 380

Met Val Thr Phe Pro Asp Val Pro Leu Gly Ile Phe Leu Phe Cys Val  
 -25 -20 -15  
 Cys Val Ile Ala Ile Gly Val Val Gln Ala Leu Ile Val Gly Tyr Ala



<210> 383  
 <211> 95  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -48...-1

<400> 383  
 Met Ala Ser Ser His Trp Asn Glu Thr Thr Thr Ser Val Tyr Gln Tyr  
                   -45                  -40                  -35  
 Leu Gly Phe Gln Val Gln Lys Ile Tyr Pro Phe His Asp Asn Trp Asn  
                   -30                  -25                  -20  
 Thr Ala Cys Phe Val Ile Leu Leu Leu Phe Ile Phe Thr Val Val Ser  
                   -15                  -10                  -5  
 Leu Val Val Leu Ala Phe Leu Tyr Glu Val Leu Asp Cys Cys Cys Cys  
 1                  5                  10                  15  
 Val Lys Asn Lys Thr Val Lys Asp Leu Lys Ser Glu Pro Asn Pro Leu  
                   20                  25                  30  
 Arg Ser Met Met Asp Asn Ile Arg Lys Arg Glu Thr Glu Val Val  
                   35                  40                  45

<210> 384  
 <211> 150  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -20...-1

<400> 384  
 Met Ala Arg His Gly Leu Pro Leu Leu Pro Leu Leu Ser Leu Leu Val  
 -20                  -15                  -10                  -5  
 Gly Ala Trp Leu Lys Leu Gly Asn Gly Gln Ala Thr Ser Met Val Gln  
                   1                  5                  10  
 Leu Gln Gly Gly Arg Phe Leu Met Gly Thr Asn Ser Pro Asp Ser Arg  
                   15                  20                  25  
 Asp Gly Glu Gly Pro Val Arg Glu Ala Thr Val Lys Pro Phe Ala Ile  
 30                  35                  40  
 Asp Ile Phe Pro Val Thr Asn Lys Asp Phe Arg Asp Phe Val Arg Glu  
 45                  50                  55                  60  
 Lys Lys Tyr Arg Thr Glu Ala Glu Met Phe Gly Trp Ser Phe Val Phe  
                   65                  70                  75  
 Glu Asp Phe Val Ser Asp Glu Leu Arg Asn Lys Ala Thr Gln Pro Met  
                   80                  85                  90  
 Lys Val Lys Phe Thr His Gly Gly Thr Gly Ser Ser Gln Thr Ala Pro  
                   95                  100                  105  
 Thr Cys Gly Arg Glu Ser Ser Pro Arg Glu Thr Lys Leu Arg Met Ala  
 110                  115                  120  
 Ser Met Glu Ser Pro Gln  
 125                  130

<210> 385  
 <211> 354  
 <212> PRT  
 <213> Homo sapiens

<400> 385

Met Ser Ala Gly Gly Gly Arg Ala Phe Ala Trp Gln Val Phe Pro Pro  
1 5 10 15  
Met Pro Thr Cys Arg Val Tyr Gly Thr Val Ala His Gln Asp Gly His  
20 25 30  
Leu Leu Val Leu Gly Gly Cys Gly Arg Ala Gly Leu Pro Leu Asp Thr  
35 40 45  
Ala Glu Thr Leu Asp Met Ala Ser His Thr Trp Leu Ala Leu Ala Pro  
50 55 60  
Leu Pro Thr Ala Arg Ala Gly Ala Ala Val Val Leu Gly Lys Gln  
65 70 75 80  
Val Leu Val Val Cys Gly Val Asp Glu Val Gln Ser Pro Val Ala Ala  
85 90 95  
Val Glu Ala Phe Leu Met Asp Glu Gly Arg Trp Glu Arg Arg Ala Thr  
100 105 110  
Leu Pro Gln Ala Ala Met Gly Val Ala Thr Val Glu Arg Asp Gly Met  
115 120 125  
Val Tyr Ala Leu Gly Gly Met Gly Pro Asp Thr Ala Pro Gln Ala Gln  
130 135 140  
Val Arg Val Tyr Asp Pro Arg Arg Asp Cys Trp Leu Ser Leu Pro Ser  
145 150 155 160  
Met Pro Thr Pro Cys Tyr Gly Ala Ser Thr Phe Leu His Gly Asn Lys  
165 170 175  
Ile Tyr Val Leu Gly Gly Arg Gln Gly Lys Leu Pro Val Thr Ala Phe  
180 185 190  
Glu Ala Phe Asp Leu Glu Ala Arg Thr Trp Thr Arg His Pro Ser Leu  
195 200 205  
Pro Ser Arg Arg Ala Phe Ala Gly Cys Ala Met Ala Glu Gly Ser Val  
210 215 220  
Phe Ser Leu Gly Gly Leu Gln Gln Pro Gly Pro His Asn Phe Tyr Ser  
225 230 235 240  
Arg Pro His Phe Val Asn Thr Val Glu Met Phe Asp Leu Glu His Gly  
245 250 255  
Ser Trp Thr Lys Leu Pro Arg Ser Leu Arg Met Arg Asp Lys Arg Ala  
260 265 270  
Asp Phe Val Val Gly Ser Leu Gly Gly His Ile Val Ala Ile Gly Gly  
275 280 285  
Leu Gly Asn Gln Pro Cys Pro Leu Gly Ser Val Glu Ser Phe Ser Leu  
290 295 300  
Ala Arg Arg Arg Trp Glu Ala Leu Pro Ala Met Pro Thr Ala Arg Cys  
305 310 315 320  
Ser Cys Ser Ser Leu Gln Ala Gly Pro Arg Leu Phe Val Ile Gly Gly  
325 330 335  
Val Ala Gln Gly Pro Ser Gln Ala Val Glu Ala Leu Cys Leu Arg Asp  
340 345 350  
Gly Val

<210> 386

<211> 207

<212> PRT

<213> Homo sapiens

<400> 386

Met Ala Leu Leu Phe Ala Arg Ser Leu Arg Leu Cys Arg Trp Gly Ala  
1 5 10 15  
Lys Arg Leu Gly Val Ala Ser Thr Glu Ala Gln Arg Gly Val Ser Phe  
20 25 30

Lys Leu Glu Glu Lys Thr Ala His Ser Ser Leu Ala Leu Phe Arg Asp  
 35 40 45  
 Asp Thr Gly Val Lys Tyr Gly Leu Val Gly Leu Glu Pro Thr Lys Val  
 50 55 60  
 Ala Leu Asn Val Glu Arg Phe Arg Glu Trp Ala Val Val Leu Ala Asp  
 65 70 75 80  
 Thr Ala Val Thr Ser Gly Arg His Tyr Trp Glu Val Thr Val Lys Arg  
 85 90 95  
 Ser Gln Gln Phe Arg Ile Gly Val Ala Asp Val Asp Met Ser Arg Asp  
 100 105 110  
 Ser Cys Ile Gly Val Asp Asp Arg Ser Trp Val Phe Thr Tyr Ala Gln  
 115 120 125  
 Arg Lys Trp Tyr Thr Met Leu Ala Asn Glu Lys Ala Pro Val Glu Gly  
 130 135 140  
 Ile Gly Gln Pro Glu Lys Val Gly Leu Leu Leu Glu Tyr Glu Ala Gln  
 145 150 155 160  
 Lys Leu Ser Leu Val Asp Val Ser Gln Val Ser Val Val His Thr Leu  
 165 170 175  
 Gln Thr Asp Phe Arg Gly Pro Val Val Pro Ala Phe Ala Leu Trp Asp  
 180 185 190  
 Gly Glu Leu Leu Thr His Ser Gly Leu Glu Val Pro Glu Gly Leu  
 195 200 205

<210> 387

<211> 210

<212> PRT

<213> Homo sapiens

<400> 387

Met Ala Ala Ser Val Glu Gln Arg Glu Gly Thr Ile Gln Val Gln Gly  
 1 5 10 15  
 Gln Ala Leu Phe Phe Arg Glu Ala Leu Pro Gly Ser Gly Gln Ala Arg  
 20 25 30  
 Phe Ser Val Leu Leu Leu His Gly Ile Arg Phe Ser Ser Glu Thr Trp  
 35 40 45  
 Gln Asn Leu Gly Thr Leu His Arg Leu Ala Gln Ala Gly Tyr Arg Ala  
 50 55 60  
 Val Ala Ile Asp Leu Pro Gly Leu Gly His Ser Lys Glu Ala Ala Ala  
 65 70 75 80  
 Pro Ala Pro Ile Gly Glu Leu Ala Pro Gly Ser Phe Leu Ala Ala Val  
 85 90 95  
 Val Asp Ala Leu Glu Leu Gly Pro Pro Val Val Ile Ser Pro Ser Leu  
 100 105 110  
 Ser Gly Met Tyr Ser Leu Pro Phe Leu Thr Ala Pro Gly Ser Gln Leu  
 115 120 125  
 Pro Gly Phe Val Pro Val Ala Pro Ile Cys Thr Asp Lys Ile Asn Ala  
 130 135 140  
 Ala Asn Tyr Ala Ser Val Lys Thr Pro Ala Leu Ile Val Tyr Gly Asp  
 145 150 155 160  
 Gln Asp Pro Met Gly Gln Thr Ser Phe Glu His Leu Lys Gln Leu Pro  
 165 170 175  
 Asn His Arg Val Leu Ile Met Lys Gly Ala Gly His Pro Cys Tyr Leu  
 180 185 190  
 Asp Lys Pro Glu Glu Trp His Thr Gly Leu Leu Asp Phe Leu Gln Gly  
 195 200 205  
 Leu Gln  
 210

<210> 388  
 <211> 375  
 <212> PRT  
 <213> Homo sapiens

<400> 388

```

Met Ala Val Thr Glu Ala Ser Leu Leu Arg Gln Cys Pro Leu Leu Leu
1          5          10          15
Pro Gln Asn Arg Ser Lys Thr Val Tyr Glu Gly Phe Ile Ser Ala Gln
          20          25          30
Gly Arg Asp Phe His Leu Arg Ile Val Leu Pro Glu Asp Leu Gln Leu
          35          40          45
Lys Asn Ala Arg Leu Leu Cys Ile Trp Gln Leu Arg Thr Ile Leu Ser
          50          55          60
Gly Tyr His Arg Ile Val Gln Gln Arg Met Gln His Ser Pro Asp Leu
65          70          75          80
Met Ser Phe Met Met Glu Leu Lys Met Leu Leu Glu Val Ala Leu Lys
          85          90          95
Asn Arg Gln Glu Leu Tyr Ala Leu Pro Pro Pro Gln Phe Tyr Ser
          100          105          110
Ser Leu Ile Glu Glu Ile Gly Thr Leu Gly Trp Asp Lys Leu Val Tyr
          115          120          125
Ala Asp Thr Cys Phe Ser Thr Ile Lys Leu Lys Ala Glu Asp Ala Ser
          130          135          140
Gly Arg Glu His Leu Ile Thr Leu Lys Leu Lys Ala Lys Tyr Pro Ala
145          150          155          160
Glu Ser Pro Asp Tyr Phe Val Asp Phe Pro Val Pro Phe Cys Ala Ser
          165          170          175
Trp Thr Pro Gln Ser Ser Leu Ile Ser Ile Tyr Ser Gln Phe Leu Ala
          180          185          190
Ala Ile Glu Ser Leu Lys Ala Phe Trp Asp Val Met Asp Glu Ile Asp
          195          200          205
Glu Lys Thr Trp Val Leu Glu Pro Glu Lys Pro Pro Arg Ser Ala Thr
          210          215          220
Ala Arg Arg Ile Ala Leu Gly Asn Asn Val Ser Ile Asn Ile Glu Val
225          230          235          240
Asp Pro Arg His Pro Thr Met Leu Pro Glu Cys Phe Phe Leu Gly Ala
          245          250          255
Asp His Val Val Lys Pro Leu Gly Ile Lys Leu Ser Arg Asn Ile His
          260          265          270
Leu Trp Asp Pro Glu Asn Ser Val Leu Gln Asn Leu Lys Asp Val Leu
          275          280          285
Glu Ile Asp Phe Pro Ala Arg Ala Ile Leu Glu Lys Ser Asp Phe Thr
          290          295          300
Met Asp Cys Gly Ile Cys Tyr Ala Tyr Gln Leu Asp Gly Thr Ile Pro
305          310          315          320
Asp Gln Val Cys Asp Asn Ser Gln Cys Gly Gln Pro Phe His Gln Ile
          325          330          335
Cys Leu Tyr Glu Trp Leu Arg Gly Leu Leu Thr Ser Arg Gln Ser Phe
          340          345          350
Asn Ile Ile Phe Gly Glu Cys Pro Tyr Cys Ser Lys Pro Ile Thr Leu
          355          360          365
Lys Met Ser Gly Arg Lys His
          370          375

```

<210> 389  
 <211> 509  
 <212> PRT



<213> Homo sapiens

<400> 389

```

Met Ala Ala Ile Gly Val His Leu Gly Cys Thr Ser Ala Cys Val Ala
1      5      10      15
Val Tyr Lys Asp Gly Arg Ala Gly Val Val Ala Asn Asp Ala Gly Asp
      20      25      30
Arg Val Thr Pro Ala Val Val Ala Tyr Ser Glu Asn Glu Glu Ile Val
      35      40      45
Gly Leu Ala Ala Lys Gln Ser Arg Ile Arg Asn Ile Ser Asn Thr Val
      50      55      60
Met Lys Val Lys Gln Ile Leu Gly Arg Ser Ser Ser Asp Pro Gln Ala
      65      70      75      80
Gln Lys Tyr Ile Ala Glu Ser Lys Cys Leu Val Ile Glu Lys Asn Gly
      85      90      95
Lys Leu Arg Tyr Glu Ile Asp Thr Gly Glu Glu Thr Lys Phe Val Asn
      100      105      110
Pro Glu Asp Val Ala Arg Leu Ile Phe Ser Lys Met Lys Glu Thr Ala
      115      120      125
His Ser Val Leu Gly Ser Asp Ala Asn Asp Val Val Ile Thr Val Pro
      130      135      140
Phe Asp Phe Gly Glu Lys Gln Lys Asn Ala Leu Gly Glu Ala Ala Arg
      145      150      155      160
Ala Ala Gly Phe Asn Val Leu Arg Leu Ile His Glu Pro Ser Ala Ala
      165      170      175
Leu Leu Ala Tyr Gly Ile Gly Gln Asp Ser Pro Thr Gly Lys Ser Asn
      180      185      190
Ile Leu Val Phe Lys Leu Gly Gly Thr Ser Leu Ser Leu Ser Val Met
      195      200      205
Glu Val Asn Ser Gly Ile Tyr Arg Val Leu Ser Thr Asn Thr Asp Asp
      210      215      220
Asn Ile Gly Gly Ala His Phe Thr Glu Thr Leu Ala Gln Tyr Leu Ala
      225      230      235      240
Ser Glu Phe Gln Arg Ser Phe Lys His Asp Val Arg Gly Asn Ala Arg
      245      250      255
Ala Met Met Lys Leu Thr Asn Ser Ala Glu Val Ala Lys His Ser Leu
      260      265      270
Ser Thr Leu Gly Ser Ala Asn Cys Phe Leu Asp Ser Leu Tyr Glu Gly
      275      280      285
Gln Asp Phe Asp Cys Asn Val Ser Arg Ala Arg Phe Glu Leu Leu Cys
      290      295      300
Ser Pro Leu Phe Asn Lys Cys Ile Glu Ala Ile Arg Gly Leu Leu Asp
      305      310      315      320
Gln Asn Gly Phe Thr Thr Asp Asp Ile Asn Lys Val Val Leu Cys Gly
      325      330      335
Gly Ser Ser Arg Ile Pro Lys Leu Gln Leu Ile Lys Asp Leu Phe
      340      345      350
Pro Ala Val Glu Leu Leu Asn Ser Ile Pro Pro Asp Glu Val Ile Pro
      355      360      365
Ile Gly Ala Ala Ile Glu Ala Gly Ile Leu Ile Gly Lys Glu Asn Leu
      370      375      380
Leu Val Glu Asp Ser Leu Met Ile Glu Cys Ser Ala Arg Asp Ile Leu
      385      390      395      400
Val Lys Gly Val Asp Glu Ser Gly Ala Ser Arg Phe Thr Val Leu Phe
      405      410      415
Pro Ser Gly Thr Pro Leu Pro Ala Arg Gln His Thr Leu Gln Ala
      420      425      430
Pro Gly Ser Ile Ser Ser Val Cys Leu Glu Leu Tyr Glu Ser Asp Gly

```

435 440 445  
 Lys Asn Ser Ala Lys Glu Glu Thr Lys Phe Ala Gln Val Val Leu Gln  
 450 455 460  
 Asp Leu Asp Lys Lys Glu Asn Gly Leu Arg Asp Ile Leu Ala Val Leu  
 465 470 475 480  
 Thr Met Lys Arg Asp Gly Ser Leu His Val Thr Cys Thr Asp Gln Glu  
 485 490 495  
 Thr Gly Lys Cys Glu Ala Ile Ser Ile Glu Ile Ala Ser  
 500 505

<210> 390  
 <211> 78  
 <212> PRT  
 <213> Homo sapiens

<400> 390  
 Met Tyr Asn Thr Gly Arg His Val Ser Leu Arg Leu Asp Lys Glu His  
 1 5 10 15  
 Leu Val Asn Ile Ser Gly Gly Pro Met Thr Tyr Ser His Arg Leu Glu  
 20 25 30  
 Glu Ile Arg Leu His Phe Gly Ser Glu Asp Ser Gln Gly Ser Glu His  
 35 40 45  
 Leu Leu Asn Gly Gln Ala Phe Ser Gly Glu Leu Gln Glu Arg Asp Leu  
 50 55 60  
 Phe Ile Leu Leu Thr Ser Val Ser Gly His Leu Pro Asp Thr  
 65 70 75

<210> 391  
 <211> 162  
 <212> PRT  
 <213> Homo sapiens

<400> 391  
 Met Ala Thr His Ala Leu Glu Ile Ala Gly Leu Phe Leu Gly Gly Val  
 1 5 10 15  
 Gly Met Val Gly Thr Val Ala Val Thr Val Met Pro Gln Trp Ile Val  
 20 25 30  
 Ser Ala Phe Ile Glu Asn Asn Ile Val Val Phe Glu Asn Phe Trp Glu  
 35 40 45  
 Gly Leu Trp Met Asn Cys Val Arg Gln Ala Asn Ile Arg Met Gln Cys  
 50 55 60  
 Lys Ile Tyr Asp Ser Leu Leu Ala Leu Ser Pro Asp Leu Gln Ala Ala  
 65 70 75 80  
 Arg Gly Leu Met Cys Ala Ala Ser Val Met Ser Phe Leu Ala Phe Met  
 85 90 95  
 Met Ala Ile Leu Gly Met Lys Cys Thr Arg Cys Thr Gly Asp Asn Glu  
 100 105 110  
 Lys Val Lys Ala His Ile Leu Leu Thr Ala Gly Ile Ile Phe Ile Ile  
 115 120 125  
 Thr Gly Met Val Val Leu Ile Pro Val Ser Trp Val Ala Asn Ala Ile  
 130 135 140  
 Ile Arg Asp Phe Tyr Asn Pro Ile Val Asn Val Ala Gln Lys Arg Glu  
 145 150 155 160  
 Leu Gly

<210> 392  
 <211> 146  
 <212> PRT

<213> Homo sapiens

<400> 392

```

Met Asn Ser Leu Leu His Phe Gly Ile Leu Leu Glu Leu Ser Leu Leu
1          5          10          15
Lys Gln Phe Lys Ser Val Tyr Val Pro Gly Asn His Thr His Gln Ala
20          25          30
Ser Tyr Lys Pro Leu Leu Lys Gln Val Val Glu Glu Ile Phe His Pro
35          40          45
Glu Arg Pro Asp Ser Val Asp Ile Glu His Met Ser Ser Gly Leu Thr
50          55          60
Asp Leu Leu Lys Thr Gly Phe Ser Met Phe Met Lys Val Ser Arg Pro
65          70          75          80
His Pro Ser Asp Tyr Pro Leu Leu Ile Leu Phe Val Val Gly Gly Val
85          90          95
Thr Val Ser Glu Val Lys Met Val Lys Asp Leu Val Ala Ser Leu Lys
100          105          110
Pro Gly Thr Gln Val Ile Val Leu Ser Thr Arg Leu Leu Lys Pro Leu
115          120          125
Asn Ile Pro Glu Leu Leu Phe Ala Thr Asp Arg Leu His Pro Asp Leu
130          135          140
Gly Phe
145

```

<210> 393

<211> 225

<212> PRT

<213> Homo sapiens

<400> 393

```

Met Ala Thr His Ala Leu Glu Ile Ala Gly Leu Phe Leu Gly Gly Val
1          5          10          15
Gly Met Val Gly Thr Val Ala Val Thr Val Met Pro Gln Trp Arg Val
20          25          30
Ser Ala Phe Ile Glu Asn Asn Ile Val Val Phe Glu Asn Phe Trp Glu
35          40          45
Gly Leu Trp Met Asn Cys Val Arg Gln Ala Asn Ile Arg Met Gln Cys
50          55          60
Lys Ile Tyr Asp Ser Leu Ala Leu Ser Pro Asp Leu Gln Ala Ala
65          70          75          80
Arg Gly Leu Met Cys Ala Ala Ser Val Met Ser Phe Leu Ala Phe Met
85          90          95
Met Ala Ile Leu Gly Met Lys Cys Thr Arg Cys Thr Gly Asp Asn Glu
100          105          110
Lys Val Lys Ala His Ile Leu Leu Thr Ala Gly Ile Ile Phe Ile Ile
115          120          125
Ala Gly Met Val Val Leu Ile Pro Val Ser Trp Val Ala Asn Ala Ile
130          135          140
Ile Arg Asp Phe Tyr Asn Pro Ile Val Asn Val Ala Gln Lys Arg Glu
145          150          155          160
Leu Gly Glu Ala Leu Tyr Leu Gly Trp Thr Thr Ala Leu Val Leu Ile
165          170          175
Val Gly Gly Ala Leu Phe Cys Cys Val Phe Cys Cys Asn Glu Lys Ser
180          185          190
Ser Ser Tyr Arg Tyr Ser Ile Pro Ser His Arg Thr Thr Gln Lys Ser
195          200          205
Tyr His Thr Gly Lys Lys Ser Pro Ser Val Tyr Ser Arg Ser Gln Tyr
210          215          220

```

Val  
225

<210> 394  
<211> 114  
<212> PRT  
<213> Homo sapiens

<400> 394  
Met Arg Leu Gln Asp Arg Ile Ala Thr Phe Phe Phe Pro Lys Gly Met  
1 5 10 15  
Met Leu Thr Thr Ala Ala Leu Met Leu Phe Phe Leu His Leu Gly Ile  
20 25 30  
Phe Ile Arg Asp Val His Asn Phe Cys Ile Thr Tyr His Tyr Asp His  
35 40 45  
Met Ser Phe His Tyr Thr Val Val Leu Met Phe Ser Gln Val Ile Ser  
50 55 60  
Ile Cys Trp Ala Ala Met Gly Ser Leu Tyr Ala Glu Met Thr Glu Asn  
65 70 75 80  
Asn Ala Gln Arg Ser His Val Leu Gln Pro Pro Val Leu Gly Val Ser  
85 90 95  
Gly His Arg Val Pro Gly Gly Ala Pro Leu Arg Pro Gly Glu Ser Glu  
100 105 110  
Gln Gly

<210> 395  
<211> 367  
<212> PRT  
<213> Homo sapiens

<400> 395  
Met Ala Thr Pro Asn Asn Leu Thr Pro Thr Asn Cys Ser Trp Trp Pro  
1 5 10 15  
Ile Ser Ala Leu Glu Ser Asp Ala Ala Lys Pro Ala Glu Ala Pro Asp  
20 25 30  
Ala Pro Glu Ala Ala Ser Pro Ala His Trp Pro Arg Glu Ser Leu Val  
35 40 45  
Leu Tyr His Trp Thr Gln Ser Phe Ser Ser Gln Lys Val Arg Leu Val  
50 55 60  
Ile Ala Glu Lys Gly Leu Val Cys Glu Glu Arg Asp Val Ser Leu Pro  
65 70 75 80  
Gln Ser Glu His Lys Glu Pro Trp Phe Met Arg Leu Asn Leu Gly Glu  
85 90 95  
Glu Val Pro Val Ile Ile His Arg Asp Asn Ile Ile Ser Asp Tyr Asp  
100 105 110  
Gln Ile Ile Asp Tyr Val Glu Arg Thr Phe Thr Gly Glu His Val Val  
115 120 125  
Ala Leu Met Pro Glu Val Gly Ser Leu Gln His Ala Arg Val Leu Gln  
130 135 140  
Tyr Arg Glu Leu Leu Asp Ala Leu Pro Met Asp Ala Tyr Thr His Gly  
145 150 155 160  
Cys Ile Leu His Pro Glu Leu Thr Thr Asp Ser Met Ile Pro Lys Tyr  
165 170 175  
Ala Thr Ala Glu Ile Arg Arg His Leu Ala Asn Ala Thr Thr Asp Leu  
180 185 190  
Met Lys Leu Asp His Glu Glu Glu Pro Gln Leu Ser Glu Pro Tyr Leu  
195 200 205  
Ser Lys Gln Lys Lys Leu Met Val Lys Ile Leu Glu His Asp Asp Val

210	215	220
Ser Tyr Leu Lys Lys Ile Leu Gly Glu Leu Ala Met Val Leu Asp Gln		
225	230	235
Ile Glu Ala Glu Leu Glu Lys Arg Lys Leu Glu Asn Glu Gly Gln Lys		240
	245	250
Cys Glu Leu Trp Leu Cys Gly Cys Ala Phe Thr Leu Ala Asp Val Leu		255
	260	265
Leu Gly Ala Thr Leu His Arg Leu Lys Phe Leu Gly Leu Ser Lys Lys		270
	275	280
Tyr Trp Glu Asp Gly Ser Arg Pro Asn Leu Gln Ser Phe Phe Glu Arg		285
	290	295
Val Gln Arg Arg Phe Ala Phe Arg Lys Val Leu Gly Asp Ile His Thr		300
305	310	315
Thr Leu Leu Ser Ala Val Ile Pro Asn Ala Phe Arg Leu Val Lys Arg		320
	325	330
Lys Pro Pro Ser Phe Phe Gly Ala Ser Phe Leu Met Gly Ser Leu Gly		335
	340	345
Gly Met Gly Tyr Phe Ala Tyr Trp Tyr Leu Lys Lys Lys Tyr Ile		350
	355	360
		365

<210> 396  
 <211> 279  
 <212> PRT  
 <213> Homo sapiens

<400> 396

Met Pro Val Cys Ala Pro Val Leu Trp Arg Ala Arg Arg Leu Cys Gly	
1	5
Met Pro Val Cys Ala Pro Val Pro Trp Arg Ala Arg Arg Leu Cys Thr	
	10
	15
Arg Ala Val Val Cys Pro Ser Ser Val Pro Phe Ile Ala Gly Gln Gly	
	20
	25
	30
Cys Thr His Met Cys Lys Pro Ala Thr Asp Pro Arg Phe Thr Arg Ser	
	35
	40
	45
Pro Leu Ala Gly Gly Val Ile Leu Gly Val Ala Leu Trp Leu Arg His	
65	70
	75
Asp Pro Gln Thr Thr Asn Leu Leu Tyr Leu Glu Leu Gly Asp Lys Pro	
	80
	85
	90
	95
Ala Pro Asn Thr Phe Tyr Val Gly Ile Tyr Ile Leu Ile Ala Val Gly	
	100
	105
	110
Ala Val Met Met Phe Val Gly Phe Leu Gly Cys Tyr Gly Ala Ile Gln	
	115
	120
	125
Glu Ser Gln Cys Leu Leu Gly Thr Phe Phe Thr Cys Leu Val Ile Leu	
	130
	135
	140
Phe Ala Cys Glu Val Ala Ala Gly Ile Trp Gly Phe Val Asn Lys Asp	
145	150
	155
Gln Ile Ala Lys Asp Val Lys Gln Phe Tyr Asp Gln Ala Leu Gln Gln	
	160
	165
	170
	175
Ala Val Val Asp Asp Ala Asn Asn Ala Lys Ala Val Val Lys Thr	
	180
	185
	190
Phe His Glu Thr Leu Asp Cys Cys Gly Ser Ser Thr Leu Thr Ala Leu	
	195
	200
	205
Thr Thr Ser Val Leu Lys Asn Asn Leu Cys Pro Ser Gly Ser Asn Ile	
	210
	215
	220
Ile Ser Asn Leu Phe Lys Glu Asp Cys His Gln Lys Ile Asp Asp Leu	
225	230
	235
Phe Ser Gly Lys Leu Tyr Leu Ile Gly Ile Ala Ala Ile Val Val Ala	
	240
	245
	250
	255

Val Ile Met Ile Phe Glu Met Ile Leu Ser Met Val Leu Cys Cys Gly  
 260 265 270  
 Ile Arg Asn Ser Ser Val Tyr  
 275

<210> 397  
 <211> 173  
 <212> PRT  
 <213> Homo sapiens

<400> 397  
 Met Cys Leu Leu Leu Gly Ala Thr Gly Val Gly Lys Thr Leu Leu Val  
 1 5 10 15  
 Lys Arg Leu Gln Glu Val Ser Ser Arg Asp Gly Lys Gly Asp Leu Gly  
 20 25 30  
 Glu Pro Pro Pro Thr Arg Pro Thr Val Gly Thr Asn Leu Thr Asp Ile  
 35 40 45  
 Val Ala Gln Arg Lys Ile Thr Ile Arg Glu Leu Gly Gly Cys Met Gly  
 50 55 60  
 Pro Ile Trp Ser Ser Tyr Tyr Gly Asn Cys Arg Ser Leu Leu Phe Val  
 65 70 75 80  
 Met Asp Ala Ser Asp Pro Thr Gln Leu Ser Ala Ser Cys Val Gln Leu  
 85 90 95  
 Leu Gly Leu Leu Ser Ala Glu Gln Leu Ala Glu Ala Ser Val Leu Ile  
 100 105 110  
 Leu Phe Asn Lys Ile Asp Leu Pro Cys Tyr Met Ser Thr Glu Glu Met  
 115 120 125  
 Lys Ser Leu Ile Arg Leu Pro Asp Ile Ile Ala Cys Ala Lys Gln Asn  
 130 135 140  
 Ile Thr Thr Ala Glu Ile Ser Ala Arg Glu Gly Thr Gly Leu Ala Gly  
 145 150 155 160  
 Val Leu Ala Trp Leu Gln Ala Thr His Arg Ala Asn Asp  
 165 170

<210> 398  
 <211> 205  
 <212> PRT  
 <213> Homo sapiens

<400> 398  
 Met Ala Ala Ala Arg Pro Ser Leu Gly Arg Val Leu Pro Gly Ser Ser  
 1 5 10 15  
 Val Leu Phe Leu Cys Asp Met Gln Glu Lys Phe Arg His Asn Ile Ala  
 20 25 30  
 Tyr Phe Pro Gln Ile Val Ser Val Ala Ala Arg Met Leu Lys Val Ala  
 35 40 45  
 Arg Leu Leu Glu Val Pro Val Met Leu Thr Glu Gln Tyr Pro Gln Gly  
 50 55 60  
 Leu Gly Pro Thr Val Pro Glu Leu Gly Thr Glu Gly Leu Arg Pro Leu  
 65 70 75 80  
 Ala Lys Thr Cys Phe Ser Met Val Pro Ala Leu Gln Gln Glu Leu Asp  
 85 90 95  
 Ser Arg Pro Gln Leu Arg Ser Val Leu Leu Cys Gly Ile Glu Ala Gln  
 100 105 110  
 Ala Cys Ile Leu Asn Thr Thr Leu Asp Leu Leu Asp Arg Gly Leu Gln  
 115 120 125  
 Val His Val Val Val Asp Ala Cys Ser Ser Arg Ser Gln Val Asp Arg  
 130 135 140

Leu Val Ala Leu Ala Arg Met Arg Gln Ser Gly Ala Phe Leu Ser Thr  
 145 150 155 160  
 Ser Glu Gly Leu Ile Leu Gln Leu Val Gly Asp Ala Val His Pro Gln  
 165 170 175  
 Phe Lys Glu Ile Gln Lys Leu Ile Lys Glu Pro Ala Pro Asp Ser Gly  
 180 185 190  
 Leu Leu Gly Leu Phe Gln Gly Gln Asn Ser Leu Leu His  
 195 200 205

<210> 399  
 <211> 180  
 <212> PRT  
 <213> Homo sapiens

<400> 399  
 Met Trp Leu Tyr Arg Asn Pro Tyr Val Glu Ala Glu Tyr Phe Pro Thr  
 1 5 10 15  
 Lys Pro Met Phe Val Ile Ala Phe Leu Ser Pro Leu Ser Leu Ile Phe  
 20 25 30  
 Leu Ala Lys Phe Leu Lys Lys Ala Asp Thr Arg Asp Ser Arg Gln Ala  
 35 40 45  
 Cys Leu Ala Ala Ser Leu Ala Leu Ala Leu Asn Gly Val Phe Thr Asn  
 50 55 60  
 Thr Ile Lys Leu Ile Val Gly Arg Pro Arg Pro Asp Phe Phe Tyr Arg  
 65 70 75 80  
 Cys Phe Pro Asp Gly Leu Ala His Ser Asp Leu Met Cys Thr Gly Asp  
 85 90 95  
 Lys Asp Val Val Asn Glu Gly Arg Lys Ser Phe Pro Ser Gly His Ser  
 100 105 110  
 Ser Phe Ala Phe Ala Gly Leu Ala Phe Ala Ser Phe Tyr Leu Ala Gly  
 115 120 125  
 Lys Leu His Cys Phe Thr Pro Gln Gly Arg Gly Lys Ser Trp Arg Phe  
 130 135 140  
 Cys Ala Phe Leu Ser Pro Leu Leu Phe Ala Ala Val Ile Ala Leu Ser  
 145 150 155 160  
 Arg Thr Cys Asp Tyr Lys His His Trp Gln Asp Leu Leu Lys Cys Thr  
 165 170 175  
 Asn Thr Ala Lys  
 180

<210> 400  
 <211> 150  
 <212> PRT  
 <213> Homo sapiens

<400> 400  
 Met Cys Thr Ala Leu Leu Leu Tyr Leu Arg Trp Cys Phe Asn Leu  
 1 5 10 15  
 Lys Leu Val Asn Val Lys Tyr Glu Pro Lys Asp Ser Leu Gly Pro Glu  
 20 25 30  
 Met Thr Phe Val Ala Asp Ala Ala Arg Gly Pro Leu Leu Ser Ser Leu  
 35 40 45  
 Asp Ser Pro Ala Asn Leu Met Ser Thr Ala Ser Val Cys Ile Ser Leu  
 50 55 60  
 Pro Glu Gly Cys Ser Gly Gly Arg Ser Pro Cys Tyr Ser Gln Lys Trp  
 65 70 75 80  
 Pro Pro Glu Val Pro Glu Lys Leu Thr Ser Leu Gly Gln Gln Ser Ser  
 85 90 95





Cys	Pro	Asp	Cys	Gly	Lys	Thr	Phe	Gly	Gln	Ala	Val	Ser	Leu	Arg	Arg
		115					120					125			
His	Arg	Gln	Met	His	Glu	Val	Arg	Ala	Pro	Pro	Gly	Thr	Phe	Ala	Cys
	130					135					140				
Thr	Glu	Cys	Gly	Gln	Asp	Phe	Ala	Gln	Glu	Ala	Gly	Leu	His	Gln	His
145					150					155					160
Tyr	Ile	Arg	His	Ala	Arg	Gly	Glu	Leu							
				165											

<210> 403

<211> 367

<212> PRT

<213> Homo sapiens

<400> 403

Met	Ala	Thr	Pro	Asn	Asn	Leu	Thr	Pro	Thr	Asn	Cys	Ser	Trp	Trp	Pro
1				5					10					15	
Ile	Ser	Ala	Leu	Glu	Ser	Asp	Ala	Ala	Lys	Pro	Ala	Glu	Ala	Pro	Asp
		20					25					30			
Ala	Pro	Glu	Ala	Ala	Ser	Pro	Ala	His	Trp	Pro	Arg	Glu	Ser	Leu	Val
	35					40					45				
Leu	Tyr	His	Trp	Thr	Gln	Ser	Phe	Ser	Ser	Gln	Lys	Val	Arg	Leu	Val
	50					55					60				
Ile	Ala	Glu	Lys	Gly	Leu	Val	Cys	Glu	Glu	Arg	Asp	Val	Ser	Leu	Pro
65					70					75					80
Gln	Ser	Glu	His	Lys	Glu	Pro	Trp	Phe	Met	Arg	Leu	Asn	Leu	Gly	Glu
				85					90					95	
Glu	Val	Pro	Val	Ile	Ile	His	Arg	Asp	Asn	Ile	Ile	Ser	Asp	Tyr	Asp
		100						105					110		
Gln	Ile	Ile	Asp	Tyr	Val	Glu	Arg	Thr	Phe	Thr	Gly	Glu	His	Val	Val
		115					120					125			
Ala	Leu	Met	Pro	Glu	Val	Gly	Ser	Leu	Gln	His	Ala	Arg	Val	Leu	Gln
	130					135					140				
Tyr	Arg	Glu	Leu	Leu	Asp	Ala	Leu	Pro	Met	Asp	Ala	Tyr	Thr	His	Gly
145					150					155					160
Cys	Ile	Leu	His	Leu	Glu	Leu	Thr	Thr	Asp	Ser	Met	Ile	Pro	Lys	Tyr
				165					170					175	
Ala	Thr	Ala	Glu	Ile	Arg	Arg	His	Leu	Ala	Asn	Ala	Thr	Thr	Asp	Leu
		180						185					190		
Met	Lys	Leu	Asp	His	Glu	Glu	Glu	Pro	Gln	Leu	Ser	Glu	Pro	Tyr	Leu
	195						200					205			
Ser	Lys	Gln	Lys	Lys	Leu	Met	Ala	Lys	Ile	Leu	Glu	His	Asp	Asp	Val
	210					215					220				
Ser	Tyr	Leu	Lys	Lys	Ile	Leu	Gly	Glu	Leu	Ala	Met	Val	Leu	Asp	Gln
225					230					235					240
Ile	Glu	Ala	Glu	Leu	Glu	Lys	Arg	Lys	Leu	Glu	Asn	Glu	Gly	Gln	Lys
				245					250					255	
Cys	Glu	Leu	Trp	Leu	Cys	Gly	Cys	Ala	Phe	Thr	Leu	Ala	Asp	Val	Leu
		260						265					270		
Leu	Gly	Ala	Thr	Leu	His	Arg	Leu	Lys	Phe	Leu	Gly	Leu	Ser	Lys	Lys
	275						280					285			
Tyr	Trp	Glu	Asp	Gly	Ser	Arg	Pro	Asn	Leu	Gln	Ser	Phe	Phe	Glu	Arg
	290					295					300				
Val	Gln	Arg	Arg	Phe	Ala	Phe	Arg	Lys	Val	Leu	Gly	Asp	Ile	His	Thr
305					310					315					320
Thr	Leu	Leu	Ser	Ala	Val	Ile	Pro	Asn	Ala	Phe	Arg	Leu	Val	Lys	Arg
				325					330					335	
Lys	Pro	Pro	Ser	Phe	Phe	Gly	Ala	Ser	Phe	Leu	Met	Gly	Ser	Leu	Gly



Met Asp Pro Gly Asp Asp Trp Leu Val Glu Ser Leu Arg Leu Tyr Gln  
1 5 10 15  
Asp Phe Tyr Ala Phe Asp Leu Ser Gly Ala Thr Arg Val Leu Glu Trp  
20 25 30  
Ile Asp Asp Lys Gly Val Phe Val Ala Gly Tyr Glu Ser Leu Lys Lys  
35 40 45  
Asn Glu Ile Leu His Leu Lys Leu Pro Leu Arg Leu Ser Val Lys Glu  
50 55 60  
Asn Lys Gly Leu Phe Pro Glu Arg Asp Phe Lys Val Arg His Gly Gly  
65 70 75 80  
Phe Ser Asp Arg Ser Ile Phe Asp Leu Lys His Val Pro His Thr Arg  
85 90 95  
Leu Leu Val Thr Ser Gly Leu Pro Gly Cys Tyr Leu Gln Val Trp Gln  
100 105 110  
Val Ala Glu Asp Ser Asp Val Ile Lys Ala Val Ser Thr Ile Ala Val  
115 120 125  
His Glu Lys Glu Glu Ser Leu Trp Pro Arg Val Ala Val Phe Ser Thr  
130 135 140  
Leu Ala Pro Gly Val Leu His Gly Ala Arg Leu Arg Ser Leu Gln Val  
145 150 155 160  
Val Asp Leu Glu Ser Arg Lys Thr Thr Tyr Thr Ser Asp Val Ser Asp  
165 170 175  
Ser Glu Glu Leu Ser Ser Leu Gln Val Leu Asp Ala Asp Thr Phe Ala  
180 185 190  
Phe Cys Cys Ala Ser Gly Arg Leu Gly Leu Val Asp Thr Arg Gln Lys  
195 200 205  
Trp Ala Pro Leu Glu Asn Arg Ser Pro Gly Pro Gly Ser Gly Gly Glu  
210 215 220  
Arg Trp Cys Ala Glu Val Gly Ser Trp Gly Gln Gly Pro Gly Pro Ser  
225 230 235 240  
Ile Ala Ser Leu Ser Ser Asp Gly Arg Leu Cys Leu Leu Asp Pro Arg  
245 250 255  
Asp Leu Cys His Pro Val Ser Ser Val Gln Cys Pro Val Ser Val Pro  
260 265 270  
Ser Pro Asp Pro Glu Leu Leu Arg Val Thr Trp Ala Pro Gly Leu Lys  
275 280 285  
Asn Cys Leu Ala Ile Ser Gly Phe Asp Gly Thr Val Gln Val Tyr Asp  
290 295 300  
Ala Thr Ser Trp Asp Gly Thr Arg Ser Gln Asp Gly Thr Arg Ser Gln  
305 310 315 320  
Val Glu Pro Leu Phe Thr His Arg Gly His Ile Phe Leu Asp Gly Asn  
325 330 335  
Gly Met Asp Pro Ala Pro Leu Val Thr Thr His Thr Trp His Pro Cys  
340 345 350  
Arg Pro Arg Thr Leu Leu Ser Ala Thr Asn Asp Ala Ser Leu His Val  
355 360 365  
Trp Asp Trp Val Asp Leu Cys Ala Pro Arg  
370 375

<210> 407

<211> 43

<212> PRT

<213> Homo sapiens

<400> 407

Met Ala Thr His Ala Leu Glu Ile Ala Gly Leu Phe Leu Gly Gly Val  
1 5 10 15  
Gly Met Val Gly Thr Val Ala Val Thr Val Met Pro Gln Trp Arg Val

[illegible]

<400>	408														
Met	Ala	Trp	Arg	Gly	Trp	Ala	Gln	Arg	Gly	Trp	Gly	Cys	Gly	Gln	Ala
1				5					10					15	
Trp	Gly	Ala	Ser	Val	Gly	Gly	Arg	Ser	Cys	Glu	Glu	Leu	Thr	Ala	Val
			20					25					30		
Leu	Thr	Pro	Gln	Leu	Leu	Gly	Arg	Arg	Phe	Asn	Phe	Ile	Gln		
		35				40					45				
Gln	Lys	Cys	Gly	Phe	Arg	Lys	Ala	Pro	Arg	Lys	Val	Glu	Pro	Arg	Arg
	50					55					60				
Ser	Asp	Pro	Gly	Thr	Ser	Gly	Glu	Ala	Tyr	Lys	Arg	Ser	Ala	Leu	Ile
65					70					75					80
Pro	Pro	Val	Glu	Glu	Thr	Val	Phe	Tyr	Pro	Ser	Pro	Tyr	Pro	Ile	Arg
				85					90					95	
Ser	Leu	Ile	Lys	Pro	Leu	Phe	Phe	Thr	Val	Gly	Phe	Thr	Gly	Cys	Ala
			100					105					110		
Phe	Gly	Ser	Ala	Ala	Ile	Trp	Gln	Tyr	Glu	Ser	Leu	Lys	Ser	Arg	Val
		115					120					125			
Gln	Ser	Tyr	Phe	Asp	Gly	Ile	Lys	Ala	Asp	Trp	Leu	Asp	Ser	Ile	Arg
	130				135						140				
Pro	Gln	Lys	Glu	Gly	Asp	Phe	Arg	Lys	Glu	Ile	Asn	Lys	Trp	Trp	Asn
145				150						155					160
Asn	Leu	Ser	Asp	Gly	Gln	Arg	Thr	Val	Thr	Gly	Ile	Ile	Ala	Ala	Asn
				165					170					175	
Val	Leu	Val	Phe	Cys	Leu	Trp	Arg	Val	Pro	Ser	Leu	Gln	Arg	Thr	Met
			180					185					190		
Ile	Arg	Tyr	Phe	Thr	Ser	Asn	Pro	Ala	Ser	Lys	Val	Leu	Cys	Ser	Pro
		195				200						205			
Met	Leu	Leu	Ser	Thr	Phe	Ser	His	Phe	Ser	Leu	Phe	His	Met	Ala	Ala
	210					215					220				
Asn	Met	Tyr	Val	Leu	Trp	Ser	Phe	Ser	Ser	Ser	Ile	Val	Asn	Ile	Leu
225				230						235					240
Gly	Gln	Glu	Gln	Phe	Met	Ala	Val	Tyr	Leu	Ser	Ala	Gly	Val	Ile	Ser
				245					250					255	
Asn	Phe	Val	Ser	Tyr	Val	Gly	Lys	Val	Ala	Thr	Gly	Arg	Tyr	Gly	Pro
			260				265						270		
Ser	Leu	Gly	Ala	Ala	Leu	Lys	Ala	Ile	Ile	Ala	Met	Asp	Thr	Ala	Gly
		275					280					285			
Met	Ile	Leu	Gly	Trp	Lys	Phe	Phe	Asp	His	Ala	Ala	His	Leu	Gly	Gly
	290					295					300				
Ala	Leu	Phe	Gly	Ile	Trp	Tyr	Val	Thr	Tyr	Gly	His	Glu	Leu	Ile	Trp
305				310						315					320
Lys	Asn	Arg	Glu	Pro	Leu	Val	Lys	Ile	Trp	His	Glu	Ile	Arg	Thr	Asn
				325					330					335	
Gly	Pro	Lys	Lys	Gly	Gly	Gly	Ser	Lys							
			340					345							

361

<213> Homo sapiens

<400> 409

Met	Lys	Arg	Ser	Gly	Asn	Pro	Gly	Ala	Glu	Val	Thr	Asn	Ser	Ser	Val
1				5					10					15	
Ala	Gly	Pro	Asp	Cys	Cys	Gly	Gly	Leu	Gly	Asn	Ile	Asp	Phe	Arg	Gln
			20					25					30		
Ala	Asp	Phe	Cys	Val	Met	Thr	Arg	Leu	Leu	Gly	Tyr	Val	Asp	Pro	Leu
		35					40					45			
Asp	Pro	Ser	Phe	Val	Ala	Ala	Val	Ile	Thr	Ile	Thr	Phe	Asn	Pro	Leu
	50					55					60				
Tyr	Trp	Asn	Val	Val	Ala	Arg	Trp	Glu	His	Lys	Thr	Arg	Lys	Leu	Ser
65					70					75				80	
Arg	Ala	Phe	Gly	Ser	Pro	Tyr	Leu	Ala	Cys	Tyr	Ser	Leu	Ser	Ile	Thr
				85					90					95	
Ile	Leu	Leu	Leu	Asn	Phe	Leu	Arg	Ser	His	Cys	Phe	Thr	Gln	Ala	Met
			100					105					110		
Leu	Ser	Gln	Pro	Arg	Met	Glu	Ser	Leu	Asp	Thr	Pro	Ala	Ala	Tyr	Ser
		115					120					125			
Leu	Val	Leu	Ala	Leu	Leu	Gly	Leu	Gly	Val	Val	Leu	Val	Leu	Ser	Ser
	130					135					140				
Phe	Phe	Ala	Leu	Gly	Phe	Ala	Gly	Thr	Phe	Leu	Gly	Asp	Tyr	Phe	Gly
145					150					155					160
Ile	Leu	Lys	Glu	Ala	Arg	Val	Thr	Val	Phe	Pro	Phe	Asn	Ile	Leu	Asp
				165					170					175	
Asn	Pro	Met	Tyr	Trp	Gly	Ser	Thr	Ala	Asn	Tyr	Leu	Gly	Trp	Ala	Ile
			180					185					190		
Met	His	Ala	Ser	Pro	Thr	Gly	Leu	Leu	Leu	Thr	Val	Leu	Val	Ala	Leu
		195					200					205			
Thr	Tyr	Ile	Val	Ala	Leu	Leu	Tyr	Glu	Glu	Pro	Phe	Thr	Ala	Glu	Ile
	210					215					220				
Tyr	Arg	Gln	Lys	Ala	Ser	Gly	Ser	His	Lys	Arg	Ser				
225					230					235					

<210> 410

<211> 121

<212> PRT

<213> Homo sapiens

<400> 410

Met	Asn	Thr	Glu	Ala	Glu	Gln	Gln	Leu	Leu	His	His	Ala	Arg	Asn	Gly
1				5					10					15	
Asn	Ala	Glu	Glu	Val	Arg	Gln	Leu	Leu	Glu	Thr	Met	Ala	Ser	Asn	Glu
			20					25					30		
Val	Ile	Ala	Asp	Ile	Asn	Cys	Lys	Gly	Arg	Ser	Lys	Ser	Asn	Leu	Gly
		35					40					45			
Trp	Thr	Pro	Leu	His	Leu	Ala	Cys	Tyr	Phe	Gly	His	Arg	Gln	Val	Val
	50					55					60				
Gln	Asp	Leu	Leu	Lys	Ala	Gly	Ala	Glu	Val	Asn	Val	Leu	Asn	Asp	Met
65					70					75				80	
Gly	Asp	Thr	Pro	Leu	His	Arg	Ala	Ala	Phe	Thr	Gly	Arg	Lys	Val	Lys
				85					90					95	
Ile	Ile	Leu	Cys	Ser	Met	Phe	Val	Ser	Glu	Val	Phe	Gly	Gly	Val	Val
			100					105					110		
Thr	Ile	Val	Phe	Ser	Val	Ile	Thr	Ile							
		115					120								

<210> 411

<211> 170  
 <212> PRT  
 <213> Homo sapiens

<400> 411  
 Met Arg Leu Gln Gly Ala Ile Phe Val Leu Leu Pro His Leu Gly Pro  
 1 5 10 15  
 Ile Leu Val Trp Leu Phe Thr Arg Asp His Met Ser Gly Trp Cys Glu  
 20 25 30  
 Gly Pro Arg Met Leu Ser Trp Cys Pro Phe Tyr Lys Val Leu Leu Leu  
 35 40 45  
 Val Gln Thr Ala Ile Tyr Ser Val Val Gly Tyr Ala Ser Tyr Leu Val  
 50 55 60  
 Trp Lys Asp Leu Gly Gly Gly Leu Gly Trp Pro Leu Ala Leu Pro Leu  
 65 70 75 80  
 Gly Leu Tyr Ala Val Gln Leu Thr Ile Ser Trp Thr Val Leu Val Leu  
 85 90 95  
 Phe Phe Thr Val His Asn Pro Gly Leu Ala Leu Leu His Leu Leu Leu  
 100 105 110  
 Leu Tyr Gly Leu Val Val Ser Thr Ala Leu Ile Trp His Pro Ile Asn  
 115 120 125  
 Lys Leu Ala Ala Leu Leu Leu Leu Pro Tyr Leu Ala Trp Leu Thr Val  
 130 135 140  
 Thr Ser Ala Leu Thr Tyr His Leu Trp Arg Asp Ser Leu Cys Pro Val  
 145 150 155 160  
 His Gln Pro Gln Pro Thr Glu Lys Ser Asp  
 165 170

<210> 412  
 <211> 236  
 <212> PRT  
 <213> Homo sapiens

<400> 412  
 Met Leu Ser Lys Gly Leu Lys Arg Lys Arg Glu Glu Glu Glu Glu Lys  
 1 5 10 15  
 Glu Pro Leu Ala Val Asp Ser Trp Trp Leu Asp Pro Gly His Thr Ala  
 20 25 30  
 Val Ala Gln Ala Pro Pro Ala Val Ala Ser Ser Ser Leu Phe Asp Leu  
 35 40 45  
 Ser Val Leu Lys Leu His His Ser Leu Gln Gln Ser Glu Pro Asp Leu  
 50 55 60  
 Arg His Leu Val Leu Val Val Asn Thr Leu Arg Arg Ile Gln Ala Ser  
 65 70 75 80  
 Met Ala Pro Ala Ala Ala Leu Pro Pro Val Pro Ser Pro Pro Ala Ala  
 85 90 95  
 Pro Ser Val Ala Asp Asn Leu Leu Ala Ser Ser Asp Ala Ala Leu Ser  
 100 105 110  
 Ala Ser Met Ala Ser Leu Leu Glu Asp Leu Ser His Ile Glu Gly Leu  
 115 120 125  
 Ser Gln Ala Pro Gln Pro Leu Ala Asp Glu Gly Pro Pro Gly Arg Ser  
 130 135 140  
 Ile Gly Gly Ala Ala Pro Ser Leu Gly Ala Leu Asp Leu Leu Gly Pro  
 145 150 155 160  
 Ala Thr Gly Cys Leu Leu Asp Asp Gly Leu Glu Gly Leu Phe Glu Asp  
 165 170 175  
 Ile Asp Thr Ser Met Tyr Asp Asn Glu Leu Trp Ala Pro Ala Ser Glu  
 180 185 190

Gly Leu Lys Pro Gly Pro Glu Asp Gly Pro Gly Lys Glu Glu Ala Pro  
 195 200 205  
 Glu Leu Asp Glu Ala Glu Leu Asp Tyr Leu Met Asp Val Leu Val Gly  
 210 215 220  
 Thr Gln Ala Leu Glu Arg Pro Pro Gly Pro Gly Arg  
 225 230 235

<210> 413  
 <211> 191  
 <212> PRT  
 <213> Homo sapiens

<400> 413  
 Met Lys Gly Leu Tyr Phe Gln Gln Ser Ser Thr Asp Glu Glu Ile Thr  
 1 5 10 15  
 Phe Val Phe Gln Glu Lys Glu Asp Leu Pro Val Thr Glu Asp Asn Phe  
 20 25 30  
 Val Lys Leu Gln Val Lys Ala Cys Ala Leu Ser Gln Ile Asn Thr Lys  
 35 40 45  
 Leu Leu Ala Glu Met Lys Met Lys Lys Asp Leu Phe Pro Val Gly Arg  
 50 55 60  
 Glu Ile Ala Gly Ile Val Leu Asp Val Gly Ser Lys Val Ser Phe Phe  
 65 70 75 80  
 Gln Pro Asp Asp Glu Val Val Gly Ile Leu Pro Leu Asp Ser Glu Asp  
 85 90 95  
 Pro Gly Leu Cys Glu Val Val Arg Val His Glu His Tyr Leu Val His  
 100 105 110  
 Lys Pro Glu Lys Val Thr Trp Thr Glu Ala Ala Gly Ser Ile Arg Asp  
 115 120 125  
 Gly Val Arg Ala Tyr Thr Ala Leu His Tyr Leu Ser His Leu Ser Pro  
 130 135 140  
 Gly Lys Ser Val Leu Ile Met Asp Gly Ala Ser Ala Phe Gly Thr Ile  
 145 150 155 160  
 Ala Ile Gln Leu Ala His His Arg Gly Ala Lys Val Phe Gln Gln His  
 165 170 175  
 Ala Ala Leu Lys Ile Ser Ser Ala Leu Lys Asp Ser Asp Leu Pro  
 180 185 190

<210> 414  
 <211> 389  
 <212> PRT  
 <213> Homo sapiens

<400> 414  
 Met Ala Glu Pro Asp Pro Ser His Pro Leu Glu Thr Gln Ala Gly Lys  
 1 5 10 15  
 Val Gln Glu Ala Gln Asp Ser Asp Ser Asp Ser Glu Gly Gly Ala Ala  
 20 25 30  
 Gly Gly Glu Ala Asp Met Asp Phe Leu Arg Asn Leu Phe Ser Gln Thr  
 35 40 45  
 Leu Ser Leu Gly Ser Gln Lys Glu Arg Leu Leu Asp Glu Leu Thr Leu  
 50 55 60  
 Glu Gly Val Ala Arg Tyr Met Gln Ser Glu Arg Cys Arg Arg Val Ile  
 65 70 75 80  
 Cys Leu Val Gly Ala Gly Ile Ser Thr Ser Ala Gly Ile Pro Asp Phe  
 85 90 95  
 Arg Ser Pro Ser Thr Gly Leu Tyr Asp Asn Leu Glu Lys Tyr His Leu  
 100 105 110

Pro Tyr Pro Glu Ala Ile Phe Glu Ile Ser Tyr Phe Lys Lys His Pro  
 115 120 125  
 Glu Pro Phe Phe Ala Leu Ala Lys Glu Leu Tyr Pro Gly Gln Phe Lys  
 130 135 140  
 Pro Thr Ile Cys His Tyr Phe Met Arg Leu Leu Lys Asp Lys Gly Leu  
 145 150 155 160  
 Leu Leu Arg Cys Tyr Thr Gln Asn Ile Asp Thr Leu Glu Arg Ile Ala  
 165 170 175  
 Gly Leu Glu Gln Glu Asp Leu Val Glu Ala His Gly Thr Phe Tyr Thr  
 180 185 190  
 Ser His Cys Val Ser Ala Ser Cys Arg His Glu Tyr Pro Leu Ser Trp  
 195 200 205  
 Met Lys Glu Lys Ile Phe Ser Glu Val Thr Pro Lys Cys Glu Asp Cys  
 210 215 220  
 Gln Ser Leu Val Lys Pro Asp Ile Val Phe Phe Gly Glu Ser Leu Pro  
 225 230 235 240  
 Ala Arg Phe Phe Ser Cys Met Gln Ser Asp Phe Leu Lys Val Asp Leu  
 245 250 255  
 Leu Leu Val Met Gly Thr Ser Leu Gln Val Gln Pro Phe Ala Ser Leu  
 260 265 270  
 Ile Ser Lys Ala Pro Leu Ser Thr Pro Arg Leu Leu Ile Asn Lys Glu  
 275 280 285  
 Lys Ala Gly Gln Ser Asp Pro Phe Leu Gly Met Ile Met Gly Leu Gly  
 290 295 300  
 Gly Gly Met Asp Phe Asp Ser Lys Lys Ala Tyr Arg Asp Val Ala Trp  
 305 310 315 320  
 Leu Gly Glu Cys Asp Gln Gly Cys Leu Ala Leu Ala Glu Leu Leu Gly  
 325 330 335  
 Trp Lys Lys Glu Leu Glu Asp Leu Val Arg Arg Glu His Ala Ser Ile  
 340 345 350  
 Asp Ala Gln Ser Gly Ala Gly Val Pro Asn Pro Ser Thr Ser Ala Ser  
 355 360 365  
 Pro Lys Lys Ser Pro Pro Pro Ala Lys Asp Glu Ala Arg Thr Thr Glu  
 370 375 380  
 Arg Glu Lys Pro Gln  
 385

<210> 415  
 <211> 481  
 <212> PRT  
 <213> Homo sapiens

<400> 415  
 Met Ser Leu Asn Leu Pro Glu Ala Ser Leu Leu Ser Arg Ala Ser Trp  
 1 5 10 15  
 Pro Glu Gln Ala Lys Glu Pro Arg Arg Glu Gly His Thr Asp Lys Gln  
 20 25 30  
 Gln Thr Glu Asp Val Leu Ala Ala Gly Leu Arg Cys Leu Pro His Leu  
 35 40 45  
 Pro Ala Ile Cys Ala Arg Arg Met Ser Pro Ala Phe Arg Ala Met Asp  
 50 55 60  
 Val Glu Pro Arg Ala Lys Gly Val Leu Leu Glu Pro Phe Val His Gln  
 65 70 75 80  
 Val Gly Gly His Ser Cys Val Leu Arg Phe Asn Glu Thr Thr Leu Cys  
 85 90 95  
 Lys Pro Leu Val Pro Arg Glu His Gln Phe Tyr Glu Thr Leu Pro Ala  
 100 105 110  
 Glu Met Arg Lys Phe Thr Pro Gln Tyr Lys Gly Val Val Ser Val Arg



		115					120					125						
Phe	Glu	Glu	Asp	Glu	Asp	Arg	Asn	Leu	Cys	Leu	Ile	Ala	Tyr	Pro	Leu			
	130					135					140							
Lys	Gly	Asp	His	Gly	Ile	Val	Asp	Ile	Val	Asp	Asn	Ser	Asp	Cys	Glu			
145					150					155					160			
Pro	Lys	Ser	Lys	Leu	Leu	Arg	Trp	Thr	Thr	Asn	Lys	Lys	His	His	Val			
				165						170					175			
Leu	Glu	Thr	Glu	Lys	Thr	Pro	Lys	Asp	Trp	Val	Arg	Gln	His	Arg	Lys			
			180					185					190					
Glu	Glu	Lys	Met	Lys	Ser	His	Lys	Leu	Glu	Glu	Glu	Phe	Glu	Trp	Leu			
		195					200					205						
Lys	Lys	Ser	Glu	Val	Leu	Tyr	Tyr	Thr	Val	Glu	Lys	Lys	Gly	Asn	Ile			
	210					215					220							
Ser	Ser	Gln	Leu	Lys	His	Tyr	Asn	Pro	Trp	Ser	Met	Lys	Cys	His	Gln			
225					230					235					240			
Gln	Gln	Leu	Gln	Arg	Met	Lys	Glu	Asn	Ala	Lys	His	Arg	Asn	Gln	Tyr			
				245					250					255				
Lys	Phe	Ile	Leu	Leu	Glu	Asn	Leu	Thr	Ser	Arg	Tyr	Glu	Val	Pro	Cys			
			260					265					270					
Val	Leu	Asp	Leu	Lys	Met	Gly	Thr	Arg	Gln	His	Gly	Asp	Asp	Ala	Ser			
		275				280					285							
Glu	Glu	Lys	Ala	Ala	Asn	Gln	Ile	Arg	Lys	Cys	Gln	Gln	Ser	Thr	Ser			
	290					295					300							
Ala	Val	Ile	Gly	Val	Arg	Val	Cys	Gly	Met	Gln	Val	Tyr	Gln	Ala	Gly			
305					310					315					320			
Ser	Gly	Gln	Leu	Met	Phe	Met	Asn	Lys	Tyr	His	Gly	Arg	Lys	Leu	Ser			
				325					330					335				
Val	Gln	Gly	Phe	Lys	Glu	Ala	Leu	Phe	Gln	Phe	Phe	His	Asn	Gly	Arg			
			340					345				350						
Tyr	Leu	Arg	Arg	Glu	Leu	Leu	Gly	Pro	Val	Leu	Lys	Lys	Leu	Thr	Glu			
		355					360					365						
Leu	Lys	Ala	Val	Leu	Glu	Arg	Gln	Glu	Ser	Tyr	Arg	Phe	Tyr	Ser	Ser			
	370					375					380							
Ser	Leu	Leu	Val	Ile	Tyr	Asp	Gly	Lys	Glu	Arg	Pro	Glu	Val	Val	Leu			
385					390					395					400			
Asp	Ser	Asp	Ala	Glu	Asp	Leu	Glu	Asp	Leu	Ser	Glu	Glu	Ser	Ala	Asp			
				405					410					415				
Glu	Ser	Ala	Gly	Ala	Tyr	Ala	Tyr	Lys	Pro	Ile	Gly	Ala	Ser	Ser	Val			
			420					425					430					
Asp	Val	Arg	Met	Ile	Asp	Phe	Ala	His	Thr	Thr	Cys	Arg	Leu	Tyr	Gly			
		435				440					445							
Glu	Asp	Thr																

```
<210> 416
<211> 354
<212> PRT
<213> Homo sapiens
```

366

35	40	45
Ala Glu Thr Leu Asp Met	Ala Ser His Thr Trp	Leu Ala Leu Ala Pro
50	55	60
Leu Pro Thr Ala Arg Ala	Gly Ala Ala Ala Val	Val Leu Gly Lys Gln
65	70	75
Val Leu Val Val Gly Gly	Val Asp Glu Val Gln	Ser Pro Val Ala Ala
85	90	95
Val Glu Ala Phe Leu Met	Asp Glu Gly Arg Trp	Glu Arg Arg Ala Thr
100	105	110
Leu Pro Gln Ala Ala Met	Gly Val Ala Thr Val	Glu Arg Asp Gly Met
115	120	125
Val Tyr Ala Leu Gly Gly	Met Gly Pro Asp Thr	Ala Pro Gln Ala Gln
130	135	140
Val Arg Val Tyr Glu Pro	Arg Arg Asp Cys Trp	Leu Ser Leu Pro Ser
145	150	155
Met Pro Thr Pro Cys Tyr	Gly Ala Ser Thr Phe	Leu His Gly Asn Lys
165	170	175
Ile Tyr Val Leu Gly Gly	Arg Gln Gly Lys Leu	Pro Val Thr Ala Phe
180	185	190
Glu Ala Phe Asp Leu Glu	Ala Arg Thr Trp Thr	Arg His Pro Ser Leu
195	200	205
Pro Ser Arg Arg Ala Phe	Ala Gly Cys Ala Met	Ala Glu Gly Ser Val
210	215	220
Phe Ser Leu Gly Gly Leu	Gln Gln Pro Gly Pro	His Asn Phe Tyr Ser
225	230	235
Arg Pro His Phe Val Asn	Thr Val Glu Met Phe	Asp Leu Glu His Gly
245	250	255
Ser Trp Thr Lys Leu Pro	Arg Ser Leu Arg Met	Arg Asp Lys Arg Ala
260	265	270
Asp Phe Val Val Gly Ser	Leu Gly His Ile Val	Ala Ile Gly Gly
275	280	285
Leu Gly Asn Gln Pro Cys	Pro Leu Gly Ser Val	Glu Ser Phe Ser Leu
290	295	300
Ala Arg Arg Arg Trp Glu	Ala Leu Pro Ala Met	Pro Thr Ala Arg Cys
305	310	315
Ser Cys Ser Ser Leu Gln	Ala Gly Pro Arg Leu	Phe Val Ile Gly Gly
325	330	335
Val Ala Gln Gly Pro Ser	Gln Ala Val Glu Ala	Leu Cys Leu Arg Asp
340	345	350
Gly Val		

<210> 417

<211> 20

<212> PRT

<213> Homo sapiens

<400> 417

Met Lys Gly Leu Tyr Phe	Gln Gln Ser Ser Thr	Asp Glu Glu Ile Thr
1	5	10
Phe Val Phe Gln		
20		

<210> 418

<211> 320

<212> PRT

<213> Homo sapiens

<400> 418

Met	Lys	Gly	Leu	Tyr	Phe	Gln	Gln	Ser	Ser	Thr	Asp	Glu	Glu	Ile	Thr
1				5					10					15	
Phe	Val	Phe	Gln	Glu	Lys	Glu	Asp	Leu	Pro	Val	Thr	Glu	Asp	Asn	Phe
			20					25					30		
Val	Lys	Leu	Gln	Val	Lys	Ala	Cys	Ala	Leu	Ser	Gln	Ile	Asn	Thr	Lys
		35					40					45			
Leu	Leu	Ala	Glu	Met	Lys	Met	Lys	Lys	Asp	Leu	Phe	Pro	Val	Gly	Arg
	50					55					60				
Glu	Ile	Ala	Gly	Ile	Val	Leu	Asp	Val	Gly	Ser	Lys	Val	Ser	Phe	Phe
65				70						75				80	
Gln	Pro	Asp	Asp	Glu	Val	Val	Gly	Ile	Leu	Pro	Leu	Asp	Ser	Glu	Asp
			85					90						95	
Pro	Gly	Leu	Cys	Glu	Val	Val	Arg	Val	His	Glu	His	Tyr	Leu	Val	His
			100					105					110		
Lys	Pro	Glu	Lys	Val	Thr	Trp	Thr	Glu	Ala	Ala	Gly	Ser	Ile	Arg	Asp
		115					120					125			
Gly	Val	Arg	Ala	Tyr	Thr	Ala	Leu	His	Tyr	Leu	Ser	His	Leu	Ser	Pro
	130					135					140				
Gly	Lys	Ser	Val	Leu	Ile	Met	Asp	Gly	Ala	Ser	Ala	Phe	Gly	Thr	Ile
145				150						155					160
Ala	Ile	Gln	Leu	Ala	His	His	Arg	Gly	Ala	Lys	Val	Ile	Ser	Thr	Ala
			165					170						175	
Cys	Ser	Leu	Glu	Asp	Lys	Gln	Cys	Leu	Glu	Arg	Phe	Arg	Pro	Pro	Ile
			180				185					190			
Ala	Arg	Val	Ile	Asp	Val	Ser	Asn	Gly	Lys	Val	His	Val	Ala	Glu	Ser
		195					200					205			
Cys	Leu	Glu	Glu	Thr	Gly	Gly	Leu	Gly	Val	Asp	Ile	Val	Leu	Asp	Ala
	210				215					220					
Gly	Val	Arg	Leu	Tyr	Ser	Lys	Asp	Asp	Glu	Pro	Ala	Val	Lys	Leu	Gln
225				230						235					240
Leu	Leu	Pro	His	Lys	His	Asp	Ile	Ile	Thr	Leu	Leu	Gly	Val	Gly	Gly
			245						250					255	
His	Trp	Val	Thr	Thr	Glu	Glu	Asn	Leu	Gln	Leu	Asp	Pro	Pro	Asp	Ser
			260				265						270		
His	Cys	Leu	Phe	Leu	Lys	Gly	Ala	Thr	Leu	Ala	Phe	Leu	Asn	Asp	Glu
		275				280						285			
Val	Trp	Asn	Leu	Ser	Asn	Val	Gln	Gln	Gly	Lys	Tyr	Leu	Tyr	Leu	Lys
	290				295						300				
Gly	Cys	Asp	Gly	Glu	Val	Ile	Asn	Trp	Cys	Phe	Gln	Thr	Ser	Val	Gly
305					310					315					320

<210> 419

<211> 159

<212> PRT

<213> Homo sapiens

<400> 419

Met	Glu	Lys	Leu	Arg	Arg	Val	Leu	Ser	Gly	Gln	Asp	Asp	Glu	Glu	Gln
1				5					10					15	
Gly	Leu	Thr	Ala	Gln	Val	Leu	Asp	Ala	Ser	Ser	Leu	Ser	Phe	Asn	Thr
			20					25					30		
Arg	Leu	Lys	Trp	Phe	Ala	Ile	Cys	Phe	Val	Cys	Gly	Val	Phe	Phe	Ser
		35					40					45			
Ile	Leu	Gly	Thr	Gly	Leu	Leu	Trp	Leu	Pro	Gly	Gly	Ile	Lys	Leu	Phe
	50					55					60				
Ala	Val	Phe	Tyr	Thr	Leu	Gly	Asn	Leu	Ala	Ala	Leu	Ala	Ser	Thr	Cys
65				70						75				80	
Phe	Leu	Met	Gly	Pro	Val	Lys	Gln	Leu	Lys	Lys	Met	Phe	Glu	Ala	Thr





Leu Arg Arg Tyr Cys Cys Pro Thr Asp Leu Gln Ala Pro Arg Ser Pro  
 20 25 30  
 Val Pro Pro Ile Arg Lys Val Gly Ile Ser Asp Val Ile Val His Ala  
 35 40 45  
 Asn Leu Ala Thr Ser Leu Lys Lys Asn Thr Cys Asn Cys Gln Ala Asp  
 50 55 60  
 Leu Leu Ser Trp Arg Ser Trp Val Asn Gly Ile Ser Cys His Cys Pro  
 65 70 75 80  
 Asn Leu Arg Pro Leu Ser Lys Ser Ile Phe Arg Asp Ser Thr Ser Leu  
 85 90 95  
 Cys Ser Leu Ser Gln Gln Arg Leu Cys Pro Leu His Ser Lys Pro Glu  
 100 105 110  
 Ala Cys Trp Gly Leu Phe Val Ser Val His Ala His Phe Arg Val Gln  
 115 120 125  
 Ala Gly Gly Arg Gly Asn Arg Val Gly Lys Lys Thr Arg Val Ser Arg  
 130 135 140  
 Asn Asp Glu Thr Leu  
 145

<210> 425  
 <211> 75  
 <212> PRT  
 <213> Homo sapiens

<400> 425  
 Met Tyr Leu Pro Pro Asn Arg Ser Glu Leu Cys Asn Phe Ala Leu Ser  
 1 5 10 15  
 Leu Asn Leu Tyr Gly Lys Gly Phe Phe Ser Leu Val Glu Lys His Asn  
 20 25 30  
 Ser Arg Asp Leu Glu Asp Arg Ala Ser Ser Gly Pro Ser Leu Ser Ser  
 35 40 45  
 Pro Ser His Pro Asp Trp Gly Tyr Ile Val Leu Ile Leu Val Ala Thr  
 50 55 60  
 Leu Gly Glu Leu Asp Thr Gln Val Gly Gly His  
 65 70 75

<210> 426  
 <211> 168  
 <212> PRT  
 <213> Homo sapiens

<400> 426  
 Met Arg Leu Thr Glu Lys Ser Glu Gly Glu Gln Gln Leu Lys Pro Asn  
 1 5 10 15  
 Asn Ser Asn Ala Pro Asn Glu Asp Gln Glu Glu Glu Ile Gln Gln Ser  
 20 25 30  
 Glu Gln His Thr Pro Ala Arg Gln Arg Thr Gln Arg Ala Asp Thr Gln  
 35 40 45  
 Pro Ser Arg Cys Arg Leu Pro Ser Arg Arg Thr Pro Thr Thr Ser Ser  
 50 55 60  
 Asp Arg Thr Ile Asn Leu Leu Glu Val Leu Pro Trp Pro Thr Glu Trp  
 65 70 75 80  
 Ile Phe Asn Pro Tyr Arg Leu Pro Ala Leu Phe Glu Leu Tyr Pro Glu  
 85 90 95  
 Phe Leu Leu Val Phe Lys Glu Ala Phe His Asp Ile Ser His Cys Leu  
 100 105 110  
 Lys Ala Gln Met Glu Lys Ile Gly Leu Pro Ile Ile Leu His Leu Phe  
 115 120 125



<400> 429

Met	Lys	Ala	Ser	Gly	Pro	Asp	Leu	Ser	Asp	Gly	Leu	His	Cys	Pro	Ser
1				5					10					15	
Leu	Ile	Arg	His	Leu	Arg	Thr	Phe	Ser	Ala	Ala	Ala	Ala	Leu	Ala	Pro
			20					25					30		
Arg	Tyr	Pro	Thr	Arg	Leu	Pro	Ser	Ser	Leu	Leu	Leu	Trp	His	Leu	Cys
		35					40					45			
Gln	Cys	Leu	His	Leu	Leu	Tyr	Ala	Val	Ser	Thr	Ser	Cys	Asn	Ser	His
	50					55					60				
Gly	Lys	Arg	Ser	Ala	Ala	Trp	Ala	Met	Thr	Arg	Thr	Glu	Asp	Thr	Asp
65					70					75				80	
Ala	Leu	Thr	Asp	Ser	Phe	Asp	Asp	Ser	Phe	Ile	Ser	Ser	Ala	Asp	
			85						90					95	

<210> 430

<211> 99

<212> PRT

<213> Homo sapiens

<400> 430

Met	Lys	Lys	Lys	Glu	Glu	Thr	Thr	Leu	Ser	Glu	Met	Glu	Pro	Val	Glu
1				5					10					15	
Pro	Gln	Tyr	Gln	Leu	Val	Asn	Ala	Glu	Ser	Thr	Ser	Pro	Phe	Leu	His
			20					25					30		
Cys	Leu	Arg	Glu	Val	Ile	Gly	Glu	Tyr	Ser	Val	His	Glu	Phe	Ser	Leu
		35				40					45				
Leu	Gly	Lys	Thr	Glu	Ser	Gln	Gly	Ile	Gly	Leu	Trp	Ile	Ala	Leu	Val
	50					55					60				
Val	Phe	Leu	Ser	Phe	Leu	Ile	Phe	Ser	Thr	Ser	Phe	Tyr	Ile	Ser	Asn
65					70					75				80	
Ala	Glu	Gln	Pro	Phe	Phe	Lys	Glu	Pro	Pro	Thr	Glu	Ala	Ala	Lys	Glu
				85					90					95	
Leu	Ser	Leu													

<210> 431

<211> 122

<212> PRT

<213> Homo sapiens

<400> 431

Ile	Arg	Ala	Thr	Met	Val	Ala	Arg	Val	Trp	Ser	Leu	Met	Arg	Phe	Leu
1				5					10					15	
Ile	Lys	Gly	Ser	Val	Ala	Gly	Gly	Ala	Val	Tyr	Leu	Val	Tyr	Asp	Gln
			20					25					30		
Glu	Leu	Leu	Gly	Pro	Ser	Asp	Lys	Ser	Gln	Ala	Ala	Leu	Gln	Lys	Ala
		35					40					45			
Gly	Glu	Val	Val	Pro	Pro	Ala	Met	Tyr	Gln	Phe	Ser	Gln	Tyr	Val	Cys
	50					55					60				
Gln	Gln	Thr	Gly	Leu	Gln	Ile	Pro	Gln	Leu	Pro	Ala	Pro	Pro	Lys	Ile
65					70					75				80	
Tyr	Phe	Pro	Ile	Arg	Asp	Ser	Trp	Asn	Ala	Gly	Ile	Met	Thr	Val	Met
			85					90					95		
Ser	Ala	Leu	Ser	Val	Ala	Pro	Ser	Lys	Ala	Arg	Glu	Tyr	Ser	Lys	Glu
			100					105					110		
Gly	Trp	Glu	Tyr	Val	Lys	Ala	Arg	Thr	Lys						
		115					120								

<210> 432



[illegible][illegible]

```

<400> 433
Met Glu Leu Glu Ala Met Ser Arg Tyr Thr Ser Pro Val Asn Pro Pro
1          5          10          15
Val Phe Pro His Leu Thr Val Val Leu Leu Ala Ile Gly Met Phe Phe
          20          25          30
Thr Ala Trp Phe Phe Val Tyr Pro Phe Thr Glu Gln Pro Glu Asp Gln
          35          40          45
His

```

[illegible]

374

[illegible]

<210> 436

<211> 45

&lt;212&gt; PRT

<400> 436

Met	Pro	Arg	Ser	Ser	Arg	Ser	Pro	Gly	Asp	Pro	Gly	Ala	Leu	Leu	Glu
1				5					10					15	
Asp	Gly	Pro	Gln	Ser	Gln	Thr	Pro	Glu	Asp	Cys	Pro	Ala	Arg	Pro	Glu
			20					25					30		
His	Gln	Gln	Asp	Gly	Arg	Gly	His	Leu	Pro	Lys	His	Glu			
		35					40					45			

<210> 437

<211> 65

<212> PRT

<213> Homo sapiens

<400> 437

[illegible]

<210> 438

<211> 112

<212> PRT

<213> Homo sapiens

<400> 438

Met	Arg	Lys	Lys	Cys	Lys	Cys	Phe	Thr	Ile	Lys	Lys	Thr	Asn	Thr	Tyr
1				5					10					15	
Glu	Glu	Ser	Asn	Ala	Gly	Asn	Glu	Gly	Gln	Lys	Glu	Ala	Ile	Ser	Ile
			20					25					30		
Cys	Ile	Cys	Arg	Arg	Asp	Gly	Leu	Leu	Pro	Leu	Trp	Val	Thr	Arg	Leu
		35					40					45			

Ser Asp Leu Val Phe Ser Lys Glu Lys Ala His Gly Met Ile Pro Leu  
50 55 60  
Leu Gly Ser His Arg Glu Lys Lys Thr Ser Lys Glu Met Lys Thr Ser  
65 70 75 80  
Ser Arg Asn Leu Arg Tyr Phe Ile Val Cys Arg Asp Ala Ser Ser Tyr  
85 90 95  
Thr Pro Gln Ser Leu Ile Ser Gly Tyr Ile Gly Pro Cys Gln His Gln  
100 105 110

<210> 439  
<211> 110  
<212> PRT  
<213> Homo sapiens

<400> 439  
Met Val Phe Gly Ala Met Val Leu Leu Val Gly Leu Glu Glu Leu Thr  
1 5 10 15  
Asn Ile Arg Asn Val Glu Arg Leu Lys Lys Asp Leu Arg Ala Ser Tyr  
20 25 30  
Cys Leu Ile Asp Ser Phe Leu Gly Asp Ser Glu Leu Ile Gly Asp Leu  
35 40 45  
Thr Gln Cys Val Asp Cys Val Ile Pro Pro Glu Gly Ser Leu Leu Gln  
50 55 60  
Ile Ser Ser Tyr Leu Tyr Leu Asn Thr Ala Leu Val Asp Leu Pro Gly  
65 70 75 80  
Val Ala Ala Ser Gln Ala Cys Asp Ser Gln Gln Val Thr Trp Leu Leu  
85 90 95  
Tyr Val Ala Asn Gly Ala Tyr Ser Ala Cys Asn Arg Pro Gly  
100 105 110

<210> 440  
<211> 121  
<212> PRT  
<213> Homo sapiens

<400> 440  
Thr Ser Ser Ser Gly Ala Glu Val Thr Met Ala Ala Ala Leu Ala Arg  
1 5 10 15  
Leu Gly Leu Arg Pro Val Lys Gln Val Arg Val Gln Phe Cys Pro Phe  
20 25 30  
Glu Lys Asn Val Glu Ser Thr Arg Thr Phe Leu Gln Thr Val Ser Ser  
35 40 45  
Glu Lys Val Arg Ser Thr Asn Leu Asn Cys Ser Val Ile Ala Asp Val  
50 55 60  
Arg His Asp Gly Ser Glu Pro Cys Val Asp Val Leu Phe Gly Asp Gly  
65 70 75 80  
His Arg Leu Ile Met Arg Gly Ala His Leu Thr Ala Leu Glu Met Leu  
85 90 95  
Thr Ala Phe Ala Ser His Ile Arg Ala Arg Asp Ala Ala Gly Ser Gly  
100 105 110  
Asp Lys Pro Gly Ala Asp Thr Gly Arg  
115 120

<210> 441  
<211> 99  
<212> PRT  
<213> Homo sapiens

<400> 441

Met Leu Ala Arg Ala Thr Phe Arg Ala Ala Ser Ala Pro Thr Leu Val  
 1 5 10 15  
 Ala Arg Arg Gly Phe Gln Ser Thr Arg Ala Gln Met Ala Ser Pro Tyr  
 20 25 30  
 His Tyr Pro Glu Gly Pro Arg Ser Asn Leu Pro Phe Asp Pro Leu Lys  
 35 40 45  
 Lys Gly Phe Ala Phe Lys Tyr Trp Gly Phe Met Gly Thr Gly Phe Ala  
 50 55 60  
 Leu Pro Phe Leu Leu Ala Val Trp Gln Thr Glu Gln Ala Val Asn Ala  
 65 70 75 80  
 Leu Arg His Gly Val Asp Met Arg Ile Gly Ile Pro Gly Asn Thr Ala  
 85 90 95  
 Phe Val Asp

<210> 442

<211> 183

<212> PRT

<213> Homo sapiens

<400> 442

Arg Glu Gly Ala Arg Ala Arg Pro Ser Pro Thr Met Ser Asp Glu Ala  
 1 5 10 15  
 Ser Ala Ile Thr Ser Tyr Glu Lys Phe Leu Thr Pro Glu Glu Pro Phe  
 20 25 30  
 Pro Leu Leu Gly Pro Pro Arg Gly Val Gly Thr Cys Pro Ser Glu Glu  
 35 40 45  
 Pro Gly Cys Leu Asp Ile Ser Asp Phe Gly Cys Gln Leu Ser Ser Cys  
 50 55 60  
 His Arg Thr Asp Pro Leu His Arg Phe His Thr Asn Arg Trp Asn Leu  
 65 70 75 80  
 Thr Ser Cys Gly Thr Ser Val Ala Ser Ser Glu Gly Ser Glu Glu Leu  
 85 90 95  
 Phe Ser Ser Val Ser Val Gly Asp Gln Asp Asp Cys Tyr Ser Leu Leu  
 100 105 110  
 Asp Asp Gln Asp Phe Thr Ser Phe Asp Leu Phe Pro Glu Gly Ser Val  
 115 120 125  
 Cys Ser Asp Val Ser Ser Ser Ile Ser Thr Tyr Trp Asp Trp Ser Asp  
 130 135 140  
 Ser Glu Phe Glu Trp Gln Leu Pro Gly Ser Asp Ile Ala Ser Gly Ser  
 145 150 155 160  
 Asp Val Leu Ser Asp Val Ile Pro Ser Ile Pro Ser Ser Pro Cys Leu  
 165 170 175  
 Leu Pro Lys Lys Lys Lys Lys  
 180

<210> 443

<211> 94

<212> PRT

<213> Homo sapiens

<400> 443

Met Ser Asp Glu Ala Ser Ala Ile Thr Ser Tyr Glu Lys Phe Leu Thr  
 1 5 10 15  
 Pro Glu Glu Pro Phe Pro Leu Leu Gly Pro Pro Arg Gly Val Gly Thr  
 20 25 30  
 Cys Pro Ser Glu Glu Pro Gly Cys Leu Asp Ile Ser Asp Phe Gly Cys  
 35 40 45

Gln Leu Ser Ser Cys His Arg Thr Asp Pro Leu His Arg Phe His Thr  
 50 55 60  
 Asn Arg Trp Asn Leu Thr Ser Cys Gly Thr Ser Val Ala Ser Ser Glu  
 65 70 75 80  
 Gly Ser Glu Glu Leu Phe Ser Ser Val Cys Trp Arg Ser Arg  
 85 90

<210> 444  
 <211> 105  
 <212> PRT  
 <213> Homo sapiens

<400> 444  
 Ile Gly Pro Arg Ala Pro Ser Pro Ser Phe Ser Val Arg Asp Val Glu  
 1 5 10 15  
 Leu Ser Asp Pro Ala Arg Glu Arg Gly Glu Met Pro Val Ala Val Gly  
 20 25 30  
 Pro Tyr Gly Gln Ser Gln Pro Ser Cys Phe Asp Arg Val Lys Met Gly  
 35 40 45  
 Phe Val Met Gly Cys Ala Val Gly Met Ala Ala Gly Ala Leu Phe Gly  
 50 55 60  
 Thr Phe Ser Cys Leu Arg Ile Gly Met Arg Gly Arg Glu Leu Met Gly  
 65 70 75 80  
 Gly Ile Gly Lys Thr Met Met Gln Ser Gly Gly Thr Phe Gly Thr Phe  
 85 90 95  
 Met Ala Ile Gly Met Gly Ile Arg Cys  
 100 105

<210> 445  
 <211> 163  
 <212> PRT  
 <213> Homo sapiens

<400> 445  
 Met Pro Arg Ser Ser Arg Ser Pro Gly Asp Pro Gly Ala Leu Leu Glu  
 1 5 10 15  
 Asp Val Ala His Asn Pro Arg Pro Arg Ile Ala Gln Arg Gly Arg  
 20 25 30  
 Asn Thr Ser Arg Met Ala Glu Asp Thr Ser Pro Asn Met Asn Asp Asn  
 35 40 45  
 Ile Leu Leu Pro Val Arg Asn Asn Asp Gln Ala Leu Gly Leu Thr Gln  
 50 55 60  
 Cys Met Leu Gly Cys Val Ser Trp Phe Thr Cys Phe Ala Cys Ser Leu  
 65 70 75 80  
 Arg Thr Gln Ala Gln Gln Val Leu Phe Asn Thr Cys Arg Cys Lys Leu  
 85 90 95  
 Leu Cys Gln Lys Leu Met Glu Lys Thr Gly Ile Leu Leu Leu Cys Ala  
 100 105 110  
 Phe Gly Val Ser Gln Gly Pro Ala Gln Ser Gln Val Glu Val Ser Leu  
 115 120 125  
 Gly Pro Gly Thr Asp Tyr Arg Thr Leu Gly Lys Thr Leu His Cys His  
 130 135 140  
 Val Thr Gln Phe Pro His Leu Pro Asp Gly Cys Cys Glu Asn Tyr  
 145 150 155 160  
 Glu Met Lys

<210> 446  
 <211> 128

<212> PRT  
<213> Homo sapiens

<400> 446  
Met Glu Asp Lys Glu Ile Pro Ile Lys Ser Glu Pro Leu Pro Lys Pro  
1 5 10 15  
Pro Ala Ser Ala Pro Pro Ser Ile Leu Val Lys Pro Glu Asn Ser Arg  
20 25 30  
Asn Gly Ile Glu Lys Gln Val Lys Thr Val Arg Phe Gln Asn Tyr Ser  
35 40 45  
Pro Pro Pro Thr Lys His Tyr Thr Ser His Pro Thr Ser Gly Lys Pro  
50 55 60  
Glu Gln Pro Ala Thr Leu Lys Ala Ser Gln Pro Glu Ala Ala Ser Leu  
65 70 75 80  
Gly Pro Glu Met Thr Val Leu Phe Ala His Arg Ser Gly Cys His Ser  
85 90 95  
Gly Gln Gln Thr Asp Leu Arg Arg Lys Ser Ala Leu Ala Lys Ala Thr  
100 105 110  
Thr Leu Val Ser Thr Ala Ser Gly Thr Gln Thr Val Phe Pro Ser Lys  
115 120 125

<210> 447  
<211> 96  
<212> PRT  
<213> Homo sapiens

<400> 447  
Met Leu Thr Arg Val Glu Glu Gln Lys Lys Met Val Lys Ala Cys Arg  
1 5 10 15  
Tyr Arg Cys Ser Ala Cys His Leu Lys Tyr Ser Pro Gln Arg Gln Lys  
20 25 30  
Glu Arg Lys Leu Ser Leu Lys Arg Gly Arg Thr Ser Gln Gln Asn Met  
35 40 45  
Ser Met Phe Trp Leu Lys Lys Leu Leu Glu Ser Gly Leu Phe Cys Ala  
50 55 60  
Met Cys Ser Pro Arg Ala Ser Thr Lys Lys Gly Phe Trp Cys Arg Pro  
65 70 75 80  
Lys Thr Thr Ile Ile Ile Asp Tyr Ser Ser Pro Arg Gln Cys Leu  
85 90 95

<210> 448  
<211> 160  
<212> PRT  
<213> Homo sapiens

<220>  
<221> UNSURE  
<222> 114  
<223> Xaa = Glu,Val

<220>  
<221> UNSURE  
<222> 113  
<223> Xaa = His,Gln

<220>  
<221> UNSURE  
<222> 115

[illegible]

Met	Gly	Lys	Ile	Ala	Leu	Gln	Leu	Lys	Ala	Thr	Leu	Glu	Asn	Ile	Thr
1				5					10					15	
Asn	Leu	Arg	Pro	Val	Gly	Glu	Asp	Phe	Arg	Trp	Tyr	Leu	Lys	Met	Lys
			20					25					30		
Cys	Gly	Asn	Cys	Gly	Glu	Ile	Ser	Asp	Lys	Trp	Gln	Tyr	Ile	Arg	Leu
			35				40					45			
Met	Asp	Ser	Val	Ala	Leu	Lys	Gly	Gly	Arg	Gly	Ser	Ala	Ser	Met	Val
	50					55				60					
Gln	Lys	Cys	Lys	Leu	Cys	Ala	Arg	Glu	Asn	Ser	Ile	Glu	Ile	Leu	Ser
65					70				75					80	
Ser	Thr	Ile	Lys	Pro	Tyr	Asn	Ala	Glu	Asp	Asn	Glu	Asn	Phe	Lys	Thr
				85					90					95	
Ile	Val	Glu	Phe	Glu	Cys	Arg	Gly	Leu	Glu	Pro	Val	Asp	Phe	Gln	Pro
			100				105						110		
Xaa	Xaa	Xaa	Leu	Leu	Leu	Lys	Val	Trp	Ser	Gln	Gly	Gln	Pro	Ser	Val
			115				120					125			
Thr	Leu	Ile	Cys	Arg	Arg	Arg	Thr	Gly	Thr	Asp	Tyr	Asp	Glu	Lys	Ala
	130					135					140				
Gln	Glu	Ser	Val	Gly	Ile	Tyr	Glu	Val	Thr	His	Gln	Phe	Val	Lys	Cys
145					150					155					160

<211> 117

<213> Hom

[illegible]

<211> 335

<213> Home

Met	Cys	Cys	Gln	Val	Cys	Glu	Ala	Val	Arg	Ser	Gly	Asn	Glu	Glu	Val
1			5						10					15	
Leu	Ala	Asp	Val	Arg	Thr	Ile	Val	Asn	Gln	Ile	Ser	Tyr	Thr	Pro	Gln
			20					25					30		
Asp	Pro	Arg	Asp	Leu	Cys	Gly	Arg	Ile	Leu	Thr	Thr	Cys	Tyr	Met	Ala

09876997-060801

	35					40				45					
Ser	Lys	Asn	Ser	Ser	Gln	Glu	Thr	Cys	Thr	Arg	Ala	Arg	Glu	Leu	Ala
	50					55					60				
Gln	Gln	Ile	Gly	Ser	His	His	Ile	Ser	Leu	Asn	Ile	Asp	Pro	Ala	Val
65					70					75					80
Lys	Ala	Val	Met	Gly	Ile	Phe	Ser	Leu	Val	Thr	Gly	Lys	Ser	Pro	Leu
				85					90					95	
Phe	Ala	Ala	His	Gly	Gly	Ser	Ser	Arg	Glu	Asn	Leu	Ala	Leu	Gln	Asn
			100					105					110		
Val	Gln	Ala	Arg	Ile	Arg	Met	Val	Leu	Ala	Tyr	Leu	Phe	Ala	Gln	Leu
	115						120				125				
Ser	Leu	Trp	Ser	Arg	Gly	Val	His	Gly	Gly	Leu	Leu	Val	Leu	Gly	Ser
	130					135					140				
Ala	Asn	Val	Asp	Glu	Ser	Leu	Leu	Gly	Tyr	Leu	Thr	Lys	Tyr	Asp	Cys
145					150					155					160
Ser	Ser	Ala	Asp	Ile	Asn	Pro	Ile	Gly	Gly	Ile	Ser	Lys	Thr	Asp	Leu
				165				170						175	
Arg	Ala	Phe	Val	Gln	Phe	Cys	Ile	Gln	Arg	Phe	Gln	Leu	Pro	Ala	Leu
		180						185					190		
Gln	Ser	Ile	Leu	Leu	Ala	Pro	Ala	Thr	Ala	Glu	Leu	Glu	Pro	Leu	Ala
	195					200						205			
Asp	Gly	Gln	Val	Ser	Gln	Thr	Asp	Glu	Glu	Asp	Met	Gly	Met	Thr	Tyr
	210					215				220					
Ala	Glu	Leu	Ser	Val	Tyr	Gly	Lys	Leu	Arg	Lys	Val	Ala	Lys	Met	Gly
225					230					235					240
Pro	Tyr	Ser	Met	Phe	Cys	Lys	Leu	Leu	Gly	Met	Trp	Arg	His	Ile	Cys
			245						250					255	
Thr	Pro	Arg	Gln	Val	Ala	Asp	Lys	Val	Lys	Arg	Phe	Phe	Ser	Lys	Tyr
			260					265					270		
Ser	Met	Asn	Arg	His	Lys	Met	Thr	Thr	Leu	Thr	Pro	Ala	Tyr	His	Ala
	275						280					285			
Glu	Asn	Tyr	Ser	Pro	Glu	Asp	Asn	Arg	Phe	Asp	Leu	Arg	Pro	Phe	Leu
	290					295				300					
Tyr	Asn	Thr	Ser	Trp	Pro	Trp	Gln	Phe	Arg	Cys	Ile	Glu	Asn	Gln	Val
305					310					315					320
Leu	Gln	Leu	Glu	Arg	Ala	Glu	Pro	Gln	Ser	Leu	Asp	Gly	Val	Asp	
				325					330					335	

<210> 451

<211> 86

<212> PRT

<213> Homo sapiens

<220>

<221> UNSURE

<222> 76

<223> Xaa = Lys,Asn

<400> 451

Met	Cys	Trp	Val	Ile	Asn	His	Ala	Ile	Leu	Pro	Arg	Met	Arg	Met	His
1				5					10					15	
Ser	Lys	Arg	Gln	Thr	Ile	Thr	Arg	His	Ser	Ala	Ser	Leu	Ser	Phe	His
			20					25					30		
Ala	Leu	Pro	Arg	Ser	Ala	Phe	Leu	Gln	Leu	Cys	Leu	Leu	Arg	Gln	Ile
	35						40					45			
His	Gln	Ile	Pro	Cys	Leu	Ser	Ile	Phe	Ser	Ser	Thr	Leu	Arg	Ala	Gln
	50					55					60				
Thr	His	Asp	Ser	Gly	Ile	Gly	Cys	Thr	Thr	Ala	Xaa	Pro	Gly	Gly	Arg



09876997.060801

65                      70                      75                      80  
Arg Gln Glu Gln Leu Arg  
85

<210> 452  
<211> 93  
<212> PRT  
<213> Homo sapiens

<400> 452  
Met Lys Ile Ala Leu Cys Gln Arg Glu Leu Pro Ser Pro Arg Ser Cys  
1                      5                      10                      15  
Leu Leu Ser Arg Asp Val Thr Gly Val Ile Cys Thr Arg Met Pro Arg  
20                      25                      30  
Leu Ala Ile Cys Ser Lys Thr Ala Gln Lys Ala Leu Pro Cys Ile Pro  
35                      40                      45  
Leu Leu His Thr Ser Pro Leu Cys Leu Gln Leu Leu Ser Ala Gly Leu  
50                      55                      60  
His Ile Tyr Ala Thr Leu Cys Lys Ser Cys Ala Ser Arg Asn His Lys  
65                      70                      75                      80  
Asn Ile Phe Leu His Leu Leu His Ser Leu Ser Ala Ala  
85                      90

<210> 453  
<211> 108  
<212> PRT  
<213> Homo sapiens

<400> 453  
Met Ala Val Arg Ala Ser Phe Glu Asn Asn Cys Glu Ile Gly Cys Phe  
1                      5                      10                      15  
Ala Lys Leu Thr Asn Thr Tyr Cys Leu Val Ala Ile Gly Gly Ser Glu  
20                      25                      30  
Asn Phe Tyr Ser Val Phe Glu Gly Glu Leu Ser Asp Thr Ile Pro Val  
35                      40                      45  
Val His Ala Ser Ile Ala Gly Cys Arg Ile Ile Gly Arg Met Cys Val  
50                      55                      60  
Gly Asp Arg Arg Asn Ser Gly Arg Cys Ala Gln Gly Gly Ser Leu Gln  
65                      70                      75                      80  
Thr Asp Ser Gly Arg Pro Gly Ala Ser Arg Lys Leu Leu Cys Leu Gln  
85                      90                      95  
Gln Ser Gly Arg Ala Gly Ala Ser Gln Asp Phe Asn  
100                      105

<210> 454  
<211> 277  
<212> PRT  
<213> Homo sapiens

<400> 454  
Met Ser Leu Cys Glu Asp Met Leu Leu Cys Asn Tyr Arg Lys Cys Arg  
1                      5                      10                      15  
Ile Lys Leu Ser Gly Tyr Ala Trp Val Thr Ala Cys Ser His Ile Phe  
20                      25                      30  
Cys Asp Gln His Gly Ser Gly Glu Phe Ser Arg Ser Pro Ala Ile Cys  
35                      40                      45  
Pro Ala Cys Asn Ser Thr Leu Ser Gly Lys Leu Asp Ile Val Arg Thr  
50                      55                      60

Glu	Leu	Ser	Pro	Ser	Glu	Glu	Tyr	Lys	Ala	Met	Val	Leu	Ala	Gly	Leu
65					70					75					80
Arg	Pro	Glu	Ile	Val	Leu	Asp	Ile	Ser	Ser	Arg	Ala	Leu	Ala	Phe	Trp
				85					90					95	
Thr	Tyr	Gln	Val	His	Gln	Glu	Arg	Leu	Tyr	Gln	Glu	Tyr	Asn	Phe	Ser
			100					105					110		
Lys	Ala	Glu	Gly	His	Leu	Lys	Gln	Met	Glu	Lys	Ile	Tyr	Thr	Gln	Gln
		115					120					125			
Ile	Gln	Ser	Lys	Asp	Val	Glu	Leu	Thr	Ser	Met	Lys	Gly	Glu	Val	Thr
	130					135					140				
Ser	Met	Lys	Lys	Val	Leu	Glu	Glu	Tyr	Lys	Lys	Lys	Phe	Ser	Asp	Ile
145					150					155					160
Ser	Glu	Lys	Leu	Met	Glu	Arg	Asn	Arg	Gln	Tyr	Gln	Lys	Leu	Gln	Gly
				165					170					175	
Leu	Tyr	Asp	Ser	Leu	Arg	Leu	Arg	Asn	Ile	Thr	Ile	Ala	Asn	His	Glu
			180					185					190		
Gly	Thr	Leu	Glu	Pro	Ser	Met	Ile	Ala	Gln	Ser	Gly	Val	Leu	Gly	Phe
		195					200					205			
Pro	Leu	Gly	Asn	Asn	Ser	Lys	Phe	Pro	Leu	Asp	Asn	Thr	Pro	Val	Arg
	210					215					220				
Asn	Arg	Gly	Asp	Gly	Asp	Gly	Asp	Phe	Gln	Phe	Arg	Pro	Phe	Phe	Ala
225					230					235					240
Gly	Ser	Pro	Thr	Ala	Pro	Glu	Pro	Ser	Asn	Ser	Phe	Phe	Ser	Phe	Val
				245					250					255	
Ser	Pro	Ser	Arg	Glu	Leu	Glu	Gln	Gln	Gln	Val	Ser	Ser	Arg	Ala	Phe
			260					265					270		
Lys	Val	Lys	Arg	Ile											
		275													

<210> 455  
 <211> 173  
 <212> PRT  
 <213> Homo sapiens

<400> 455

Met	Leu	Val	Met	Tyr	Leu	Leu	Ala	Ala	Leu	Phe	Gly	Tyr	Leu	Thr	Phe
1			5						10					15	
Tyr	Gly	Glu	Val	Glu	Asp	Glu	Leu	Leu	His	Ala	Tyr	Ser	Lys	Val	Tyr
			20					25					30		
Thr	Leu	Asp	Ile	Pro	Leu	Leu	Met	Val	Arg	Leu	Ala	Val	Leu	Val	Ala
		35					40					45			
Val	Thr	Leu	Thr	Val	Pro	Ile	Val	Leu	Phe	Pro	Ile	Arg	Thr	Ser	Val
	50					55					60				
Ile	Thr	Leu	Leu	Phe	Pro	Lys	Arg	Pro	Phe	Ser	Trp	Ile	Arg	His	Phe
65					70					75					80
Leu	Ile	Ala	Ala	Val	Leu	Ile	Ala	Leu	Asn	Asn	Val	Leu	Val	Ile	Leu
			85						90					95	
Val	Pro	Thr	Ile	Lys	Tyr	Ile	Phe	Gly	Phe	Ile	Gly	Ala	Ser	Ser	Ala
			100					105					110		
Thr	Met	Leu	Ile	Phe	Ile	Leu	Pro	Ala	Val	Phe	Tyr	Leu	Lys	Leu	Val
		115					120					125			
Lys	Lys	Glu	Thr	Phe	Arg	Ser	Pro	Gln	Lys	Val	Gly	Ala	Leu	Ile	Phe
	130					135					140				
Leu	Val	Val	Gly	Ile	Phe	Phe	Met	Ile	Gly	Ser	Met	Ala	Leu	Ile	Ile
145					150					155					160
Ile	Asp	Trp	Ile	Tyr	Asp	Pro	Pro	Asn	Ser	Lys	His	His			
				165					170						

<210> 456  
 <211> 370  
 <212> PRT  
 <213> Homo sapiens

<400> 456

Met	Ser	Ala	Ser	Ala	Ala	Thr	Gly	Val	Phe	Val	Leu	Ser	Leu	Ser	Ala
1				5					10					15	
Ile	Pro	Val	Thr	Tyr	Val	Phe	Asn	His	Leu	Ala	Ala	Gln	His	Asp	Ser
			20					25					30		
Trp	Thr	Ile	Val	Gly	Val	Ala	Ala	Leu	Ile	Leu	Phe	Leu	Val	Ala	Leu
		35					40					45			
Leu	Ala	Arg	Val	Leu	Val	Lys	Arg	Lys	Pro	Pro	Arg	Asp	Pro	Leu	Phe
	50					55					60				
Tyr	Val	Tyr	Ala	Val	Phe	Gly	Phe	Thr	Ser	Val	Val	Asn	Leu	Ile	Ile
65					70					75				80	
Gly	Leu	Glu	Gln	Asp	Gly	Ile	Ile	Asp	Gly	Phe	Met	Thr	His	Tyr	Leu
			85					90					95		
Arg	Glu	Gly	Glu	Pro	Tyr	Leu	Asn	Thr	Ala	Tyr	Gly	His	Met	Ile	Cys
			100					105					110		
Tyr	Trp	Asp	Gly	Ser	Ala	His	Tyr	Leu	Met	Tyr	Leu	Val	Met	Val	Ala
		115					120					125			
Ala	Ile	Ala	Trp	Glu	Glu	Thr	Tyr	Arg	Thr	Ile	Gly	Leu	Tyr	Trp	Val
	130					135					140				
Gly	Ser	Ile	Ile	Met	Ser	Val	Val	Val	Phe	Val	Pro	Gly	Asn	Ile	Val
145					150					155				160	
Gly	Lys	Tyr	Gly	Thr	Arg	Ile	Cys	Pro	Ala	Phe	Phe	Leu	Ser	Ile	Pro
				165				170						175	
Tyr	Thr	Cys	Leu	Pro	Val	Trp	Ala	Gly	Phe	Arg	Ile	Tyr	Asn	Gln	Pro
			180					185					190		
Ser	Glu	Asn	Tyr	Asn	Tyr	Pro	Ser	Lys	Val	Ile	Gln	Glu	Ala	Gln	Ala
		195					200					205			
Lys	Asp	Leu	Leu	Arg	Arg	Pro	Phe	Asp	Leu	Met	Leu	Val	Val	Cys	Leu
	210					215					220				
Leu	Leu	Ala	Thr	Gly	Phe	Cys	Leu	Phe	Arg	Gly	Leu	Ile	Ala	Leu	Asp
225					230					235				240	
Cys	Pro	Ser	Glu	Leu	Cys	Arg	Leu	Tyr	Thr	Gln	Phe	Gln	Glu	Pro	Tyr
				245					250					255	
Leu	Lys	Asp	Pro	Ala	Ala	Tyr	Pro	Lys	Ile	Gln	Met	Leu	Ala	Tyr	Met
			260					265					270		
Phe	Tyr	Ser	Val	Pro	Tyr	Phe	Val	Thr	Ala	Leu	Tyr	Gly	Leu	Val	Val
		275					280					285			
Pro	Gly	Cys	Ser	Trp	Met	Pro	Asp	Ile	Thr	Leu	Ile	His	Ala	Gly	Gly
	290					295					300				
Leu	Ala	Gln	Ala	Gln	Phe	Ser	His	Ile	Gly	Ala	Ser	Leu	His	Ala	Arg
305					310					315				320	
Thr	Ala	Tyr	Val	Tyr	Arg	Val	Pro	Glu	Glu	Ala	Lys	Ile	Leu	Phe	Leu
				325					330					335	
Ala	Leu	Asn	Ile	Ala	Tyr	Gly	Val	Leu	Pro	Gln	Leu	Leu	Ala	Tyr	Arg
			340					345					350		
Cys	Ile	Tyr	Lys	Pro	Glu	Phe	Phe	Ile	Lys	Thr	Lys	Ala	Glu	Glu	Lys
		355					360					365			
Val	Glu														
	370														

<210> 457  
 <211> 393  
 <212> PRT

<213> Homo sapiens

<400> 457

Met	Thr	Tyr	Arg	Trp	Gly	Thr	Leu	Leu	Met	Lys	Arg	Lys	Phe	Glu	Glu
1				5					10					15	
Pro	Arg	Pro	Gly	Phe	His	Gly	Val	Leu	Gly	Ile	Asn	Ser	Ile	Thr	Gly
			20					25					30		
Lys	Glu	Glu	Pro	Leu	Tyr	Pro	Ser	Tyr	Lys	Arg	Gln	Leu	Arg	Ile	Tyr
		35					40					45			
Leu	Val	Ser	Leu	Pro	Phe	Val	Cys	Leu	Cys	Leu	Tyr	Phe	Ser	Leu	Tyr
	50					55					60				
Val	Met	Met	Ile	Tyr	Phe	Asp	Met	Glu	Val	Trp	Ala	Leu	Gly	Leu	His
65					70					75					80
Glu	Asn	Ser	Gly	Ser	Glu	Trp	Thr	Ser	Val	Leu	Leu	Tyr	Val	Pro	Ser
				85					90					95	
Ile	Ile	Tyr	Ala	Ile	Val	Ile	Glu	Ile	Met	Asn	Arg	Leu	Tyr	Arg	Tyr
			100					105						110	
Ala	Ala	Glu	Phe	Leu	Thr	Ser	Trp	Glu	Asn	His	Arg	Leu	Glu	Ser	Ala
		115					120					125			
Tyr	Gln	Asn	His	Leu	Ile	Leu	Lys	Val	Leu	Val	Phe	Asn	Phe	Leu	Asn
	130					135					140				
Cys	Phe	Ala	Ser	Leu	Phe	Tyr	Ile	Ala	Phe	Val	Leu	Lys	Asp	Met	Lys
145					150					155					160
Leu	Leu	Arg	Gln	Ser	Leu	Ala	Thr	Leu	Leu	Ile	Thr	Ser	Gln	Ile	Leu
				165					170					175	
Asn	Gln	Ile	Met	Glu	Ser	Phe	Leu	Pro	Tyr	Trp	Leu	Gln	Arg	Lys	His
			180					185					190		
Gly	Val	Arg	Val	Lys	Arg	Lys	Val	Gln	Ala	Leu	Lys	Ala	Asp	Ile	Asp
	195						200					205			
Ala	Thr	Leu	Tyr	Glu	Gln	Val	Ile	Leu	Glu	Lys	Glu	Met	Gly	Thr	Tyr
	210					215					220				
Leu	Gly	Thr	Phe	Asp	Asp	Tyr	Leu	Glu	Leu	Phe	Leu	Gln	Phe	Gly	Tyr
225					230					235					240
Val	Ser	Leu	Phe	Ser	Cys	Val	Tyr	Pro	Leu	Ala	Ala	Ala	Phe	Ala	Val
				245					250					255	
Leu	Asn	Asn	Phe	Thr	Glu	Val	Asn	Ser	Asp	Ala	Leu	Lys	Met	Cys	Arg
			260					265					270		
Val	Phe	Lys	Arg	Pro	Phe	Ser	Glu	Pro	Ser	Ala	Asn	Ile	Gly	Val	Trp
	275						280					285			
Gln	Leu	Ala	Phe	Glu	Thr	Met	Ser	Val	Ile	Ser	Val	Val	Thr	Asn	Cys
	290					295					300				
Ala	Leu	Ile	Gly	Met	Ser	Pro	Gln	Val	Asn	Ala	Val	Phe	Pro	Glu	Ser
305					310					315					320
Lys	Ala	Asp	Leu	Ile	Leu	Ile	Val	Val	Ala	Val	Glu	His	Ala	Leu	Leu
				325					330					335	
Ala	Leu	Lys	Phe	Ile	Leu	Ala	Phe	Ala	Ile	Pro	Asp	Lys	Pro	Arg	His
			340					345					350		
Ile	Gln	Met	Lys	Leu	Ala	Arg	Leu	Glu	Phe	Glu	Ser	Leu	Glu	Ala	Leu
	355						360					365			
Lys	Gln	Gln	Gln	Met	Lys	Leu	Val	Thr	Glu	Asn	Leu	Lys	Glu	Glu	Pro
	370					375					380				
Met	Glu	Ser	Gly	Lys	Glu	Lys	Ala	Thr							
385					390										

<210> 458

<211> 116

<212> PRT

<213> Homo sapiens

<400> 458

```

Met Val Gly Gly Glu Ala Ala Ala Ala Val Glu Glu Leu Val Ser Gly
1          5          10          15
Val Arg Gln Ala Ala Asp Phe Ala Glu Gln Phe Arg Ser Tyr Ser Glu
          20          25          30
Ser Glu Lys Gln Trp Lys Ala Arg Met Glu Phe Ile Leu Arg His Leu
          35          40          45
Pro Asp Tyr Arg Asp Pro Pro Asp Gly Ser Gly Arg Leu Asp Gln Leu
          50          55          60
Leu Ser Leu Ser Met Val Trp Ala Asn His Leu Phe Leu Gly Cys Ser
65          70          75          80
Tyr Asn Lys Asp Leu Leu Asp Lys Val Met Glu Met Ala Asp Gly Ile
          85          90          95
Glu Val Glu Asp Leu Pro Gln Phe Thr Thr Arg Ser Glu Leu Met Lys
          100          105          110
Lys His Gln Ser
          115

```

<210> 459

<211> 163

<212> PRT

<213> Homo sapiens

<400> 459

```

Met Glu His Tyr Arg Lys Ala Gly Ser Val Glu Leu Pro Ala Pro Ser
1          5          10          15
Pro Met Pro Gln Leu Pro Pro Asp Thr Leu Glu Met Arg Val Arg Asp
          20          25          30
Gly Ser Lys Ile Arg Asn Leu Leu Gly Leu Ala Leu Gly Arg Leu Glu
          35          40          45
Gly Gly Ser Ala Arg His Val Val Phe Ser Gly Ser Gly Arg Ala Ala
          50          55          60
Gly Lys Ala Val Ser Cys Ala Glu Ile Val Lys Arg Arg Val Pro Gly
65          70          75          80
Leu His Gln Leu Thr Lys Leu Arg Phe Leu Gln Thr Glu Asp Ser Trp
          85          90          95
Val Pro Ala Ser Pro Asp Thr Gly Leu Asp Pro Leu Thr Val Arg Arg
          100          105          110
His Val Pro Ala Val Trp Val Leu Leu Ser Arg Asp Pro Leu Asp Pro
          115          120          125
Asn Glu Cys Gly Tyr Gln Pro Pro Gly Ala Pro Pro Gly Leu Gly Ser
          130          135          140
Met Pro Ser Ser Ser Cys Gly Pro Arg Ser Arg Arg Arg Ala Arg Asp
145          150          155          160
Thr Arg Ser

```

<210> 460

<211> 230

<212> PRT

<213> Homo sapiens

<400> 460

```

Met Val Val Phe Gly Tyr Glu Ala Gly Thr Lys Pro Arg Asp Ser Gly
1          5          10          15
Val Val Pro Val Gly Thr Glu Glu Ala Pro Lys Val Phe Lys Met Ala
          20          25          30
Ala Ser Met His Gly Gln Pro Ser Pro Ser Leu Glu Asp Ala Lys Leu

```

Arg	Arg	35	Pro	Met	Val	Ile	Glu	40	Ile	Ile	Glu	Lys	Asn	45	Phe	Asp	Tyr	Leu
50							55						60					
Arg	Lys	Glu	Met	Thr	Gln	Asn	Ile	Tyr	Gln	Met	Ala	Thr	Phe	Gly	Thr			
65					70				75					80				
Thr	Ala	Gly	Phe	Ser	Gly	Ile	Phe	Ser	Asn	Phe	Leu	Phe	Arg	Arg	Cys			
				85				90					95					
Phe	Lys	Val	Lys	His	Asp	Ala	Leu	Lys	Thr	Tyr	Ala	Ser	Leu	Ala	Thr			
			100					105					110					
Leu	Pro	Phe	Leu	Ser	Thr	Val	Val	Thr	Asp	Lys	Leu	Phe	Val	Ile	Asp			
		115					120						125					
Ala	Leu	Tyr	Ser	Asp	Asn	Ile	Ser	Lys	Glu	Asn	Cys	Val	Phe	Arg	Ser			
		130				135					140							
Ser	Leu	Ile	Gly	Ile	Val	Cys	Gly	Val	Phe	Tyr	Pro	Ser	Ser	Leu	Ala			
145					150				155					160				
Phe	Thr	Lys	Asn	Gly	Arg	Leu	Ala	Thr	Lys	Tyr	His	Thr	Val	Pro	Leu			
			165					170					175					
Pro	Pro	Lys	Gly	Arg	Val	Leu	Ile	His	Trp	Met	Thr	Leu	Cys	Gln	Thr			
		180					185						190					
Gln	Met	Lys	Leu	Met	Ala	Ile	Pro	Leu	Val	Phe	Gln	Ile	Met	Phe	Gly			
		195				200					205							
Ile	Leu	Asn	Gly	Leu	Tyr	His	Tyr	Ala	Val	Phe	Glu	Glu	Thr	Leu	Glu			
	210					215					220							
Lys	Thr	Ile	His	Glu	Glu													
225					230													

<210> 461  
 <211> 101  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> UNSURE  
 <222> 95  
 <223> Xaa = Cys, Trp

Met	Glu	Arg	Pro	Asp	Lys	Ala	Ala	Leu	Asn	Ala	Leu	Gln	Pro	Pro	Glu
1				5					10				15		
Phe	Arg	Asn	Glu	Ser	Ser	Leu	Ala	Ser	Thr	Leu	Lys	Thr	Leu	Leu	Phe
		20					25					30			
Phe	Thr	Ala	Leu	Met	Ile	Thr	Val	Pro	Ile	Gly	Leu	Tyr	Phe	Thr	Thr
		35				40					45				
Lys	Ser	Tyr	Ile	Phe	Glu	Gly	Ala	Leu	Gly	Met	Ser	Asn	Arg	Asp	Ser
	50				55				60						
Tyr	Phe	Tyr	Ala	Ala	Ile	Val	Ala	Val	Val	Ala	Val	His	Val	Val	Leu
65					70				75						80
Ala	Leu	Phe	Val	Tyr	Val	Ala	Trp	Asn	Glu	Gly	Ser	Arg	Gln	Xaa	Arg
			85					90					95		
Glu	Gly	Lys	Gln	Asp											
			100												

<210> 462  
 <211> 93  
 <212> PRT  
 <213> Homo sapiens

<400> 462

Met Asp Ser Leu Arg Lys Met Leu Ile Ser Val Ala Met Leu Gly Ala  
 1 5 10 15  
 Gly Ala Gly Val Gly Tyr Ala Leu Leu Val Ile Val Thr Pro Gly Glu  
 20 25 30  
 Arg Arg Lys Gln Glu Met Leu Lys Glu Met Pro Leu Gln Asp Pro Arg  
 35 40 45  
 Ser Arg Glu Glu Ala Ala Arg Thr Gln Gln Leu Leu Leu Ala Thr Leu  
 50 55 60  
 Gln Glu Ala Ala Thr Thr Gln Glu Asn Val Ala Trp Arg Lys Asn Trp  
 65 70 75 80  
 Met Val Gly Gly Glu Gly Gly Ala Gly Gly Arg Ser Pro  
 85 90

<210> 463  
 <211> 133  
 <212> PRT  
 <213> Homo sapiens

<400> 463  
 Met Gly His Gly Asp Glu Ile Val Leu Ala Asp Leu Asn Phe Pro Ala  
 1 5 10 15  
 Ser Ser Ile Cys Gln Cys Gly Pro Met Glu Ile Arg Ala Asp Gly Leu  
 20 25 30  
 Gly Ile Pro Gln Leu Leu Glu Ala Val Leu Lys Leu Leu Pro Leu Asp  
 35 40 45  
 Thr Tyr Val Glu Ser Pro Ala Ala Val Met Glu Leu Val Pro Ser Asp  
 50 55 60  
 Lys Glu Arg Gly Leu Gln Thr Pro Val Trp Thr Glu Tyr Glu Ser Ile  
 65 70 75 80  
 Leu Arg Arg Ala Gly Cys Val Arg Ala Leu Ala Lys Ile Glu Arg Phe  
 85 90 95  
 Glu Phe Tyr Glu Arg Ala Lys Lys Ala Phe Ala Val Val Ala Thr Gly  
 100 105 110  
 Glu Thr Ala Leu Tyr Gly Asn Leu Ile Leu Arg Lys Gly Val Leu Ala  
 115 120 125  
 Leu Asn Pro Leu Leu  
 130

<210> 464  
 <211> 95  
 <212> PRT  
 <213> Homo sapiens

<400> 464  
 Met Gly His Gly Asp Glu Ile Val Leu Ala Asp Leu Asn Phe Pro Ala  
 1 5 10 15  
 Ser Ser Ile Cys Gln Cys Gly Pro Met Glu Ile Arg Ala Asp Gly Leu  
 20 25 30  
 Gly Ile Pro Gln Leu Leu Glu Ala Val Leu Ala Ala Ala Pro Gly His  
 35 40 45  
 Leu Cys Gly Glu Ser Gly Cys Ser His Gly Ala Gly Ala Gln Arg Gln  
 50 55 60  
 Gly Glu Gly Pro Ala Asp Pro Ser Val Asp Gly Val Arg Val His Pro  
 65 70 75 80  
 Thr Gln Gly Arg Leu Cys Glu Ser Pro Gly Lys Asp Arg Glu Val  
 85 90 95

<210> 465

<211> 93  
 <212> PRT  
 <213> Homo sapiens

<400> 465  
 Met Thr Pro Ile Lys Leu Leu Asn Leu Thr Ser Arg Tyr Asn Phe Arg  
 1 5 10 15  
 Arg Thr Phe Gly Ile Glu Leu Ser Ser Asn Ser Ser Tyr Cys Lys Arg  
 20 25 30  
 Gly Asn Gly Tyr Arg Ser Arg Val Pro Lys Glu Cys Glu Cys Asn Trp  
 35 40 45  
 Leu His Leu Glu Ser Asp Thr Leu Lys Lys Leu Pro Ile Ile Ser Pro  
 50 55 60  
 Ser Trp Thr Cys Arg Ile Ile Leu Phe Leu Tyr Phe Ser Gly Gln Leu  
 65 70 75 80  
 Leu Gln Leu Ser Leu Ser Cys Leu Gln Leu Ile Lys Leu  
 85 90

<210> 466  
 <211> 500  
 <212> PRT  
 <213> Homo sapiens

<400> 466  
 Met Glu Val Ser Thr Asn Pro Ser Ser Asn Ile Asp Pro Gly Asn Tyr  
 1 5 10 15  
 Val Glu Met Asn Asp Ser Ile Thr His Leu Pro Ser Lys Val Val Ile  
 20 25 30  
 Gln Asp Ile Thr Met Glu Leu His Cys Pro Leu Cys Asn Asp Trp Phe  
 35 40 45  
 Arg Asp Pro Leu Met Leu Ser Cys Gly His Asn Phe Cys Glu Ala Cys  
 50 55 60  
 Ile Gln Asp Phe Trp Arg Leu Gln Ala Lys Glu Thr Phe Cys Pro Glu  
 65 70 75 80  
 Cys Lys Met Leu Cys Gln Tyr Asn Asn Cys Thr Phe Asn Pro Val Leu  
 85 90 95  
 Asp Lys Leu Val Glu Lys Ile Lys Lys Leu Pro Leu Leu Lys Gly His  
 100 105 110  
 Pro Gln Cys Pro Glu His Gly Glu Asn Leu Lys Leu Phe Ser Lys Pro  
 115 120 125  
 Asp Gly Lys Leu Ile Cys Phe Gln Cys Lys Asp Ala Arg Leu Ser Val  
 130 135 140  
 Gly Gln Ser Lys Glu Phe Leu Gln Ile Ser Asp Ala Val His Phe Phe  
 145 150 155 160  
 Met Glu Glu Leu Ala Ile Gln Gln Gly Gln Leu Glu Thr Thr Leu Lys  
 165 170 175  
 Glu Leu Gln Thr Leu Arg Asn Met Gln Lys Glu Ala Ile Ala Ala His  
 180 185 190  
 Lys Glu Asn Lys Leu His Leu Gln Gln His Val Ser Met Glu Phe Leu  
 195 200 205  
 Lys Leu His Gln Phe Leu His Ser Lys Glu Lys Asp Ile Leu Thr Glu  
 210 215 220  
 Leu Arg Glu Glu Gly Lys Ala Leu Asn Glu Glu Met Glu Leu Asn Leu  
 225 230 235 240  
 Ser Gln Leu Gln Glu Gln Cys Leu Leu Ala Lys Asp Met Leu Val Ser  
 245 250 255  
 Ile Gln Ala Lys Thr Glu Gln Gln Asn Ser Phe Asp Phe Leu Lys Asp  
 260 265 270



09876597.060801

```

Ile Thr Thr Leu Leu His Ser Leu Glu Gln Gly Met Lys Val Leu Ala
    275                280                285
Thr Arg Glu Leu Ile Ser Arg Lys Leu Asn Leu Gly Gln Tyr Lys Gly
    290                295                300
Pro Ile Gln Tyr Met Val Trp Arg Glu Met Gln Asp Thr Leu Cys Pro
    305                310                315                320
Gly Leu Ser Pro Leu Thr Leu Asp Pro Lys Thr Ala His Pro Asn Leu
    325                330                335
Val Leu Ser Lys Ser Gln Thr Ser Val Trp His Gly Asp Ile Lys Lys
    340                345                350
Ile Met Pro Asp Asp Pro Glu Arg Phe Asp Ser Ser Val Ala Val Leu
    355                360                365
Gly Ser Arg Gly Phe Thr Ser Gly Lys Trp Tyr Trp Glu Val Glu Val
    370                375                380
Ala Lys Lys Thr Lys Trp Thr Val Gly Val Val Arg Glu Ser Ile Ile
    385                390                395                400
Arg Lys Gly Ser Cys Pro Leu Thr Pro Glu Gln Gly Phe Trp Leu Leu
    405                410                415
Arg Leu Arg Asn Gln Thr Asp Leu Lys Ala Leu Asp Leu Pro Ser Phe
    420                425                430
Ser Leu Thr Leu Thr Asn Asn Leu Asp Lys Val Gly Ile Tyr Leu Asp
    435                440                445
Tyr Glu Gly Gly Gln Leu Ser Phe Tyr Asn Ala Lys Thr Met Thr His
    450                455                460
Ile Tyr Thr Phe Ser Asn Thr Phe Met Glu Lys Leu Tyr Pro Tyr Phe
    465                470                475                480
Cys Pro Cys Leu Asn Asp Gly Arg Glu Asn Lys Glu Pro Leu His Ile
    485                490                495
Leu His Pro Gln
    500

```

<210> 467  
 <211> 140  
 <212> PRT  
 <213> Homo sapiens

```

<400> 467
Met Val Leu Thr Lys Pro Leu Gln Arg Asn Gly Ser Met Met Ser Phe
1      5      10      15
Glu Asn Val Lys Glu Lys Ser Arg Glu Gly Gly Pro His Ala His Thr
20     25     30
Pro Glu Glu Glu Leu Cys Phe Val Val Thr His Tyr Pro Gln Val Gln
35     40     45
Thr Thr Leu Asn Leu Phe Phe His Ile Phe Lys Val Leu Thr Gln Pro
50     55     60
Leu Ser Leu Leu Trp Gly Cys Asp Gln Lys Pro Arg Thr Val Pro Thr
65     70     75     80
Leu Gly Asn Gly Ala Trp Asp Thr Cys Gln Gln His Ile Arg Thr Ser
85     90     95
Ser Trp Thr Ala Asn Thr Leu Val Ile Gln Asn Gln His Ser Arg Glu
100    105    110
Ser Thr Val Ser Val Cys Leu Phe Met Leu Ile Arg Met Gln His Ile
115    120    125
Leu Lys Thr Asp Thr Leu Gln Phe Arg Ile Cys
130    135    140

```

<210> 468  
 <211> 100

<212> PRT  
<213> Homo sapiens

<400> 468  
Met Tyr Met Leu Leu Ser Pro His Arg Leu Arg Glu Gln Ala Gly Val  
1 5 10 15  
Arg Gly Ser Ile Arg Thr Ala Asn Arg Thr Glu Asp Gly Leu Lys Ile  
20 25 30  
Arg Glu Ala Glu Ser Leu Pro Gln Ser Asn Thr Ala Asp Phe Lys Cys  
35 40 45  
Leu His Ser Ala Ser Leu Gln Ala Pro Gly Gly Ile Leu Met Gly  
50 55 60  
Pro Ala Ser Ser Pro Trp Thr Leu Ala Val Glu Gly Glu Lys Arg Thr  
65 70 75 80  
Ser Ala Pro Pro Leu Arg Glu Ser Leu Met Pro Thr Lys Gly Leu Gly  
85 90 95  
Trp Trp Thr Gln  
100

<210> 469  
<211> 119  
<212> PRT  
<213> Homo sapiens

<400> 469  
Met Ala Ser Tyr Ser Gly Phe Ser Gly Leu Leu Glu Ile Arg Tyr Gly  
1 5 10 15  
Pro Gly His Arg Ser Cys Leu Pro Gln Phe Ala Phe Phe Pro Gln Pro  
20 25 30  
Pro Leu Pro Arg Pro Arg Ile Cys Met Trp Val Leu Ala Glu Leu Leu  
35 40 45  
Glu Leu Gly Cys Pro Glu Gln Ser Leu Arg Asp Ala Ile Thr Leu Asp  
50 55 60  
Leu Phe Cys His Ala Leu Ile Phe Cys Arg Gln Gln Gly Phe Ser Leu  
65 70 75 80  
Glu Gln Thr Ser Ala Cys Ala Leu Leu Gln Asp Leu His Lys Ala  
85 90 95  
Cys Ile Gly Glu Arg Gly Gln Leu Pro Gly Leu Ser Pro Arg Glu Lys  
100 105 110  
Arg Asn Arg Ala Trp His Lys  
115

<210> 470  
<211> 140  
<212> PRT  
<213> Homo sapiens

<400> 470  
Met Arg Ser Glu Cys Val Leu Gly Ala Ala Ser Asp Ser Gly Gln Glu  
1 5 10 15  
Ala Pro Arg Asp Thr Trp Phe Leu Gln Gly Trp Lys Ala Ser Arg Arg  
20 25 30  
Phe Leu Ile Lys Gly Ser Val Ala Gly Gly Ala Val Tyr Leu Val Tyr  
35 40 45  
Asp Gln Glu Leu Leu Gly Pro Ser Asp Lys Ser Gln Ala Ala Leu Gln  
50 55 60  
Lys Ala Gly Glu Val Val Pro Pro Ala Met Tyr Gln Phe Ser Gln Tyr  
65 70 75 80

Val Cys Gln Gln Thr Gly Leu Gln Ile Pro Gln Leu Pro Ala Pro Pro  
 85 90 95  
 Lys Ile Tyr Phe Pro Ile Arg Asp Ser Trp Asn Ala Gly Ile Met Thr  
 100 105 110  
 Val Met Ser Ala Leu Ser Val Ala Pro Ser Lys Ala Arg Glu Tyr Ser  
 115 120 125  
 Lys Glu Gly Trp Glu Tyr Val Lys Ala Arg Thr Lys  
 130 135 140

<210> 471  
 <211> 109  
 <212> PRT  
 <213> Homo sapiens

<400> 471  
 Met Phe His Leu Arg Thr Cys Ala Ala Lys Leu Arg Pro Leu Thr Ala  
 1 5 10 15  
 Ser Gln Thr Val Lys Thr Phe Ser Gln Asn Arg Pro Ala Ala Ala Arg  
 20 25 30  
 Thr Phe Gln Gln Ile Arg Cys Tyr Ser Ala Pro Val Ala Ala Glu Pro  
 35 40 45  
 Phe Leu Ser Gly Thr Ser Ser Asn Tyr Val Glu Glu Met Tyr Cys Ala  
 50 55 60  
 Trp Leu Glu Asn Pro Lys Ser Val His Lys Thr Gly Ser His Cys Cys  
 65 70 75 80  
 Pro Gly Trp Ser Ala Val Ala Gly Ser Arg Leu Ala Ala Thr Ser Asp  
 85 90 95  
 Ser Trp Val Gln Val Ile Leu Met Pro Gln Pro Pro Glu  
 100 105

<210> 472  
 <211> 100  
 <212> PRT  
 <213> Homo sapiens

<400> 472  
 Met Phe His Leu Arg Thr Cys Ala Ala Lys Leu Arg Pro Leu Thr Ala  
 1 5 10 15  
 Ser Gln Thr Val Lys Thr Phe Ser Gln Asn Arg Pro Ala Ala Ala Arg  
 20 25 30  
 Thr Phe Gln Gln Ile Arg Ala Ile Leu His Leu Leu Leu Leu Ser Pro  
 35 40 45  
 Phe Ser Val Gly Leu Val Arg Thr Met Trp Arg Arg Cys Thr Val Leu  
 50 55 60  
 Gly Trp Lys Thr Pro Lys Val Tyr Ile Arg Gln Gly Pro Thr Val Val  
 65 70 75 80  
 Gln Ala Gly Val Gln Trp Arg Asp Leu Gly Leu Leu Gln Pro Pro Thr  
 85 90 95  
 Pro Gly Phe Lys  
 100

<210> 473  
 <211> 141  
 <212> PRT  
 <213> Homo sapiens

<400> 473  
 Met Ala Pro Lys Val Phe Arg Gln Tyr Trp Asp Ile Pro Asp Gly Thr

1		5		10		15
Asp	Cys	His	Arg	Lys	Ala	Tyr
		20		25		30
Gly	Leu	Thr	Ala	Ala	Ala	Tyr
		35		40		45
Phe	Leu	Glu	Gly	Val	Ala	Lys
		50		55		60
Ala	Val	Gly	Ala	Val	Phe	Gly
		65		70		75
Arg	Glu	Lys	Pro	Asp	Asp	Pro
		85		90		95
Gly	Gly	Leu	Thr	Leu	Gly	Ala
		100		105		110
Ala	Ala	Cys	Val	Tyr	Phe	Gly
		115		120		125
Arg	Leu	Glu	Gly	Trp	Glu	Val
		130		135		140

<210> 474  
 <211> 134  
 <212> PRT  
 <213> Homo sapiens

<400> 474															
Met	Ala	Thr	His	Pro	Asp	Gly	Phe	Arg	Leu	Glu	Gly	Pro	Leu	Ala	Ala
1			5					10					15		
Ala	His	Ser	Pro	Gly	Pro	Cys	Thr	Val	Leu	Tyr	Glu	Gly	Pro	Val	Arg
		20				25						30			
Gly	Leu	Cys	Pro	Phe	Ala	Pro	Arg	Asn	Ser	Asn	Thr	Met	Ala	Ala	Ala
		35				40						45			
Ala	Leu	Ala	Ala	Pro	Ser	Leu	Gly	Phe	Asp	Gly	Val	Ile	Gly	Val	Leu
		50				55					60				
Val	Ala	Asp	Thr	Ser	Leu	Thr	Asp	Met	His	Val	Val	Asp	Val	Glu	Leu
		65			70				75					80	
Ser	Gly	Pro	Arg	Gly	Pro	Thr	Gly	Arg	Ser	Phe	Ala	Val	His	Thr	Arg
			85					90					95		
Arg	Glu	Asn	Pro	Ala	Glu	Pro	Gly	Ala	Val	Thr	Gly	Ser	Ala	Thr	Val
		100					105						110		
Thr	Ala	Phe	Trp	Arg	Ser	Leu	Leu	Ala	Cys	Cys	Gln	Leu	Pro	Ser	Arg
		115				120						125			
Pro	Gly	Ile	His	Leu	Cys										
		130													

<210> 475  
 <211> 134  
 <212> PRT  
 <213> Homo sapiens

<400> 475															
Met	Ala	Thr	His	Pro	Asp	Gly	Phe	Arg	Leu	Glu	Gly	Pro	Leu	Ala	Ala
1			5					10					15		
Ala	His	Ser	Pro	Gly	Pro	Cys	Thr	Val	Leu	Tyr	Glu	Gly	Pro	Val	Arg
		20				25						30			
Gly	Leu	Cys	Pro	Phe	Ala	Pro	Arg	Asn	Ser	Asn	Thr	Met	Ser	Ala	Ala
		35				40						45			
Ala	Leu	Ala	Ala	Pro	Ser	Leu	Gly	Phe	Asp	Gly	Val	Ile	Gly	Val	Leu
		50				55					60				
Val	Ala	Asp	Thr	Ser	Leu	Thr	Asp	Met	His	Val	Val	Asp	Val	Glu	Leu

65 70 75 80  
 Ser Gly Pro Arg Gly Pro Thr Cys Arg Ser Phe Ala Val His Thr Arg  
 85 90 95  
 Arg Glu Asn Pro Ala Glu Pro Gly Ala Val Thr Gly Ser Ala Thr Val  
 100 105 110  
 Thr Ala Phe Trp Arg Ser Leu Leu Ala Cys Cys Gln Leu Pro Ser Arg  
 115 120 125  
 Pro Gly Ile His Leu Cys  
 130

<210> 476  
 <211> 85  
 <212> PRT  
 <213> Homo sapiens

<400> 476  
 Met Leu Lys Val Glu Ala Thr Gly Ser Pro Glu Glu Gly Trp Ala Gly  
 1 5 10 15  
 Gly Glu Pro Arg Thr Gly Ala Pro Ala Asn Ser Pro Ser Cys Pro Gln  
 20 25 30  
 Glu Met Pro Leu Gln Asp Pro Arg Ser Arg Glu Glu Ala Ala Arg Thr  
 35 40 45  
 Gln Gln Leu Leu Leu Ala Thr Leu Gln Glu Ala Ala Thr Thr Gln Glu  
 50 55 60  
 Asn Val Ala Trp Arg Lys Asn Trp Met Val Gly Gly Glu Gly Gly Ala  
 65 70 75 80  
 Ser Gly Arg Ser Pro  
 85

<210> 477  
 <211> 116  
 <212> PRT  
 <213> Homo sapiens

<400> 477  
 Met Gly Arg Pro Trp Met Val Met Ile Leu Glu Ser Lys Ser Glu Glu  
 1 5 10 15  
 Lys Met Trp Tyr Gly Val Phe Leu Trp Ala Leu Val Ser Ser Leu Phe  
 20 25 30  
 Phe His Val Pro Ala Gly Leu Leu Ala Leu Phe Thr Leu Arg His His  
 35 40 45  
 Lys Tyr Gly Arg Phe Met Ser Val Ser Ile Leu Leu Met Gly Ile Val  
 50 55 60  
 Gly Pro Ile Thr Ala Gly Ile Leu Thr Ser Ala Ala Ile Ala Gly Val  
 65 70 75 80  
 Tyr Arg Ala Ala Gly Lys Glu Met Ile Pro Phe Glu Ala Leu Thr Leu  
 85 90 95  
 Gly Thr Gly Gln Thr Phe Cys Val Leu Val Val Ser Phe Leu Arg Ile  
 100 105 110  
 Leu Ala Thr Leu  
 115

<210> 478  
 <211> 104  
 <212> PRT  
 <213> Homo sapiens

<400> 478

Met Asn Arg Tyr Cys Gly Lys Ile Phe Val Ser Val Met Val Lys Leu  
 1 5 10 15  
 Gln Lys Asn Lys Leu Thr Ser Phe Pro Arg Gln Pro Leu Leu Thr Phe  
 20 25 30  
 Phe Glu Tyr Leu Glu Lys Val Leu Cys Ser Gly Leu Phe Ser His Ser  
 35 40 45  
 Ala Lys Ser His His Asp Leu Leu Thr Arg His Pro Tyr Glu Thr Ala  
 50 55 60  
 Ala Pro Leu Leu Ser Ser His Leu Ile Leu Thr Glu Ala Leu Arg Asn  
 65 70 75 80  
 Gly Leu Gly Lys Cys His Asp Pro His Phe Thr Gly Glu Glu Thr Glu  
 85 90 95  
 Ala Gln Arg Gly Lys Leu Thr Thr  
 100

<210> 479  
 <211> 439  
 <212> PRT  
 <213> Homo sapiens

<400> 479  
 Leu Gly Asp His Gly Trp Glu Leu Ser Leu Glu Glu Asp Ala Gln Leu  
 1 5 10 15  
 Trp Gly Gly Val Val Lys Ser Cys Phe Glu Gly Lys Gly Pro Gln Arg  
 20 25 30  
 Glu Ala Gln Pro Ala Ser Pro Gln Ala Ala Pro Pro Gly Pro Thr Asn  
 35 40 45  
 Glu Ala Gln Met Ala Ala Ala Ala Leu Ala Arg Leu Glu Gln Lys  
 50 55 60  
 Gln Ser Arg Ala Trp Gly Pro Thr Ser Gln Asp Thr Ile Arg Asn Gln  
 65 70 75 80  
 Val Arg Lys Glu Leu Gln Ala Glu Ala Thr Val Ser Gly Ser Pro Glu  
 85 90 95  
 Ala Pro Gly Thr Asn Val Val Ser Glu Pro Arg Glu Glu Gly Ser Ala  
 100 105 110  
 His Leu Ala Val Pro Gly Val Tyr Phe Thr Cys Pro Leu Thr Gly Ala  
 115 120 125  
 Thr Leu Arg Lys Asp Gln Arg Asp Ala Cys Ile Lys Glu Ala Ile Leu  
 130 135 140  
 Leu His Phe Ser Thr Asp Pro Val Ala Ala Ser Ile Met Lys Ile Tyr  
 145 150 155 160  
 Thr Phe Asn Lys Asp Gln Asp Arg Val Lys Leu Gly Val Asp Thr Ile  
 165 170 175  
 Ala Lys Tyr Leu Asp Asn Ile His Leu His Pro Glu Glu Glu Lys Tyr  
 180 185 190  
 Arg Lys Ile Lys Leu Gln Asn Lys Val Phe Gln Glu Arg Ile Asn Cys  
 195 200 205  
 Leu Glu Gly Thr His Glu Phe Phe Glu Ala Ile Gly Phe Gln Lys Val  
 210 215 220  
 Leu Leu Pro Ala Gln Asp Gln Glu Asp Pro Glu Glu Phe Tyr Val Leu  
 225 230 235 240  
 Ser Glu Thr Thr Leu Ala Gln Pro Gln Ser Leu Glu Arg His Lys Glu  
 245 250 255  
 Gln Leu Leu Ala Ala Glu Pro Val Arg Ala Lys Leu Asp Arg Gln Arg  
 260 265 270  
 Arg Val Phe Gln Pro Ser Pro Leu Ala Ser Gln Phe Glu Leu Pro Gly  
 275 280 285  
 Asp Phe Phe Asn Leu Thr Ala Glu Glu Ile Lys Arg Glu Gln Arg Leu

290 295 300  
 Arg Ser Glu Ala Val Glu Arg Leu Ser Val Leu Arg Thr Lys Ala Met  
 305 310 315 320  
 Arg Glu Lys Glu Glu Gln Arg Gly Leu Arg Lys Tyr Asn Tyr Thr Leu  
 325 330 335  
 Leu Arg Val Arg Leu Pro Asp Gly Cys Leu Leu Gln Gly Thr Phe Tyr  
 340 345 350  
 Ala Arg Glu Arg Leu Gly Ala Val Tyr Gly Phe Val Arg Glu Ala Leu  
 355 360 365  
 Gln Ser Asp Trp Leu Pro Phe Glu Leu Leu Ala Ser Gly Gly Gln Lys  
 370 375 380  
 Leu Ser Glu Asp Glu Asn Leu Ala Leu Asn Glu Cys Gly Leu Val Pro  
 385 390 395 400  
 Ser Ala Leu Leu Thr Phe Ser Trp Asp Met Ala Val Leu Glu Asp Ile  
 405 410 415  
 Lys Ala Ala Gly Ala Glu Pro Asp Ser Ile Leu Lys Pro Glu Leu Leu  
 420 425 430  
 Ser Ala Ile Glu Lys Leu Leu  
 435

<210> 480  
 <211> 116  
 <212> PRT  
 <213> Homo sapiens

<400> 480  
 Met Trp Ala Arg Leu Pro His Thr Pro Glu Gln Met Gly His Arg Leu  
 1 5 10 15  
 Ile Gly Pro Lys Glu Ala Ser Leu His Val Val Pro Ser Trp Pro Ala  
 20 25 30  
 Arg Lys Met Glu Gly Leu Leu Ala Gly Leu Ser Ser Ser Pro Arg Lys  
 35 40 45  
 Ser Cys Trp Pro Phe Trp Val His Gly Pro Lys Val His Glu Gly Gly  
 50 55 60  
 Ser Ala Cys Glu Thr Ser Ser Ser Trp Val Glu Gly Leu Gly Leu Arg  
 65 70 75 80  
 Arg Val Thr Ser Val His Ser Leu Cys Gln Gly Leu Gly Ala Ser Val  
 85 90 95  
 Gln Leu Leu Pro Gly Pro Pro Pro Thr Thr Thr Ser Asp Lys Asn Asn  
 100 105 110  
 Tyr Thr Ser Gly  
 115

<210> 481  
 <211> 171  
 <212> PRT  
 <213> Homo sapiens

<400> 481  
 Met Gln Pro Ala Glu Arg Ser Arg Val Pro Arg Ile Asp Pro Tyr Gly  
 1 5 10 15  
 Phe Glu Arg Pro Glu Asp Phe Asp Asp Ala Ala Tyr Glu Lys Phe Phe  
 20 25 30  
 Ser Ser Tyr Leu Val Thr Leu Thr Arg Arg Ala Ile Lys Trp Ser Arg  
 35 40 45  
 Leu Leu Gln Gly Gly Gly Val Pro Arg Ser Arg Thr Val Lys Arg Tyr  
 50 55 60  
 Val Arg Lys Gly Val Pro Leu Glu His Arg Ala Arg Val Trp Met Val

65                      70                      75                      80  
 Leu Ser Gly Ala Gln Ala Gln Met Asp Gln Asn Pro Gly Tyr Tyr His  
                             85                      90                      95  
 Gln Leu Leu Gln Gly Glu Arg Asn Pro Arg Leu Glu Asp Ala Ile Arg  
                             100                      105                      110  
 Thr Asp Leu Asn Arg Thr Phe Pro Asp Asn Val Lys Phe Arg Lys Thr  
                             115                      120                      125  
 Thr Asp Pro Cys Leu Gln Arg Thr Leu Tyr Asn Val Leu Leu Ala Tyr  
                             130                      135                      140  
 Gly His His Asn Gln Gly Val Gly Tyr Cys Gln Gly Met Asn Phe Ile  
 145                      150                      155                      160  
 Ala Gly Tyr Leu Ile Leu Ile Thr Asn Asn Glu  
                             165                      170

<210> 482  
 <211> 177  
 <212> PRT  
 <213> Homo sapiens

<400> 482  
 Met Gln Pro Ala Glu Arg Ser Arg Val Pro Arg Ile Asp Pro Tyr Gly  
 1                      5                      10                      15  
 Phe Glu Arg Pro Glu Asp Phe Asp Asp Ala Ala Tyr Glu Lys Phe Phe  
                             20                      25                      30  
 Ser Ser Tyr Leu Val Thr Leu Thr Arg Arg Ala Ile Lys Trp Ser Arg  
                             35                      40                      45  
 Leu Leu Gln Gly Gly Gly Val Pro Arg Ser Arg Thr Val Lys Arg Tyr  
                             50                      55                      60  
 Val Arg Lys Gly Val Pro Leu Glu His Arg Ala Arg Val Trp Met Val  
 65                      70                      75                      80  
 Leu Ser Gly Ala Gln Ala Gln Met Asp Gln Asn Pro Gly Tyr Tyr His  
                             85                      90                      95  
 Gln Leu Leu Gln Gly Glu Arg Asn Pro Arg Leu Glu Asp Ala Ile Arg  
                             100                      105                      110  
 Thr Asp Leu Asn Arg Thr Phe Pro Asp Asn Val Lys Phe Arg Lys Thr  
                             115                      120                      125  
 Thr Asp Pro Cys Leu Gln Arg Thr Leu Tyr Asn Val Leu Leu Ala Tyr  
                             130                      135                      140  
 Gly His His Asn Gln Gly Val Gly Tyr Cys Gln Gly Met Asn Phe Ile  
 145                      150                      155                      160  
 Ala Gly Tyr Leu Ile Leu Ile Thr Asn Asn Asp Lys Asn Leu Phe Gly  
                             165                      170                      175  
 Cys



US 0987699703P1



Creation date: 06-01-2003  
Indexing Officer: JHERNANDEZ - Jesusa Hernandez  
Team: CENTRALSCANPRINT  
Dossier: 09876997

Legal Date: 07-08-2001

No.	Dccode	Number of pages
1	CRFE	6

Total number of pages: 6

Remarks:

Order of re-scan issued on .....